



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 96137

TO: Lorraine Spector
Location: cm1/10b11/10b19 ✓
Art Unit: 1647
Monday, June 16, 2003

Case Serial Number: 877804

From: Susan Hanley
Location: Biotech-Chem Library
CM1-6B05
Phone: 305-4053

susan.hanley@uspto.gov

Search Notes



STIC SEARCH RESULTS FEEDBACK FORM

Biotech-Chem Library

Questions about the scope or the results of the search? Contact *the searcher or contact:*

Mary Hale, Information Branch Supervisor
308-4258, CM1-1E01

Voluntary Results Feedback Form

➤ I am an examiner in Workgroup: Example: 1610

➤ Relevant prior art **found**, search results used as follows:

- ☐ 102 rejection
- ☐ 103 rejection
- ☐ Cited as being of interest.
- ☐ Helped examiner better understand the invention.
- ☐ Helped examiner better understand the state of the art in their technology.

Types of relevant prior art found:

- ☐ Foreign Patent(s)
- ☐ Non-Patent Literature
(journal articles, conference proceedings, new product announcements etc.)

➤ Relevant prior art **not found**:

- ☐ Results verified the lack of relevant prior art (helped determine patentability).
- ☐ Results were not useful in determining patentability or understanding the invention.

Comments:

Drop off or send completed forms to STIC/Biotech-Chem Library CM1 - Circ. Desk



Query Match 100.0%; Score 2366; DB 10; Length 2366;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2366; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

181 GACAGAGATTCCGACCGGACCTCCCGCGGAACGCCATTGAACAGGCTTTGTGCTACCCAA 240
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2221 AAATGGCAATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2280
2281 ACTGATCAGGGACCAATTAACCCCTTTGGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCT 2340
2281 ACTGATCAGGGACCAATTAACCCCTTTGGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCT 2340
2341 CAAATAAAACAAAGCAAAACCCGACA 2366
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Qy	1868	CTCATCACTGTCTCCAAAGGCCAGAGATTCTCCTAGTCTGTCTTACCCCATCAATCTTGT	1927
Db	1801	CTCATCACTGTGTCCAAAGCAAGAGATTCTCTGGTGTGTCTTACCCCATCAACTCTGT	1860
Qy	1928	GCCAACTCTTTCTCTACGCCATTTTCACCAAGAACTTCCGCAAGGAGTTCTTTCATCTCCG	1987
Db	1861	GCCAAACCCCTTCTCTATGCCATCTTTACCAAAAACCTTTGCGAGAGATTTCCTTCATCTCG	1920
Qy	1988	CTGAGCAAGTTTGGCTGTTATGAATGCAAGCCAGATTTTACAGGACAGAAAACCTCATCC	2047
Db	1921	CTGAGCAAGTGTGGCTGCTATGAATGCAAGCCAAATTTATAGGACAGAAAACCTTCATCC	1980
Qy	2048	GCTACCCACAACCTTCATGCCCCAAGAGCGCACTGCTCTCAGCTCCGACAGTGCACCAAT	2107
Db	1981	ACTGTCCACAACACCCATCCAAGGAATGGCCACTGCTCTCAGCTCCGACAGTGCACCAAT	2040
Qy	2108	-----AGTTACGTGCTGTGTCCTCTTAATCATTCATCCCAAGAACTAA	2149
Db	2041	GGTTCACACTTACATACATCTGTCCCTCTAAGTCATTTAGCCCCAAAACCTAA	2088

RESULT 3

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US-09-804-626-3
; Sequence 3, Application US/09804626
; Patent No. US20020128190A1
; GENERAL INFORMATION:
;
; APPLICANT: Lobel, Leslie
; APPLICANT: Lustbader, Joyce
; TITLE OF INVENTION: EXPRESSION OF
; TITLE OF INVENTION: GONADOTROPIN
; FILE REFERENCE: 0575/62259/JPM/SHS
; CURRENT APPLICATION NUMBER: US/09/
; CURRENT FILING DATE: 2001-03-09
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 1551
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-09-804-626-3

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Query Match	33.2%	Score 784.8	DB 10	Length 1551
Best Local Similarity	86.3%	Pred. No. 3.3e-239		
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Qy	152	AGGTCCTTTCTCTGCCAAGACAGCAAGGTGACAGAGATTCCGACCGACCTCCCCCGGAAC	211	
Db	502	AGGTTTTTCTCTGCCAAGAGAGCAAGGTGACAGAGATTCTCTGACCTCCCGAGGAAT	561	
Qy	212	GCCATTGAATCTGAGGTTTGTGCTCACCAAAGCTTCGAGTCATCCCGAAAGGATCATTTGCT	271	
Db	562	GCCATTGAATCTGAGGTTTGTCTCACCAAAGCTTCGAGTCATCCAAAAGGTGCATTTTCA	621	
Qy	272	GGATTTGAGACCTGGAGAAATAGAGATCTCTCAGATGATGCTCTGGAAAGTATAGAG	331	
Db	622	GGATTTGGGACCTGGAGAAATAGAGATCTCTCAGATGATGCTCTGGAGGTGATAGAG	681	
Qy	332	GCAGATGTGTTCTCCAAACCTACCCAAAGTTGCATGAAATTAGGATTGAAAAGGCCAACAT	391	
Db	682	GCAGATGTGTTCTCCAACTTCCCAAATTTACATGAAATTAGAATGAAAAGGCCAACAC	741	
Qy	392	CTTCTGTACATCAACCCGGAGGCTTCCAGAAATCTCCCAAGTCTCCAGATATCTGTTAATA	451	
Db	742	CTGCTCTACATCAACCCGTGAGGCTTCCAGAACTTCCCAACCTTCAATATCTGTTAATA	801	
Qy	452	TCCAACACAGGCATTAAAGCACTTGCACGCTGTTCCACAAGATCCAGTCTCTCCAAAAGTT	511	
Db	802	TCCAACACAGGATTAAAGCACTTCCAGATGTTCCACAGATTCTCTCCAAAAGGTT	861	
Qy	512	CTACTAGACATTCAGATATACATAAATCCACATTCGTTGCCAGGAATCTCTCATGGGA	571	
Db	862	TTACTTGACATTCAGATATACATAAATCCACAAATTCACAAATTTGAAAGAAATCTTTGTTGGGG	921	

RESULT 4

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US-09-804-626-5
; Sequence 5, Application US/09804626
; Patent No. US20020128190A1
; GENERAL INFORMATION:
; APPLICANT: Lustbader, Joyce
; APPLICANT: Lobel, Leslie
; TITLE OF INVENTION: EXPRESSION OF
; TITLE OF INVENTION: GONADOTROPIN
; FILE REFERENCE: 0575/62259 JPM/SHS
; CURRENT APPLICATION NUMBER: US/09/
; CURRENT FILING DATE: 2001-03-09
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
; LENGTH: 2100
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-09-804-626-5

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	Query Match	28,0%	Score 663;	DB 10;	Length 2100;
	Best Local Similarity	61.9%;	Pred. No. 3.3e-200;		
	Matches 1116;	Conservative 0;	Mismatches 670;	Indels 21;	Gaps 3;
Qy	247	AGTCATCCCGAAGGATCATTTGCTGGATTTGGAGACCTGGAGAAAATACAGATGCTCTCA	306		
Db	186	AGTGATCCCATCTCAAGCTTTCAGAGGACTTAATGAGGTCAATAAAATTTGAAATCTCTCA	245		
Qy	307	GAATGATGCTTCGAGAGTAATACAGGCAGATGTGTTCTCCAACTACCCCAAGTTGCATGA	366		
Db	246	GATTGATTCCTCGAAGAGTAAAGCTATGCTTTGACAACCTCTCAATTTGTCTGA	305		

Matches 1108; Conservative 0; Mismatches 677; Indels 21; Gaps 4;

Qy	247	AGTCATCCCGAAAGGATCATTTGCTGGATTTGGAGACCTGGAGAAAATAGAGATCTCTCA	306
Db	241	AGTAATTCATCACAAGCTTTACGGGGCACTTAATGAGGTCGTAAAAATTGAATCTCTCA	300
Qy	307	GAATGATGCTTGGAACTAATAGAGGCGAGATGTCTTCCAACCTACCCAAAGTTGCATGA	366
Db	301	GAGTGATTCCTGTGAAAGGATAGAAGCTAATGCCCTTTGACAACCTCCTCAATTTGTCGA	360
Qy	367	AATTAGGATTGAAAAGGCCAACATCTTCTGATACATCAACCGGAGGCCCTTCAGAAATCT	426
Db	361	ACTACTGATCCAGAAACCAAAAACCTGCTATACATTTGAACCTGTGTCCTTTTACAAAACCT	420
Qy	427	CCCCAGTCTCAGATATCTGTTAATATCCAACACAGGCATTAAGCACATTGCCAGCTGTTC	486
Db	421	CCCTCGGTTAAATACCTGAGCATCTGTACACAGGCNTCCGAACCTTCCAGATGTTAC	480
Qy	487	CAAGATCCAGTCTCTCCAA---AAGGTTCTACTAGACATTCAGAGTAACATAAACATCCA	543
Db	481	GAAGATCTCCTCTCTGAAATTAATTTCAATCTGGAATCTGTGATAACTTACACATAAC	540
Qy	544	CATCGTTGCCAGGAACCTCCTCATCGGACATGAGTTTTGAAAGTGTGATTTTATGGCGTAG	603
Db	541	CACCATACCCGGGAATGCTTTCCAAAGGGATGAATAACGAGTCTGTTCACACTNAAACCTGA	600
Qy	604	TAAGAAATGGGATTGAAGAAATACACAACCTGTGCATTCACCGGAACCTCAGCTAGATGAAC	663
Db	601	TGGAATGGGATTTCAAGAGTACAAAGCCATGCATTCATGGAAGGAGCTCTAATCTCGCT	660
Qy	664	GAATCTAAGCGATTAACAAATTAATTTGGAAGAAATTCGCTTAATGACGTTTTCCAGGGAGCCT	723
Db	661	GGAGCTAAAAGAAAACATCTACCTGGAGAGAAGTGCACAGTGGAGCCCTTCAGGGGGCCAC	720
Qy	724	TGGCCAGTCATTTTAGATATCTCAAGSACAAAGGTCCATTCCTTACCAACACCATGCGTT	783
Db	721	GGGGCCACGATCTCGTATATTTCTCCACCAAAATGACAGGCCCTGCCGAGCCACCGGGCT	780
Qy	784	AGAAAATCTGAAGAAGCTGAGGGCCAGGTCAACATACCGCTTGAAAAGCTCCCTAATCT	843
Db	781	GGACTCCATTCAGACGCTCATCGCCCTGCTTCTCTACTCACTGAAACACACTGCCCTCCAA	840
Qy	844	GGACAAGTTTGTCAACCCTATGAGAGGCCAGCTCACTACCCAGGCCACTGCTGTGCTTT	903
Db	841	AGAAAAATTCACGAGCCTCCTGTGCGCAGGCTGACCTACCCAGCCACTGCTGCGCCTT	900
Qy	904	TGCAAACTTGAAGGGGCAATCTCTGAATTCATCCAAATTTGCACAAAGTCTATTTTAAG	963
Db	901	-----CAGGAATTTGCCGAAGAAAGACAGAAATTTTTCATTTTCCATTTTGTG	947
Qy	964	GCAAGATATTGATGATATGACTCAAAATTTGGGGATCAGAGAGTCTCTCTGATAGATGTA	1023
Db	948	AAAATTTCTCCAAACATGCGAAGCACAGTTAGAAAAGCAGATACCGACGCTTTATT	1007
Qy	1024	ACCAGTTATGGAAAAGGATCTGACATGATGTACAATGAAATTTGATTTATGACTTATGTAA	1083
Db	1008	CCGCCATCTTTGAGGAGAA--TGAACATCAGTGGCTGGGATATGATTATGGCTTCTG--	1062
Qy	1084	TGAAGTTGTTGATGTGACCTGCTCACCAGGCGAGATGCAATTAATCCATGTGAGAGTAT	1143
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Qy	1144	CATGGGTACAAACATCCTCAGGGTCTTGATATGGTTTATTAGCATCCTGCCCACTACTGG	1203
Db	1123	TATGGGTATGCTTCCCTTAGGGTCTTGATTTGGCTGATTAATATACTAGCCATCTTTGG	1182
Qy	1204	GAACACACAGTGTGTTGGTCTTGACCCACAGCCAAATACAAACTAACTGTGCCCGGTT	1263
Db	1183	CAACCTGACAGTCTCTTTGTTCTCTTGACCAAGTCCGTTATAAACTGACAGTGCCCGCCT	1242
Qy	1264	TCTTATGTGTAACCTCGCCTTCGCTGATCTCTGCATAGGCATCTACTTGTCTACTATAGC	1323
Db	1243	CCTCATGTGTAATCTTCTTTTGAGACTTTTGATGGGGCTTACTGCTGCTCATTCG	1302

RESULT 6

RESULT 6
US-10-045-624B-1

US-10-043-624B-I
; sequence 1, Application US/10045624B; Sequence 1, Application US/1004
; Publication No. US20030009778A1; PUBLICATION NO: US20
; GENERAL INFORMATION:

APPLICANT: Allen, Keith D.

; TITLE OF INVENTION: TRANSGENIC MICE CONTAINING THYROID

; TITLE OF INVENTION: TRANSGENIC MICE CONTAINING THYROID
 ; TITLE OF INVENTION: STIMULATING HORMONE RECEPTOR (TSH-R) GENE DISRUPTIONS
 ; FILE REFERENCE: R-666

FILE REFERENCE: K 000
; CURRENT APPLICATION NUMBER: US/10/045,624B

; CURRENT APPLICATION NUMBER: US/1
 ; CURRENT FILING DATE: 2002-08-19

; CURRENT FILING DATE: 2002-08-19
; PRIOR APPLICATION NUMBER: US 10/045,624

; PRIOR APPLICATION NUMB
; PRIOR FILING DATE: 200

, PRIOR FILING DATE: 2001-10-26
 ; NUMBER OF SEQ ID NOS: 4

; NUMBER OF :
; SOFTWARE:

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; SOFTWARE: FAS
; SEO ID NO 1

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; SEQ ID NO 1
:      LENGTH: 21

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; LENGTH: 2312
; TYPE: DNA

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RESULT 9
US-09-864-761-4143
; Sequence 4143, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aeonica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263,6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annonmax Sequence Listing Engine vers. 1.1
; SEQ ID NO 4143
; LENGTH: 407
; TYPE: DNA
; ORGANISM: Homo sapiens

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: OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 2.5
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: OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 2.7
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: OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2.1
: OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 2.3
: OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.9
US-09-864-761-4113
Query Match 6.18; Score 144.6; DB 10; Length 407;
Best Local Similarity 82.9; Pred No 3.2e-35;
Matches 165; Conservative 0; Mismatches 34; Indels 0; Gaps 0;
QY 739 AGATATCTCAAGGACCAAGGCTCCATTCCTTACCAACACATGCTTAGAAAATCTGAAGAA 798
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DB 339 GCTCATGAGGCGCAGGTCAACATACCGCTCTGAAAAGCTCCCTAATCTGGACAAAGTTGTGAC 388
QY 919 GCAATCTCTGAGTCAT 937
DB 389 GCAATCTGAGTCATCT 407
RESULT 10
US-09-864-761-20897
: Sequence 20897, Application US/09864761
: Patent No. US20020048763A1
: GENERAL INFORMATION:
: APPLICANT: Penn, Sharon R.
: APPLICANT: Hanzel, David R.
: TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
: TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
: FILE REFERENCE: Asclon-X-1
: CURRENT APPLICATION NUMBER: US/09/864.761
: PRIOR FILING DATE: 2001-05-23
: PRIOR APPLICATION NUMBER: US 60/180,312
: PRIOR FILING DATE: 2000-02-04
: PRIOR APPLICATION NUMBER: US 60/207,456
: PRIOR FILING DATE: 2000-05-26
: PRIOR APPLICATION NUMBER: US 09/632,366
: PRIOR FILING DATE: 2000-08-03
: PRIOR APPLICATION NUMBER: GB 24263.6
: PRIOR FILING DATE: 2000-10-04
: PRIOR APPLICATION NUMBER: US 60/236,359
: PRIOR FILING DATE: 2000-09-27
: PRIOR APPLICATION NUMBER: PCT/US01/00666
: PRIOR FILING DATE: 2001-01-30
: PRIOR APPLICATION NUMBER: PCT/US01/00667
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: PRIOR APPLICATION NUMBER: PCT/US01/00664
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: PRIOR FILING DATE: 2000-09-21
: PRIOR APPLICATION NUMBER: US 09/608,408
: PRIOR FILING DATE: 2000-06-30
: PRIOR APPLICATION NUMBER: US 09/774,203
: PRIOR FILING DATE: 2001-01-29
: NUMBER OF SEQ ID NOS: 49117
: SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
: SEQ ID NO 20897
: Length 185
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: OTHER INFORMATION: MAP TO AC007189.6
: OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 2.3
: OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 2.5
: OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 2
: OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 2.7
: OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.9
: OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2.4
: OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.1
: OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2.1
: OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 2.3
: OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.9
: OTHER INFORMATION: NT HIT: g14503792, EVALUATE 1.00e-100
: OTHER INFORMATION: SWISSPROT HIT: P23945, EVALUATE 1.00e-30
US-09-864-761-20897
Query Match 6.08; Score 141.8; DB 10; Length 185;
Best Local Similarity 85.48; Pred No 1.4e-34;
Matches 158; Conservative 0; Mismatches 27; Indels 0; Gaps 0;
QY 740 GATATCTCAAGGACCAAGGCTCCATTCCTTACCAACACATGCTTAGAAAATCTGAAGAA 799
DB 1 GATATTTCAAGAACAAAGATCCATTCCTGCTAGCTATGCTTAGAAAATCTTAAGAA 60
QY 800 CTGAGGCGCAGGTCAACATACCGCTCTGAAAAGCTCCCTAATCTGGACAAAGTTGTGAC 859
DB 61 CTGAGGCGCAGGTCAACATACCGCTCTGAAAAGCTCCCTAATCTGGACAAAGTTGTGAC 120
QY 860 GTCATGAGGCGCAGGTCAACATACCGCTCTGAAAAGCTCCCTAATCTGGACAAAGTTGTGAC 919
DB 121 GTCATGAGGCGCAGGTCAACATACCGCTCTGAAAAGCTCCCTAATCTGGACAAAGTTGTGAC 180
QY 920 CAAT 924
DB 181 CAAT 185
RESULT 11
US-10-251-385-263
: Sequence 263, Application US/10251385
: Publication No. US20030105292A1
: GENERAL INFORMATION:
: APPLICANT: Behn, Dominic P.
: APPLICANT: Chalmers, Derek T.
: TITLE OF INVENTION: Human WUS20030105292A1-Endogenous, Constitutively Activated Human
: TITLE OF INVENTION: Protein-Coupled
: TITLE OF INVENTION: Receptors
: FILE REFERENCE: AREN-0040
: CURRENT APPLICATION NUMBER: US/10/251,385
: PRIOR FILING DATE: 2002-09-20
: PRIOR APPLICATION NUMBER: US/09/170,496
: PRIOR FILING DATE: 1998-10-13
: NUMBER OF SEQ ID NOS: 294
: SOFTWARE: PatentIn version 3.1

Oy 1742 CTAACATGTTGCTCTCATCAGGACCAAGATTGCGAAGCGATGCGCAGACTCATC 1801
Db 2260 GGAGACCTGGAGAAATTT---GGAGCTGCTCTATGMAAAACACATTCGCTGTGCTC 2316
Oy 1803 TTACAGATCTTCTGTCATGCGCCCACTTTTCATCTTTTCCATTTCTGCTCCCTCAAG 1861
Db 2317 TTACACCACTGATCTCAAACTGCGCTGCTGCTTTCTTGTGCTCTCTCTCTTTAANAAC 2376
Oy 1862 GTGCGCTCATCATGTTGCTCAGGCGCAAGATTCTCTAGTCTTCTGTTCTACCCCATCAAT 1921
Db 2377 TTACATTTATCATGCTCTGAGTAAATTAAGTTTATCTCTGCTGCTGCTGCTGCTCTCT 2436
Oy 1922 CTGCTGCGCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1981
Db 2437 GCATGCTCAATCCCTCTCTACATCTTGTTCATCTCTCTCTCTCTCTCTCTCTCTCTCT 2496
Oy 1982 ATCTCG 1987
Db 2497 AGCCTG 2502

RESULT 13
US-09-822-846-124
; Sequence 124, Application US/09822846
; Publication No. US2003007139A1
; GENERAL INFORMATION:
; APPLICANT: Jacobs, Kenneth
; APPLICANT: Jacoby, John M.
; APPLICANT: Taylor, Edward R.
; APPLICANT: Collins, Lisa A.
; APPLICANT: Evans, Cheryl
; APPLICANT: Merberg, David
; APPLICANT: Treacy, Maurice
; APPLICANT: Agostino, Michael J.
; APPLICANT: Steininger II, Robert J.
; APPLICANT: Bowman, Michael R.
; APPLICANT: Spaulding, Vikki
; APPLICANT: Wong, Gordon G.
; APPLICANT: Clark, Hilary
; APPLICANT: Fechtel, Kim
; APPLICANT: Hoves, Steven H.
; APPLICANT: Resnick, Richard J.
; APPLICANT: Gunkota, Kamalakar
; APPLICANT: Graham, James R.
; APPLICANT: Genzyme, Inc.
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL SECRETED PROTEINS
; FILE REFERENCE: GIN 6400
; CURRENT APPLICATION NUMBER: US/09/822,846
; CURRENT FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: 60/195,605
; PRIOR FILING DATE: 2000-04-06
; NUMBER OF SEQ ID NOS: 629
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 124
; LENGTH: 3429
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-822-846-124

Query Match 2.98; Score 67.8; DB 9; Length 3429;
Best Local Similarity 43.24; P-Val 5.3e-10;
Matches 373; Conservative 0; Mismatches 487; Indels 3; Gaps 1;
Oy 1103 TGCTCAACCAAGCCAGATCTTATCCATGTGAGATATCATGGGTACACATCTCTC 1162
Db 376 TGACACCTTCACACAGGTCTTTTACGCTGTGAATATTTACTGGCAGCTGGATGAT 435
Oy 1163 AGGCTCTGTATGTTTATAGCATCTCGCCATTTACTGGGACACACACATCTGCTGTG 1222
Db 436 CGTCTACTGTGCTGCTCATTTCTGCTGCTCATATTTTTCACCTGCTGCTGTTATTTA 495
Oy 1223 GTCTGACCAAGCCAACTAACAATCTGCGCCGGTTCTTATGTGTACCTCGCC 1282

Db 496 ACAACATTTGCTCTCTACATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 555
Oy 1283 TTGCTGATCTCTGCTAGGACATCTACTTGTCTACTTATAGCATCATCTGCTGCTGCTGCT 1342
Db 556 GTCTCTAATCTTATCATGGGAATCTACTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 615
Oy 1343 AAGAGCCAGTACCAACTATGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1402
Db 616 TGGGCGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 675
Oy 1403 GGTCTTTTCTACTGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1462
Db 676 GGTCTTTTCTACTGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 735
Oy 1463 CAAAGATGGCATACATACACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1522
Db 736 CAAAGATGGCATACATACACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 795
Oy 1523 GCTGCGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1582
Db 796 TTCCGGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 855
Oy 1583 TTTGCTATGCTAGTACATGAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 1642
Db 856 TTCCATAGAGGGGAATATCTGCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 915
Oy 1643 TTGTCACAGCTGCTATGTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1702
Db 916 CCAATCTTAGGATTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 975
Oy 1703 TGTGCTCTATACCACTATCTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1762
Db 976 CCGCTATCTACACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1035
Oy 1763 AGGACAGCAAGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1822
Db 1036 CAATCTAGCATGTT---AGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1092
Oy 1823 GCGCCCATTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1882
Db 1093 TGCCCTGTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1152
Oy 1883 AAGGCAAGATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1942
Db 1153 ATAGTGAAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1212
Oy 1943 TAGCCATTTTCAACCAAGCTT 1965
Db 1213 TATGTTTCTTCAACCAAGCTT 1235

RESULT 14
US-09-862-767A-1
; Sequence 1, Application US/09862767A
; Patent No. US20020034786A1
; GENERAL INFORMATION:
; APPLICANT: Pan, Yang
; TITLE OF INVENTION: TANGO-72 AND TANGO-77 NUCLEIC ACID MOLECULES AND POLYPEPTIDES
; FILE REFERENCE: MBIO1997-008P1RCP1CNI(M)
; CURRENT APPLICATION NUMBER: US/09/862,767A
; CURRENT FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: US 09/127,856
; PRIOR FILING DATE: 1998-08-03
; PRIOR APPLICATION NUMBER: US 60/054,646
; PRIOR FILING DATE: 1998-08-04
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Pse-Seq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 3688
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:

NAME/KEY: CDS
LOCATION: (2)...(1894)
US-09-862-767A-1

Query Match 2.9%; Score 67.8; DB 10; Length 3688;
Best Local Similarity 43.2%; Pred. No. 5.6e-10;
Matches 373; Conservative 0; Mismatches 487; Indels 3; Gaps 1;

QY 1103 TGCTCACCAAGCCAGATGATTAATCCATGTGAAGATATCATGGGTGACAACTCTCTC 1162
DB 605 TGACACCTTCAACAGGTCCTTTAAGCCCTGTGAATATTTACTGGGAAGCTGGATGATT 664
QY 1163 AGGGCTTTGATATGCTTTTATAGCATCTGCGCAATTTACTGGGAACACACACATGCTGGTG 1222
DB 665 CGCTTACTGTGCTGCTTCTTCTGCTGCTATTTTTCACACCTGCTGTTATTTA 724
QY 1223 GTCTGACCAACAGCCATACAACTAATCTGTCGCCCGTTCCTTATGTGTAACCTCGCC 1282
DB 725 ACAACATTTGCACTTTGTACATCACTGCTTGTCCAAATTTGTTATAGGCTTGATTTCT 784
QY 1283 TTCGCTGATCTCTGCATAGGATCTTGTCTTATAGCATCAGTTGACATCCATACC 1342
DB 785 GTGCTACTTATTCATGGGAATCTTATGTCATCTTCTTGTGCTGTGCTGCC 844
QY 1343 AAGAGCCAGTACCAACTATGCCATTTGACTGGCAACAGGAGGCTGTGATGCTGCT 1402
DB 845 TGGGCGAGATTCGCTGAATTTGGCATTTGGTGGGAATCTGGCAGTGGCTGCAAGTAGCT 904
QY 1403 GCGTTTTTCACTGCTTTTGGCCAGTGAATGCTGCTACACATGACAGCCATCACCTTA 1462
DB 905 GGGTTTCTGCAAGTTTCTCTCAGAAAGTGCATATTTTATTAATGCTAGCACTGTC 964
QY 1463 GAAAGTGGCATACCATACATGCTATGCAACTGGAATGGAATGGAAGAGCAATCTCAACAG 1522
DB 965 GAAAGAGCTTATCTGCAAAAGATATAATGAAATGGAAGAGCAATCTCAACAG 1024
QY 1523 GCTGCGAGGCTCATGGTATGGGCTGGAGCTTTTGGCTTGGCAGTGTCTCTTCCCATC 1582
DB 1025 TTCCGGGTGCTGCTTTTGGCTTTCTAGTGCTACAGTAGCAGGCTGTTTCCCTT 1084
QY 1583 TTGGCATCAGTAGCTACATGAAAGTAGCATCTGCTGCCCATGGATATGACAGCCCT 1642
DB 1085 TTCCATAGAGGGGAATTTCTGCATCACCCCTTTGTTGGCATTTCTCAGAGGTGAAGG 1144
QY 1643 TTGTCACAGCTATGTTATGCTGCTTCTTCTCAATGCTGCTGCTTCTGCTGCTATC 1702
DB 1145 CCATCATTAGGATCACTGTAAGCTTAGTGCTATTAACTCACTAGCATTTTATTAAG 1204
QY 1703 TGTGCTGCTATACCCACATCTACCTCACAGTGAAGATCCCTACCATTTGTCTCATCA 1762
DB 1205 GCGTTATCTACATAAGCTATCTGCACTTTGGAAGAGAGGACCTCTCAGAAACTCA 1264
QY 1763 AGGACACCAAGATGCGCAAGGCAATGGCCACATCTTACAGACTTTCTGTCAGT 1822
DB 1265 CAATCTAGCATGATT---AAGCATGTGCTGCTGCTAATCTTCAACAAATTCATCTTTTC 1321
QY 1823 GCGCCCATTTTCTTTTCCCATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1882
DB 1322 TGCCCTGTGCGGTTTTTTCATTTGCAACATTTGATCATGCAATCTCTATATACGCCGAA 1381
QY 1883 AAGGCCAAGATCTCTAGTCTGTTCTACCCCATCAATTTCTGTCCTTCTTCTTCTTCT 1942
DB 1382 ATAAAGTCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1441
QY 1943 TAGGCAATTTTCAACCAAGATTT 1965
DB 1442 TATGTTTCTTCAACCAAGATTT 1464

RESULT 15
US-09-864-761-8142
Sequence 8142, Application US/09864761
Patent No. US20020048763A1

GENERAL INFORMATION:
APPLICANT: Penn, Sharon G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO
FILE REFERENCE: Aecmice-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117,
SEQ ID NO 8142
LENGTH: 580
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AC010582.6
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 4.9
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 4.7
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 4.7
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 7
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2.4
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 6.1
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 7
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 5.9
US-09-864-761-8142

Query Match 2.3%; Score 53.8; DB 10; Length 580;
Best Local Similarity 56.5%; Pred. No. 4.1e-06;
Matches 100; Conservative 0; Mismatches 77; Indels 0; Gaps 0;

QY 740 GATATCTCAAGGACAAAGGCTCCATCCCTTACCAACCATCGCTTAGAAAATCTGAAGAAG 799
DB 24 GACGTGCTCTCAAAACCAAGTGTCTACTGCTCCCTTCCATCCAAAGGCTGGAGCACCTGAAGGAA 83
QY 800 CTGAGGGCCAGGTCAACATACCCCTTGAAAGAGCTCCCTTAATCTGGACAAAGTTTGTACC 859

84 CTGATGACGAGAAACACCTGGACTCTTAGGAACTTCCACTTTCCTTGAGTTTCTTCAC 143
860 CTCATGGAGGCGAGCTCAGCTACCGAGCCACTGCTGCTTTTCCAACTTGAG 916
144 CTCACAGGGCTGACCTTCTTAGCGAGGCCACTGCTGCTTTTAAAGATCAGAG 200

Search completed: June 16, 2003, 13:31:34
Job time : 331 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 16, 2003, 05:17:26 ; Search time 5925 Seconds
(without alignments)
11621.475 Million cell updates/sec

Title: US-09-877-804-5
Perfect score: 2366
Sequence: 1 aggaagctgggaatctgtg.....aaacaagcaaaacccgaca 2366

Scoring table: IDENTITY.MUC
Gapex 10.0, Gapext 1.0

Searched: 2054640 seqs. 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 04

Maximum Match 1004

Listing first 45 summaries

Database :

1: gb-ba.*
2: gb-ba.*
3: gb-ba.*
4: gb-ba.*
5: gb-ba.*
6: gb-ba.*
7: gb-ba.*
8: gb-ba.*
9: gb-ba.*
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36: gb-ba.*
37: gb-ba.*
38: gb-ba.*
39: gb-ba.*
40: gb-ba.*
41: gb-ba.*

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	ID	Description
1	2366	100.0	2366	10	RATFSHTRA L02842 Rattus sp.
2	1872.6	79.1	2079	10	AF095642 Mus muscu
3	1699.6	71.8	2393	9	HUMFSHRE M65085 Human foll
4	1681	71.0	2222	6	A76125 Sequence 1
5	1680	71.0	2186	9	HUMFSHREC M95489 H.sepiens f
6	1677.6	70.9	2179	6	AR003719 Sequence
7	1677.6	70.9	2179	6	AR003719 Sequence
8	1677.6	70.9	2179	6	AR003719 Sequence
9	1677.6	70.9	2179	6	AR003719 Sequence
10	1647.2	69.6	2375	4	BOVFSHR S23219 follicle-st
11	1646.4	69.6	2375	4	BOVFSHR S23219 follicle-st
12	1645	69.5	2241	4	AF035377 AF025377 Sus scro
13	1627.6	68.8	2088	9	MFSHHR S70150 follitropin
14	1623.4	68.6	2319	4	S70150 follitropin
15	1590.4	67.2	2400	10	AY082514 Cavia por
16	1564.6	66.1	2089	4	PIGFORE L31966 Sus scrofa
17	1543.4	65.2	2064	4	EAU73659 U73659 Equus asinu
18	1522.2	64.3	2428	4	SHPFTR L36115 Ovis aries
19	1367.6	57.8	1410	10	S81117S10 S81119 follicle-st
20	1220.6	51.6	187310	2	AC101870 Mus muscu
21	1129.4	47.7	3115	5	DB7871 DB7871 Gallus gall
22	1125.2	47.6	2468	5	GGU51097 GGU51097 Homo sapi
23	1001.2	42.3	154589	9	AC007189 AC007189 Cynops py
24	952.2	42.1	3075	5	AB005387 AB005387 follicle-st
25	952.6	41.2	1449	9	S73526 S73526 Sequence
26	952.6	41.2	1449	9	S73526 Sequence
27	952.6	41.2	1449	9	S73526 Sequence
28	943.2	39.9	1243	6	AX174765 AX174765 Sequence
29	943.2	39.9	1243	6	AX174765 Sequence
30	943.2	39.9	1243	6	AX174765 Sequence
31	816	34.5	2116	5	PS129253 PS129253 Podarcis
32	685	29.0	921	4	AF415208 AF415208 Alluoropod
33	663	28.0	2032	6	AR146400 AR146400 Sequence
34	663	28.0	2100	9	S57793 S57793 Homo sapien
35	663	28.0	2987	6	AR146399 AR146399 Sequence
36	663	28.0	2987	6	AR146399 Sequence
37	663	28.0	2987	6	AR146399 Sequence
38	662.8	28.0	2987	6	AR146399 Sequence
39	657.0	27.8	2453	4	BTU05004 BTU05004 Bos tauru
40	656.8	27.8	2453	4	BTU05004 Bos tauru
41	656.8	27.8	2453	4	BTU05004 Bos tauru
42	647.2	27.4	2183	4	PIGLHRCGA M9525 Porcine lut
43	646.8	27.3	1890	4	BTU07230 BTU07230 Bos tauru
44	640.8	27.1	2902	10	RATLHRCG M26199 Rat lutropl
45	625.8	26.4	3019	9	HUMLHRCG M73746 Homo sapien

ALIGNMENTS

RESULT 1	RATFSHTRA	RATFSHTRA	2366 bp	mRNA	linear	ROD 06-AUG-2002
LOCUS	Rattus sp.	follicle stimulating hormone receptor (FSHR) mRNA,				
DEFINITION	Complete cds.					
ACCESSION	L02842.1	GI-204183				
VERSION	L02842.1	GI-204183				
KEYWORDS	follicle stimulating hormone (FSH) receptor.					
SOURCE	Rattus sp.					
ORGANISM	Rattus sp.					
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;					
	Rattus.					
REFERENCE	1 (bases 1 to 2366)					
AUTHORS	Sprenkel,R., Braun,T., Nikolic,K., Segaloff,D.L. and Seeburg,P.H.					

Pred. No. is the number of results predicted by chance to have a

Db	1561	CGCAGCTGCTCTCTCTCCCATCTTTTCCGCTACAGTACATGAAAGTGCAGCATCTGCCT	1620
Oy	1621	GCCATGAGATATCGACAGAGCCCTTTGTGCAGCTGTATGTATATGGCCCTCTCTGTCTCTCAA	1680
Db	1621	GCCATGAGATATCGACAGAGCCCTTTGTGCAGCTGTATGTATATGGCCCTCTCTGTCTCTCAA	1680
Oy	1681	TGTCTTGCCCTTTGTGGTCATCTGTGGCTGCTATACCCACATCTACTACATCAGAGAGAA	1740
Db	1681	TGTCTTGCCCTTTGTGGTCATCTGTGGCTGCTATACCCACATCTACTACATCAGAGAGAA	1740
Oy	1741	TCTTACATCTTTGTCTCATCAGCAGCAGCAGATATGCCAGGCGATGGCCACACTCAT	1800
Db	1741	TCTTACATCTTTGTCTCATCAGCAGCAGCAGATATGCCAGGCGATGGCCACACTCAT	1800
Oy	1801	CTTTCACAGACTTCTCTGCATGGCCGCCCATTTTCATTTTGTGGCATTTTCTGCCTCCCTCAA	1860
Db	1801	CTTTCACAGACTTCTCTGCATGGCCGCCCATTTTCATTTTGTGGCATTTTCTGCCTCCCTCAA	1860
Oy	1861	GGTGGCGCTCATCTACTGTGTGCAAGGCCAAGATTCCTCTAGTTCTGTCTACCCCATCAA	1920
Db	1861	GGTGGCGCTCATCTACTGTGTGCAAGGCCAAGATTCCTCTAGTTCTGTCTACCCCATCAA	1920
Oy	1921	TGTCTTGCCCATCTCTCTGTGAGCGCATTTTCACAGAGATTCGCGAGGCACTCTTT	1980
Db	1921	TGTCTTGCCCATCTCTCTGTGAGCGCATTTTCACAGAGATTCGCGAGGCACTCTTT	1980
Oy	1981	CATCTGCTCTGAGCAAGTTTGGCTCTTATGAATGCAAGCCACAGATTTTACAGACAGAGAAC	2040
Db	1981	CATCTGCTCTGAGCAAGTTTGGCTCTTATGAATGCAAGCCACAGATTTTACAGACAGAGAAC	2040
Oy	2041	CTCATCCGCTACCCACAACTTCCATGCCCGAAAGAGCCATCTCTCAGCTTCCCAAGT	2100
Db	2041	CTCATCCGCTACCCACAACTTCCATGCCCGAAAGAGCCATCTCTCAGCTTCCCAAGT	2100
Oy	2101	CACCAATAGTTAGTGGCTGTGCCCTCTTATCATATATGCCAGAACTAAATCAATGTG	2160
Db	2101	CACCAATAGTTAGTGGCTGTGCCCTCTTATCATATATGCCAGAACTAAATCAATGTG	2160
Oy	2161	AAATGGATCTCACCCTTGAAGACAATATGACTCTCTCTGAGAGCAGCCCATGGACT	2220
Db	2161	AAATGGATCTCACCCTTGAAGACAATATGACTCTCTCTGAGAGCAGCCCATGGACT	2220
Oy	2221	AAATGGCAATCTACTGCACATCTCATCTATTAATCTCTCTGGGTCTCTGCATGGCAG	2280
Db	2221	AAATGGCAATCTACTGCACATCTCATCTATTAATCTCTCTGGGTCTCTGCATGGCAG	2280
Oy	2281	ACTGATCAGGAGCAATTAATACCCCTTTGGCTCTCTGCACATTTAATAATGGTAAACAG	2340
Db	2281	ACTGATCAGGAGCAATTAATACCCCTTTGGCTCTCTGCACATTTAATAATGGTAAACAG	2340
Oy	2341	CAATATACAGCAAGCAAAACGCCACA	2366
Db	2341	CAATATACAGCAAGCAAAACGCCACA	2366
RESULT 2			
AF095642			
LOCUS	AF095642	2079 bp	linear
DEFINITION	Mus musculus follicle stimulating hormone receptor (Fshr) mRNA,		
ACCESSION	AF095642.1	GI:3789955	
VERSION	AF095642		
RETRIEVED			
SEQUENCE			
ORGANISM			
REFERENCE			
AUTHORS			
TITLE			
NOTE			

C566T transition in exon 7 of the coding sequence
 Biol. Reprod. 60 (6). 1515-1527 (1999)
 2 (bases 1 to 2079)
 Tene-Sempere,M., Menna,P.R. and Huhtaniemi,I.
 Direct Submission
 Submitted (23-SEP-1998) Physiology, Biomedicine, Klinemyllynkatu
 10, Turku 20520, Finland
 Location/Qualifiers
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 Origin
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 Best Local Similarity 93.8%; Pred. No. 0;
 Matches 1950; Conservative 0; Mismatches 129; Indels 0; Gaps 0;
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2111 TACGCT 2149
2041 TACGCT 2079

RESULT 3

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LOCUS Human follicle stimulating hormone receptor mRNA linear PRI 08-NOV-1994
DEFINITION Human follicle stimulating hormone receptor mRNA, complete cds.
ACCESSION M65085
VERSION M65085.1 GI:182770
KEYWORDS follicle stimulating hormone (FSH) receptor.
SOURCE Human, cDNA to mRNA.
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 2393)
AUTHORS Minegishi, T., Nakamura, K., Takakura, Y., Ibuki, Y., Igarashi, M. and Minegishi, T. [corrected to Minegishi, T.
TITLE Cloning and sequencing of human FSH receptor cDNA
JOURNAL Blochem. Biophys. Res. Commun. 175 (3), 1125-1130 (1991)
MEDLINE 9122171
PUBMED 1709010
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RESULT 4

A76125 2222 bp DNA linear PAT 19-OCT-1999
 LOCUS
 DEFINITION
 A76125 Sequence 1 from Patent WO9320199.
 A76125
 VERSION
 KEYWORDS
 SOURCE

ORGANISM

Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 DiJkema, R. and De, L.R.
 HUMAN GONADOTROPIN RECEPTOR (FSH RECEPTOR)
 Patent: WO 9320199-A 1 14-OCT-1993;
 AK20 NV (NL); DIJKEMA REIN (NL)
 Location/Qualifiers

FEATURES

source

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BASE COUNT

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ORIGIN

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 Best Local Similarity 86.1%; Pred. No. 0;
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RESULT 6

AR003719

LOCUS

DEFINITION

2179 bp

DNA

linear

PAT 04-DEC-1998

Sequence 1 from patent US 5744448.

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Qy	1564	AGCTGCTCTTCCCATCATCTTTGGCATAGCTAGCTACATGAAGTGACATCTGCGCTGCC	1623
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Db 2171 GTGAAAATG 2179

RESULT 7
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DEFINITION Sequence 1 from patent US 5851768.
ACCESSION AR067576
VERSION AR067576.1 GI:5998798
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 2179)
AUTHORS de la Chapelle, A., Huhtaniemi, I. and Alttomaki, K.
TITLE Method for diagnosis of ovarian dysgenesis
JOURNAL Patent: US 5851768-A 1 22-DEC-1998;
FEATURES Location/Qualifiers
source 1..2179
BASE COUNT 575 a 560 c 445 g 599 t
ORIGIN

Query Match 70.9%; Score 1677.6; DB 6; Length 2179;
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RESULT 8
AR207283
LOCUS 2179 bp DNA linear PAT 20-JUN-2002
DEFINITION Sequence 1 from patent US 6,372,711.
ACCESSION AR207283
VERSION AR207283.1 GI:21506147
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 2179)
AUTHORS Reillon,C.;Ann., Cheng,S.;Yen., Nugent,N.;Patrice, and
TITLE Schleichardt,R.;Lynn, human PSH using human PSH receptor
JOURNAL PNAS
PAGES 1151-1155
PUBDATE 1996-APR-2002
FEATURES Location/Qualifiers
SOURCE 1-2179
BASE COUNT 575 a 560 c 445 g 599 t
ORIGIN
Query Match 70.9%; Score 1677.6; DB 6; Length 2179;

Best Local Similarity 86.5%; Pred. No. 0;
Matches 1876; Conservative 0; Mismatches 284; Indels 9; Gaps 2;
Oy 7 CTGGGGAATCTGTGGAAAGTCTTCCGCTGATGCAAGAAAGTCCGCTGAATGATATAAT 66
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RESULT 10
BOVESHR BOVESHR 2375 bp mRNA linear MAM 13-OCT-1994
LOCUS Bovine foallicle stimulating hormone receptor (FSHR) mRNA, complete
DEFINITION cds.


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ACCESSION L22319
VERSION L22319.1 GI:404671
KEYWORDS follicle stimulating hormone (FSH) receptor.
SOURCE Bos taurus (strain Holstein) cDNA to mRNA.
ORGANISM Bos taurus
Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Bovinae; Bos.
REFERENCE 1 (bases 1 to 2375)
AUTHORS Houde,A., Lambert,A., Saumande,J., Silversides,D.W. and
Lussier,J.G.
TITLE Structure of the bovine follicle-stimulating hormone receptor
complementary DNA and expression in bovine tissues
JOURNAL Mol. Reprod. Dev. 39 (2), 127-135 (1994)
MEDLINE 95127199
PUBMED 7826612
REFERENCE 2 (bases 1 to 2375)
AUTHORS Lussier,J.G.
TITLE Direct Submission
JOURNAL Submitted (30-SEP-1993) Jacques G. Lussier, CRRA, Faculty of
Veterinary Medicine, University of Montreal, P.O. Box 5,000, 3,200
Sicotte, St-Hyacinthe, Quebec, J2S 7C6, Canada
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TITLE Molecular cloning of the testicular follicle stimulating hormone receptor of the non human primate Macaca fascicularis and identification of multiple transcripts in the testis
JOURNAL Biochem. Biophys. Res. Commun. 196 (3), 1066-1072 (1993)
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REFERENCE 1 (bases 1 to 2319)
AUTHORS Robert, P., Anselme, S., Christophe, S., Benifla, J.L., Bellet, D.,
 Koman, A., and Bidart, J.M.
TITLE Cloning and sequencing of the equine testicular follitropin
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JOURNAL Biochem. Biophys. Res. Commun. 201 (1), 201-207 (1994)
MEDLINE 94256980
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Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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24: /SID52/gcgdata/geneseq/geneseq-emb1/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2359.6	99.7	2366	11	AAQ06634
2	1681	71.0	2222	14	AAQ50013
3	1676.6	70.9	2179	18	AAQ63181
4	1673.4	70.7	2180	13	AAQ29377
5	975.6	41.2	2140	22	AAF90547
6	943.2	39.9	1243	22	AAF90546
7	818.8	34.6	1316	18	AAQ45148
8	799.8	33.8	1300	19	AAV33371
9	799.8	33.8	1300	19	AAV33372

10	661.4	28.0	2987	13	AAQ22937	Sequence encoding
11	640.8	27.1	2902	11	AAQ06633	Clone encoding rat
12	604	25.5	3082	19	AAV27200	Homo sapiens Lir re
13	496	21.0	642	21	AAQ71467	Single nucleotide
14	494.4	20.9	642	21	AAQ71470	Single nucleotide
15	483.2	20.8	638	21	AAQ71464	Single nucleotide
16	483.2	20.8	638	21	AAQ71472	Single nucleotide
17	483.2	20.8	638	21	AAQ71476	Single nucleotide
18	493.2	20.8	638	21	AAQ71479	Single nucleotide
19	493.2	20.8	638	21	AAQ71482	Single nucleotide
20	470.6	19.9	2115	12	AAQ11120	Exon 4 of Human Lu
21	459.8	19.4	2512	24	AAQ37912	Mouse thyroid stim
22	448.8	19.0	5270	13	AAQ25387	Rat thyrotropin re
23	446.2	18.9	4417	12	AAQ12163	Sequence encoding
24	445.8	18.8	2415	12	AAQ12868	Human Thyroid Stim
25	445.8	18.8	3710	12	AAQ12164	Sequence encoding
26	444.2	18.8	2292	23	AB197930	Non-endogenous hum
27	444.2	18.8	2292	23	AB197933	Non-endogenous hum
28	444.2	18.8	2469	12	AAQ12529	Human Thyroid Stim
29	442.6	18.7	2292	23	AB197936	Non-endogenous hum
30	442.6	18.7	2292	23	AB197942	Non-endogenous hum
31	441	18.6	2292	23	AB197948	Non-endogenous hum
32	441	18.6	2292	23	AB197948	Non-endogenous hum
33	439.4	18.6	2292	23	AB197945	Non-endogenous hum
34	439.4	18.6	3549	23	AB198035	Human TSH receptor
35	436.2	18.4	2292	23	AB197951	Human TSH receptor
36	436.2	18.4	2413	12	AAQ11124	Homo sapiens TSH r
37	420.2	17.8	2410	18	AAQ63176	Drosophila melanog
38	420.2	17.8	2410	19	AAV27198	D. melanogaster pe
39	253.2	10.7	3158	23	ABL13245	Drosophila melanog
40	193.6	8.2	2586	23	AAH49414	Drosophila melanog
41	193.6	8.2	3909	23	ABL14533	Drosophila melanog
42	193.6	8.2	12248	23	ABL14532	Human TSH-receptor
43	153.2	6.5	411	12	AAQ11640	Human breast cell
44	144.6	6.1	407	22	ABA45519	Human foetal liver
45	144.6	6.1	407	22	ABA56015	

ALIGNMENTS

RESULT 1

AAQ06634

ID AAQ06634 standard; DNA: 2366 BP.

AC AAQ06634;

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FT	/tag= f
PT	/note= "primer for GST-PSH-R2"
PX	
PN	WO9320199-A.
PO	14-OCT-1993.
XX	
PF	29-MAR-1993; 93MO-EP00780.
PR	30-MAR-1992; 92EP-0200886.
PP	(ALKU) AKZO NV.
PA	
PI	De Leeuw R, Dijkema R;
DR	WFI: 1993-336907/42.
OR	P-FSDb: AHR42082.
PT	New follicle stimulating hormone receptor - and derived antibodies, anti-idiotypic antibodies, and transfected cells, useful e.g. in diagnosis and as antidote for FSH overstimulation
PT	
PS	Disclosure: Page 20-23; 42pp; English.
XX	
CC	The primers given in AAQ50029-34 were used in the cloning of GST-PSH-R1, GST-PSH-R2 and GST-PSH-R3 fusion protein constructs.
CC	Screening of the human testis cDNA library with a hPSH-R specific probe resulted in five recombinant phages positive in hybridisation.
CC	Sequence analysis was performed of the 2222 bp fragment of pGEM32cl (AAQ50013).
CC	
XX	
SQ	Sequence 2222 BP; 598 A; 565 C; 453 G; 606 T; 0 other:
Query Match 71.0% Score 1681 DB 14 Length 2222:	
Best Local Similarity 86.1%; Pred No. 0;	
Matches 1886; Conservative 0; Mismatches 295; Indels 9; Gaps 2:	
OY	7 CTGGGAATCTGTGGAAATTTTTCGCCTCATGACAGAAAAGACTCGGTGAATGGATAAAT 66
DB	21 CTCAGATCTGTGGAGTCTTTCTCTGCAATGCCAGAAGAAATCAGGTGGATGATGCAT 80
OY	67 AAGGATGCGCTTGCTCTCGTCTCTTCTGGCATTTCTTGGGCAGCGGATCTGGATGTCA 126
DB	81 AATTATGGCCCTGCTCTCGTGTCTTTGTTCGCAATTCCTGAGCTTGGGCTCAGGATGTCA 140
OY	127 TCATGGCTGTGTCAATGCTCTTAATAGGGCTTTCTCTGCCAAGACAGCAAGGTGACAGA 186
DB	141 TCATCGATCTGTCACTGCTCTACAGGGTTTTCTGCCNAGAGCAAGTAGTGACAGA 200
OY	187 GATTCGACACCGACTCCCCCGGAAGCGCAATTGAAGTGTGTGCTCACCAAGCTTGG 246
DB	201 GATTCCTTCTGACTCCCGGAGGATGCCATTGAAGTGTGTGCTCACCAAGCTTGG 260
OY	247 AGTCATCCCAAGAGATCATTTGCTGGATTTTGGAGACCTCGCAAAATAGAGATCTCTCA 306
DB	261 AGTCATCCAAAGGTGCATTTTCAGGATTTGGGGACCTCGSAAAAATAGAGATCTCTCA 320
OY	307 GAATGATCTCTTGSAGTAATAGAGCAGATGTGTCTTCCAAGCTACCAGGTTCGATGA 366
DB	321 GAATGATCTCTTGSAGGTGATAGAGCAGATGTGTCTTCCAAGCTTCCCAAAATACATGA 380
OY	367 AATTAGANTTAAAGGCCAACATTTCTGTACATCAACCCGGAGGCTTCCAGATCT 426
DB	381 AATTAGATTAAGAGGCCAACACATGCTCTACATCAACCCGTAGGCTTTCAGAGCTT 440
OY	427 CCCAGTCTCAGATCTGTTAATTCGACAGCGGATTAAGGATCTTGGCAGCTTCA 486
DB	441 TCCCAGCTTCAATCTGTTAATTCACAACAGAGTAAATGAAGACCTTCCAGATGTCTCA 500
OY	487 CAAGATCCAGTCTTCCAAAGGGTTCTACTAGACATTCAGATTAACATTAAGATCCACAT 546
DB	501 CAAGATCTCATTTCTCCAAAAGTTTTTACTTGACATTCAGATTAACATTAAGATCCACAC 560


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QY 1204 GAACACCAAGTCTGGTGGTCTGACACCAAGCCAACTACAACTAAGTGTGCCCGGTT 1263
DB 1211 GAACATCATGTGCTAGTGTCTTACCTACAGCCCAATATAAATCAAGTCCCGAGTT 1270
QY 1264 TCTTATGTGAACCTCGCTTGGCTGATCTCTGATAGGCACTACTTGTCTACTTATAGC 1323
DB 1271 CCTTATGTGAACCTCGCTTGGCTGATCTCTGATGATGGAATCTACCTGCTCTATTGC 1330
QY 1324 ATCAGTTGACATCCATACCAAGAGCAGGATGACACAACTATGCAATGAGTGCACAAAGG 1383
DB 1331 ATCAGTTGATATCCATACCAAGAGCAATATACAACTATGCAATGAGTGCACAAAGT 1390
QY 1384 AGCAGCTGTGATGCTGCTGCTTTTCACTGCTCTTTGGCAGTGAACCTGAGTCTACAC 1443
DB 1391 GCGAGCTGTGATGCTGCTGCTTTTCACTGCTCTTTGGCAGTGAACCTGAGTCTACAC 1450
QY 1444 ATTGACAGCCATCACCTTGAAGATGGCATACCATCACATGCTATGCAACTGGAATG 1503
DB 1451 TCTGACAGCTATCACCTTGAAGATGGCATACCATCACATGCAACTGGAATG 1510
QY 1504 CAAGTGCAGCTCCGCGATGCTGCCAGCTGCTATGTTGGGCTGGACTTTTGCCTTCC 1563
DB 1511 CAAGTGCAGCTCCGCGATGCTGCCAGTGTCTATGTTGGGCTGGACTTTTGCCTTCC 1570
QY 1564 AGCTGCTCTCTTCCCTCTTTGGCATCAGTACATGAAAGTGAAGTGAAGTGAAGTGAAG 1623
DB 1571 AGCTGCTCTCTTCCCTCTTTGGCATCAGTACATGAAAGTGAAGTGAAGTGAAGTGAAG 1630
QY 1624 CATGATATGACAGCCCTTTGTCAGCTGTATGTTATGGCCCTCTTGTCTCTCAATGT 1683
DB 1631 CATGATATGACAGCCCTTTGTCAGCTGTATGTTATGGCCCTCTTGTCTCTCAATGT 1690
QY 1684 CTTGGCTTTTGGTCTGCTGCTGCTATACCCACATCTACCTCAGAGTGAAGTCC 1743
DB 1691 CTTGGCTTTTGGTCTGCTGCTGCTATACCCACATCTACCTCAGAGTGAAGTCC 1750
QY 1744 TACCATTTGTCTCATCAAGGACACCAAGATTTGCCAGCGCATGCGCACATCTCATCTT 1803
DB 1751 CAACATCGTCTCTCTCTAGTGACACCAAGATTTGCCAGCGCATGCGCACATCTCATCTT 1810
QY 1804 CACAGACTTTCTCTGATGCGCCCAATTTCAATTTCTTGGCATTTTCTGCTCTCCCTCAAGT 1863
DB 1811 CACTGACTTCTCTGATGCGCCCAATTTCAATTTCTTGGCATTTTCTGCTCTCCCTCAAGT 1870
QY 1864 GCGCTCATCAGTCTGCAAGGCGCAAGATTTCTCTGATGCTTCTTACCCCATCAATTC 1923
DB 1871 GCGCTCATCAGTCTGCAAGGCGCAAGATTTCTCTGATGCTTCTTACCCCATCAATTC 1930
QY 1924 TTGTGCAATCTCTCTTCTACGCCATTTTCAACAAAGATTTCTGCTGCTGCTGCTGCTGCT 1983
DB 1931 CTGTGCAACCCCTCTCTATGCTATGCTATTTACCAAAATTTCTGCGAGATTTCTTCTAT 1990
QY 1984 CTTGCTGAGCAAGTTTGGCTGTTATGAAATGCAAGCCAGATTTACAGGACAGAAACCTC 2043
DB 1991 TCTGCTGAGCAAGTTTGGCTGTTATGAAATGCAAGCCAGATTTATAGGACAGAAACCTC 2050
QY 2044 ATCCGCTTACCAACATTTCCATCCGGAAGAGCACTGCTCTGCTGCTGCTGCTGCTGCTGCT 2103
DB 2051 ATCCATGCTCCACACACCCATCCAGGAATGCGCACTGCTCTGCTGCTGCTGCTGCTGCTGCT 2110
QY 2104 CAAT-----AGTTAGCTGCTTGTCTCTTAACTATTCATCCAGAACTATAAATCAAT 2157
DB 2111 CAATGGTTCCATTTACATCTTGTCTCTTAACTATTCATCCAGAACTATAAATCAAT 2170
QY 2158 GTGAAAT 2165
DB 2171 GTGAAAT 2178
```

RESULT 4

AAQ29377

ID AAQ29377 standard; DNA; 2180 BP.

```
XX AAQ29377;
XX AC
XX DT 04-MAR-1993 (first entry)
XX FSHR DNA.
XX DE
XX KW Human: follicle stimulating hormone receptor; maturation;
XX OS spermatogenesis; birth control; ss.
XX FH Homo sapiens.
XX Key Location/Qualifiers
XX CDS 75..2159
XX FT /*tag= a
XX FT sig_peptide 75..126
XX FT mat_peptide /*tag= b
XX FT 127..2159
XX FT /*tag= c
XX PN W09216620-A.
XX PD 01-OCT-1992.
XX PF 02-JAN-1992: 92WO-US00122.
XX PR 15-MAR-1991: 91US-0670085.
XX PA (ISTF ) ARS APPL RES SYST HOLDING NV.
XX PI Cheng SVY, Kelton CA, Nugent NP, Schweickhardt RL;
XX DR WPI: 1992-349206/42.
XX DR P-PSDB; AAR29377.
XX PT Pure human FSH receptor, fragments and mutants - for preventing
XX PT follicle growth, maturation and spermatogenesis, also for use of
XX PS appropriate cell lines for bio-assays of FSH
XX PS Claim 7; Page 25; 48pp; English.
XX CC The DNA sequence encoding human follicle stimulating hormone
XX CC receptor (FSHR) was obtd. by screening a lambda gt11 cDNA library
XX CC constructed from RNA extracted from human testis and amplified, with
XX CC a rat FSHR cDNA clone as a probe. Positive colonies were used for
XX CC a secondary screen which isolated five putative human FSHR clones.
XX CC None of the clones contained the complete hFSHR coding region but
XX CC could be overlapped using GCG to give the complete sequence. hFSHR
XX CC binds to FSH to reduce endogenous FSH bioactivity, in females to
XX CC prevent follicle growth and maturation and in males to prevent
XX CC spermatogenesis, i.e. as a birth control agent.
XX SQ Sequence 2180 BP; 577 A; 560 C; 444 G; 599 T; 0 other;
```

Query Match 70.7%; Score 1673.4; DB 13; Length 2180;
Best Local Similarity 86.6%; Pred. No. 0;
Matches 1869; Conservative 0; Mismatches 280; Indels 9; Gaps 2;

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QY 18 GTGGAAGTTTTCGGCTGATGTCAGAAAGATCGGTGAATGAATGAATGAATGAATGAATGAAT 77
DB 23 GAGGTTTTCCTGCAAAATGCAAGGAAGAAATCAGTGGATGATGATGATGATGATGATGATGAT 82
QY 78 TGTCTCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 137
DB 83 TGTCTCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 142
QY 138 GTCATTTCTCTAATAGGCTCTTTCTCTGCAAGACAGCAAGGTCAGAGATTCAGGACCG 197
DB 143 GTCACCTCTCTAAGAGGTTTCTCTGCAAGACAGCAAGGTCAGAGATTCAGGACCG 202
QY 198 ACCTCCCGGAGAGCCGCTTGAATGAGTTTGTCTGCTCACCAGCTTCGAGTCAATCCGA 257
DB 203 ACCTCCCGGAGAGTGCATGAGTTTGTCTGCTCACCAGCTTCGAGTCAATCCGA 262
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FT		/codon_start= 104
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FT		/tag= d
FT	primer_bind	/note= "primer A1"
FT		/complement (225..244)
FT		/tag= e
FT	primer_bind	/note= "primer B1"
FT		254..273
FT		/tag= f
FT	primer_bind	/note= "primer A2"
FT		/complement (468..487)
FT		/tag= g
FT	primer_bind	/note= "primer C1"
FT		493..512
FT		/tag= h
FT	primer_bind	/note= "primer B2"
FT		/complement (675..694)
FT		/tag= i
FT	primer_bind	/note= "primer D1"
FT		713..732
FT		/tag= j
FT	primer_bind	/note= "primer C2"
FT		/complement (850..869)
FT		/tag= k
FT	primer_bind	/note= "primer E1"
FT		904..923
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FT		/tag= q
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PN	WO200144502-A2.	
XX		
PD	21-JUN-2001.	
XX		
PF	18-DEC-2000; 2000WO-EPI2886.	
XX		
XX	16-DEC-1999; 99EP-0125148.	
PR	29-FEB-2000; 2000US-0185670.	

The present sequence is that of the exon 10 region of the human follicle stimulating hormone (FSH) receptor gene on chromosome 2p21. This region of the gene encodes the transmembrane and intracellular domain (see AAB82468) of the FSH receptor. A claimed method for determining the dosage of FSH required in the treatment of infertility of a woman comprises determination of the FSH receptor variant by isolating genomic DNA from a blood sample of the woman and determining whether the isolated DNA codes for the FSH receptor variant Ala307/Ser680 or Thr307/Asn680. This is achieved by partial amplification of the FSH receptor DNA by using a pair of primers that flank the DNA coding for amino acids 307 and/or 680 of the FSH receptor protein. The amplified DNA is then digested, preferably using BstI, and the FSH receptor variant is determined by restriction fragment length polymorphism. Suitable primers are given in AAF90530-43. Women bearing the homozygous FSH receptor variant Ala307/Ser680 may be given a high dosage of FSH. Women bearing the homozygous FSH receptor variant Thr307/Asn680 may be given a low dosage of FSH, while women with a heterozygous state may be given an intermediate dosage of FSH.

Sequence 1450 Bp; 356 A; 387 C; 283 G; 424 T; 0 other;

Query Match	41.28;	Score 975.6;	DB 22;	Length 1450;
Best Local Similarity	86.4%;	Pred. No. 1.3e-293;		
Matches 1103;	Conservative 0;	Mismatches 164;	Indels 9;	Gaps 2;
Qy 923	ATCTCTGAACATTCATCCAAATTTGCAACAAGTCTATTTTAAGGCAAGATATTTGATGATG	982		
Db 101	AGCTCTGAGCTTCATCCAAATTTGCAACAATCTATTTTAAGGCAAGATTTGATATATG	160		
Qy 983	ACTCAAAATGGGGATCAGAGAGTCTCTCTGATAGATG---ATGAACCCAGTTATGGAAAA	1039		
Db 161	ACTCAGACTAGGGGTGAGAGATCCTCTCTGCGAAGACAATGAGTCCAGCTACAGCAGA	220		
Qy 1040	GGATCTCACATGATGATCAATGAATTTGATATGACTTATGACTTATGAAGTTGTTGATGTG	1099		
Db 221	GGATTTGACATGAGTACATGAGTTGGATGACTATGACTTATGCAATGAAGTTGGTTGAGCTG	280		
Qy 1100	ACCTGCTCACCACAGCCAGATGCAATTTAAATCCATGTGAAGATATCATGGGGTACAAACATC	1159		
Db 281	ACCTGCTCCCTTAAGCCAGATGCAATTCACCCATGTGAAGTATCATGGGGTACAAACATC	340		
Qy 1160	CTCAGGGTCTTGATATGGTTTATAGCATCCTTGCCATTACTGGGAACACACAGATGCTG	1219		
Db 341	CTCAGATCTCTGATATGGTTTATCAGCATCCTTGCCATCATCTGGGAACATCATAGTGCTA	400		
Qy 1220	GTGGTCTGTACCACAGCCAAATACAACTAACTGTGCCCGGTTCTTATGTCTGAACCTC	1279		
Db 401	GTGATCTTAATCCAGCCCAATATAACTCACAGTCCCCAGGTTCTTATGTGCAACCTG	460		
Qy 1280	GCCTTCGCTGATCTCTGCATAGGCATCTACTTGTCTATTAGCATCAGTTGACATCCAT	1339		
Db 461	GCCTTTGCTGATCTCTGCATGGAACTCACTGCTGCTCATTGATGATATCCAT	520		
Qy 1340	ACCAAGAGCCAGTACCACAACTATGCCATTTGCTGGCAACACAGAGCAGCGCTGTGATGCT	1399		
Db 521	ACCAAGAGCCAAATATCAAACTATGCCATTTGCTGGCAAACTGCGGAGCGCTGTGATGCT	580		
Qy 1400	GCTGGCTTTTTCAGTGTCTTTGGCAGTGAACCTGTGCTGCTACACATGTGACAGCCATCACC	1459		
Db 581	GCTGGCTTTTTCAGTGTCTTTGGCAGTGAACCTGTGCTGCTACACTGTGACAGCTATCACC	640		
Qy 1460	CTAGAAAGATGGCATACCATCACACATGCTATGCAACTGGAATGCAAGTGCAGCTCCGG	1519		
Db 641	TTGAAAGATGGCATACCATCACGCATGCCATGCAGCTGCAGTGCAGGTCGAGCTCCG	700		
Qy 1520	CATGCTGCCAGGTCATGGTATTTGGGCTGGCACTTTTGGCTTGGAGCTGCTCTCTTCCTCC	1579		
Db 701	CATGCTGCCAGTGCATGGTATGGGCTGGATTTTGTCTTTTGGAGCTGCTCTCTTCCTCC	760		


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Db 544 TTGGAAGATGGCATACCATCAGCATGCCATGCGAGCTGCAGGTGCAGCTCCGC 603
Qy 1520 CATGCTGCCAGCTCATGGTATTTGGGCTGACATTTTGGCTTCGAGCTGCTCTTCCCC 1579
Db 604 CATGCTGCCAGCTCATGGTATTTGGGCTGAGTATTTGCTTTTCGAGCTGCCCTTTCC 663
Qy 1580 ATCTTTGGCATCAGTACATGAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 1639
Db 664 ATCTTTGGCATCAGCTCATGAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 723
Qy 1640 CTTTGTGACAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1699
Db 724 CTTTGTGACAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 783
Qy 1700 ATCTGTGGCTGCTATACCCACATCTACCTCAGAGTGAAGTGAAGTGAAGTGAAGT 1759
Db 784 ATCTGTGGCTGCTATACCCACATCTACCTCAGAGTGAAGTGAAGTGAAGTGAAGT 843
Qy 1760 TCAAGCCACACCAAGATTTGCCAAGCGCATGCGCCACATCTATCTTACAGACTTTCTCTGC 1819
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Db 1023 CTCTAGCCCATTTTCAACCAAGATTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCT 1082
Qy 2000 GGCTGTTATGAATGCAAGCCCAAGATTTACAGGACAGAAACCTTACCTCCGCTACCCACAAC 2059
Db 1083 GGCTGTTATGAATGCAAGCCCAAGATTTATAGGACAGAAACCTTACCTCCGCTACCCACAAC 1142
Qy 2060 TTCCATGCCGGAAGAGCACTCTCTGCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCT 2113
Db 1143 ACCATCCAGGAATGGCCACTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCT 1202
Qy 2114 GTGCTTCTGCTTCTTATCATTCATCCAGCAATAAA 2151
Db 1203 ATACTTGTCTCTAGTCAATTTAGCCCAAACTAAA 1240
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RESULT 7

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AAT45148
ID .AAT45148 standard; cdna; 1316 BP.
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```
XX AC AAT45148;
XX DT 09-MAR-1997 (first entry)
XX DE Gonadotropin receptor hFSHR-EC CDNA.
XX KW Gonadotropin receptor; follicle stimulating hormone receptor; FSHR;
XX KW baculovirus; AcNPV; Spodoptera frugiperda; insect; Sf9;
XX KW contraceptive; mimetic; antagonist; ss.
XX OS Chimeric Homo sapiens;
XX OS Chimeric Autographa californica nuclear polyhedrosis virus.
XX PH Key Location/Qualifiers
FT promoter 1..996
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FT FT folding and secretion in insect host cells"
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FT FT tripeptide linker"
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XX W09638575-A1.
XX PN 05-DEC-1996.
XX PD 03-JUN-1996; 96WO-1B00709.
XX PF 02-JUN-1995; 95US-0460576.
XX PR (ISTE ) ARS APPLIED RES SYSTEMS HOLDING NV.
XX PA Buckler DR, Cheng SVY, Prentice HL, Sisk WP;
XX PI WPI; 1997-034385/03.
XX DR P-PSDB; AAW06532.
XX XX
XX PT Baculovirus transfer vector expresses gonadotropin receptor
XX PT extracellular domain - can be linked to affinity column to extract
XX PT hormone mimetic(s) or antagonists
XX PS Example 2; Fig 3; 66pp; English.
XX CC A CDNA construct (AAT45148) codes for human follicle stimulating
XX CC hormone receptor extracellular domain (hFSHR-EC) in which the
XX CC native signal peptide is replaced by the gp67 signal peptide of
XX CC a baculovirus (AcNPV). It is obtd. by PCR amplification (see also
XX CC AAT45149-50) of hFSHR cDNA and ligation into baculovirus transfer
XX CC vector pACGP67-A. The construct allows prodn. of soluble hFSHR-EC
XX CC in insect host cells. The hFSHR-EC can be used as an affinity
XX CC ligand to extract hormone mimetics or antagonists, and to purify
XX CC gonadotropins, or can be used to modulate hormone action in vivo,
XX CC e.g. as a contraceptive.
XX XX
SQ Sequence 1316 BP; 405 A; 291 C; 268 G; 352 T; 0 other;
```

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Query Match 34.6%; Score 818.8; DB 18; Length 1316;
Best Local Similarity 87.1%; Pred. No. 1.3e-244;
Matches 911; Conservative 0; Mismatches 132; Indels 3; Gaps 1;
Qy 122 TGTCTATCATGCTGTGTCTATCTCTAATAGGCTCTTTCTCTGCCAAGACAGAGGTG 181
Db 261 TGTCTATCATGCTGTGTCTATCTCTAATAGGCTCTTTCTCTGCCAAGACAGAGGTG 320
Qy 182 ACAGAGATTCGCGACCGACCTCCCGGACCGATTCGCTGAGTGTGTGTCTCACCAG 241
Db 321 ACAGAGATTCGCTGACCTCCCGGACCGATTCGCTGAGTGTGTGTCTCACCAG 380
Qy 242 CTTCGAGTTCATCCGAAAGATTCATTTGCTGGATTTGGAGCTTGGAGAAATAGAGATC 301
Db 381 CTTCGAGTTCATCCAAAAGGTGCTATTTTACGAGTTTGGGACCTGGAGAAATAGAGATC 440
Qy 302 TCTCAGAATGATCTCTTGGAGGTATAGAGGAGAGATGTGTCTTCCAACTTACCAAGTTG 361
Db 441 TCTCAGAATGATCTCTTGGAGGTATAGAGGAGAGATGTGTCTTCCAACTTCCCAATTA 500
```


Best Local Similarity 87.0%; Pred. No. 6e-144; Matches 557; Conservative 1; Mismatches 76; Indels 6; Gaps 1;	
QY	1518 GCATGCTGCCAGCGTCATGGTATTGGCGCGACTTTTGGCTTCCGACGTGCTCTTCCT 1577
Db	1 GCATGCTGCCAGGTGTCATGGTGATGGCGTGGATTTTTTGGCTTTTGCAGCTGGCCCTCTTTC 60
QY	1578 CCATCTTTGGCATCAGTAGCTACATGAAGTAGGACATCGCTTGGCCATGGATATCGACA 1637
Db	61 CCATCTTTGGCATACAGCACTACATGAAGTAGGACATCGCTTGGCCATGGATATCGACA 120
QY	1638 GCCCTTGTGCACAGCTGATGTATTATGGCGCCCTCTTGTCTCAATCTCTGGCTTTTGTGG 1699
Db	121 GCCCTTGTGCACAGCTGATGTATCTCTCTCTCTGTGTGTCAATCTCTGGCTTTTGTGG 180
QY	1698 TCATCTGTGGCTGTATACCGACATCTACCTTCACAGTCAGGAGATCTACATCTGTGTCT 1757
Db	181 TCATCTGTGGCTGTATATCCATCATCTACCTTCACAGTCAGGAGATCTACATCTGTGTCT 240
QY	1758 CATCAAGCGACACCAAGATTGCGAAGCGATGGCCACACTCATCTTCACAGACTTTCTCT 1817
Db	241 CCTCTAGTGACACCAAGATCGCCAAAGCGCATGGCCATGCTCATCTTCACTGACTTCTCT 300
QY	1818 GCATGGCGCCCAATTTCATCTTTGCCATCTTCTGCTTCCCTCAAGTGGCGCTCATCACTG 1877
Db	301 GCATGGCACCCATTTCTTTCTTGGCCATTTCTGCTTCCCTCAAGTGGCGCTCATCACTG 360
QY	1878 TGTCCAAAGCGCAAGATTCTCCTTACTTCTGTCTTACCCATCAATCTTGTGGCAATCCTT 1937
Db	361 TGTCCAAAGCAAGATTCTGTGTCTGTCTTTCACCCCATCAACTCTGTGGCAACCCCT 420
QY	1938 TCTCTACGCCAATTTTCCAAAGAACTTCCGACGGAGCTTCTTCATCTCTGTGAGCAAGT 1997
Db	421 TCTCTATATGCCATCTTTTACCAAAACTTTTGGCAGAGATTTCTTCATCTCTGTGAGCAAGT 480
QY	1998 TTGGCTGTATGAATCGAAGCGCAGATTTCAGGACAGAAACCTTCATCGCGCTACCCCA 2057
Db	481 GTGGCTGTATGAATCGAAGCGCAGCTGTCTGTGAGCGCCAGATTCATCCATCTGCCACA 540
QY	2058 ACCTTCATCGCGAAGTACGCGACCTGCTGTGAGCGCCAGATTCATCCATCTGCCACA 540
Db	541 ACACCTTCAGGAGTATGGCCACTGCTCTTCAGCTCCCGAGATTCACATGTGTTCACATT 600
QY	2112 ACGCTCTGTGCTCTTTATCATCTTCATCCGACACTAAA 2151
Db	601 ACATACTGTGCTCTTAAGTCATCTTATGCCAAACTAAA 640

RESULT 14	
AAC71470	
1D	AAC71470 standard; DNA; 642 BP.
1X	
AC	
AC	AAC71470;
XX	
DT	09-FEB-2001 (first entry)
DT	
XX	
XX	Single nucleotide polymorphism containing sequence #433.
DE	
XX	Single nucleotide polymorphism. SNP; human; genetic disease;
KW	disease susceptibility; cardiovascular system; endocrine system;
KW	neurological system; forensic testing; paternity testing; ds.
XX	
XX	Homo sapiens.
OS	
XX	WC200058519-A2.
XX	
XX	
PD	05-OCT-2000.
XX	
PF	30-MAR-2000; 2000WO-US08440.
XX	
XX	
PR	31-MAR-1999; 99US-0127248.
XX	
XX	
PA	(WHED) WHITEHEAD INST BIOMEDICAL RES.

XX
PA (WHED) WHITEHEAD INST BIOMEDICAL RES.

(AFFY-) AFFYMETRIX INC.
Althshuler D, Cargill M, Daley GO, Ireland JS, Lander ES;
Lipshutz RJ, Patil N, Sklar P;
WPI: 2000-611722/58.
Nucleic acid selected from one of 106 genes comprising single nucleotide polymorphisms, allele-specific oligonucleotides to the genes are useful for phenotypic correlations, forensics, paternity testing, medicine and genetic analysis.
Claim 1: Fig 5: 214pp: English.
The present invention is concerned with a number of human single nucleotide polymorphisms (SNPs) which the inventors identified in human genes. These SNPs can be used in disease diagnosis and prediction of an individual's susceptibility to disease, in forensic and paternity testing and in genetic mapping. In particular, the SNPs of the invention can be used to diagnose susceptibility to diseases of the cardiovascular, endocrine and neurological systems, such as coronary artery disease, schizophrenia, cancer, autoimmune diseases, Alzheimer's and Parkinson's diseases.
Note: The degenerate codon within the sequence represents the position of an SNP, for example the letter S represents a polymorphism where the nucleotide may be C or G.
Sequence 642 BP; 138 A; 200 C; 117 G; 186 T; 1 other;
Query Match 20.9%; Score 494.4; DB 21; Length 642;
Best Local Similarity 86.9%; Pred. No. 1.9e-143;
Matches 556; Conservative 1; Mismatches 77; Indels 6; Gaps 1;
QY 1518 GGCATGCTGCCAGCTCATGTGATGGGTGGCTGACATTTTGCCTCCAGCTGCTCTCTCC 1577
DB 1 GGCATGCTGCCAGCTCATGTGATGGGTGGCTGACATTTTGCCTCCAGCTGCTCTCTCC 60
QY 1578 CCATCTTTGGCATCATAGTACATACATGAAGTGGAGCATCTGCCTGCCCATGGATATCGACA 1637
DB 61 CCATCTTTGGCATCATAGTACATACATGAAGTGGAGCATCTGCCTGCCCATGGATATCGACA 120
QY 1638 GCCCTTTGTCAGCTGATGTATGATGGCTCTCTGCTCAATGCTCTGCGCTTTGGG 1697
DB 121 GSCCTTTGTCAGCTGATGTATGATGGCTCTCTGCTCAATGCTCTGCGCTTTGGG 180
QY 1698 TCATCTGTGGCTGTATACCCACATCTACCTCACAGTGGAGTCTTACCATTGCTCTCT 1757
DB 181 TCATCTGTGGCTGTATATCCATCTACCTCACAGTGGAGTCTTACCATTGCTCTCTCT 240
QY 1758 CATCAAGCGACACCAAGATGTCGAAGCGCATGGCCACACTCATCTTTCACAGACTTTCTCT 1817
DB 241 CCTCTAGTGACACCAAGATGTCGAAGCGCATGGCCACACTCATCTTTCACAGACTTTCTCT 300
QY 1818 GCATGCCCCCATTTTCATCTTTGCGCATTTTGCCTCCCTCAAGTGGCGGTCATCACTG 1877
DB 301 GCATGCCCCCATTTTCATCTTTGCGCATTTTGCCTCCCTCAAGTGGCGGCTCATCACTG 360
QY 1878 TGTCACAGCGCAAGATCTCTCTAGTGTCTTCTACCCCATCAATTTGTCGCAATCTCT 1937
DB 361 TGTCACAGCAAGATCTCTCTAGTGTCTTCTACCCCATCAATTTGTCGCAATCTCT 420
QY 1938 TCCTCTAGCCCATTTTCACCAAGAACTTCCGAGGAGTCTTCTTCACTGCTGAGCAAGT 1997
DB 421 TCCTCTAGCCCATTTTCACCAAGAACTTTCGAGAGATTTCTTCACTGCTGAGCAAGT 480
QY 1998 TTGGCTGTATGAATGCAAGCCAGATTTTACAGAGAGAAACCTTCATCCGTCACCCACA 2057
DB 481 GTGGCTGTATGAATGCAAGCCAGATTTTACAGAGAGAAACCTTCATCCGTCACCCACA 540
QY 2058 ACTTCCATGCCCGCAAGAGGAGCTGCTCTCTAGCTTCCAGAGTCCCAAT-----AGTT 2111
DB 541 ACACCCATCCAGGAATGGCCACTGCTCTTACGCTCCCGAGAGTCCCAATGGTTCCTCACTT 600

QY 2112 ACGTCTGTGCTCCTTATCATTCATCCAGCACTAAAA 2151
DB 601 ACATACTTGTCCCTTAAGTCAATTTAGCCCAAACTAAAA 640
RESULT 15
AAC71464
ID AAC71464 standard; DNA; 638 BP.
AC AAC71464;
XX
DT 09-FEB-2001 (first entry)
XX
DE Single nucleotide polymorphism containing sequence #431.
XX
KW Single nucleotide polymorphism; SNP; human; genetic disease;
KW disease susceptibility; cardiovascular system; endocrine system;
KW neurological system; forensic testing; paternity testing; ds.
OS Homo sapiens.
XX
PN WO200058519-A2.
XX
PD 05-OCT-2000.
XX
PF 30-MAR-2000; 2000WO-US08440.
XX
PR 31-MAR-1999; 99US-0127248.
XX
PA (WHED) WHITEHEAD INST BIOMEDICAL RES.
PA (AFFY-) AFFYMETRIX INC.
XX
PI Althshuler D, Cargill M, Daley GO, Ireland JS, Lander ES;
PI Lipshutz RJ, Patil N, Sklar P;
XX
DR WPI: 2000-611722/58.
XX
PT Nucleic acid selected from one of 106 genes comprising single nucleotide polymorphisms, allele-specific oligonucleotides to the genes are useful for phenotypic correlations, forensics, paternity testing, medicine and genetic analysis.
PT
PS Claim 1: Fig 5: 214pp: English.
XX
CC The present invention is concerned with a number of human single nucleotide polymorphisms (SNPs) which the inventors identified in human genes. These SNPs can be used in disease diagnosis and prediction of an individual's susceptibility to disease, in forensic and paternity testing and in genetic mapping. In particular, the SNPs of the invention can be used to diagnose susceptibility to diseases of the cardiovascular, endocrine and neurological systems, such as coronary artery disease, schizophrenia, cancer, autoimmune diseases, Alzheimer's and Parkinson's diseases.
CC Note: The degenerate codon within the sequence represents the position of an SNP, for example the letter S represents a polymorphism where the nucleotide may be C or G.
XX
SQ Sequence 638 BP; 162 A; 158 C; 144 G; 173 T; 1 other;
Query Match 20.8%; Score 493.2; DB 21; Length 638;
Best Local Similarity 86.9%; Pred. No. 4.5e-143;
Matches 553; Conservative 1; Mismatches 79; Indels 3; Gaps 1;
QY 925 CTCGAACTTCATCCAAATTTGCAACAAGTCTATTTAAGGCAAGATTTGATGATATGAC 984
DB 2 CTCGAGCTTCATCCAAATTTGCAACAAGTCTATTTAAGGCAAGATTTGATGATATGAC 61
QY 985 TCAAAATGGGGATCAGAGAGTCTCTCTCATAGATC---ATGACCCAGCTTATGGAAAGG 1041
DB 62 TCAGRCTAGGGTTCAGAGATCTCTCTCGGACAGCAATAGTCCAGCTCAGCAGAGG 121
QY 1042 ATCTGACATGATGTACAATGAATTTGATTATGACCTTATGATGAAGTTGTTGATGTGAC 1101

Db	122	ATTTCACATGACGTACACATGAGTTTCACCTATGACTTATGCAATGAAGTGGTTGACCGTAC	181
Oy	1102	CTGCTCACCAAGAGCAGATGCATTTAATCCATGTGAGATATCATGGGGTACAACATGCT	1161
Db	182	CTCTGCCCTTAAGCCAGATGCATTCACCCATGTGAGATATCATGGGGTACAACATGCT	241
Oy	1162	CAGGCTCTGATATGTGTTTATTAGCATCTCGGCCATCTACGTGGGAACACACAGTGTGGT	1221
Db	242	CAGATCTGTATATGTGTTTTCACATCTCTGGCCATCACTGGGAACATCATGTGGTGTGCT	301
Oy	1222	GGTCTGCACACAGCAGCAATCAACTGATGGCCCGGTTCTTATGTGTGTAACCTGGC	1281
Db	302	GATCTTAAGTACCGACCATTAATCACTACAGTCCCGAGTCTCTATGTGTGCACCTGGC	361
Oy	1282	CTTTCGCTGATCTTCGATAGGCATCTACTTGCCTACTATATAGCATCAGTGCAGATCCATAC	1341
Db	362	CTTTGCTGATCTTCGATTTGGAATCTACTCTGCTGCTCATTTGCATCAGTTGATATCCATAC	421
Oy	1342	CMAAGCCAGTATACACAACTATGSCATTGACTGGCAACAGAGACGCGCTGTGATGCTGC	1401
Db	422	CMAAGGCAATATACAACTATGSCAATATGACTGGCAAACTGGGGCAGCGCTGTGATGCTGC	481
Oy	1402	TGCTTTTTTCAGCTGTCTTTCGAGTGAATCTGCAGTCTTACAAATTTGACAGCCATACGCT	1461
Db	482	TGGATTTTCACTGTCTTTCGAGTGAATCTGCAGTCTTACAAATTTGACAGCCATACGCT	541
Oy	1462	AGAAAGATGGCATACCATCACATCATCTGCAATCGGAATCGAATGAGTGCAGCTCGGCCA	1521
Db	542	GGAAAGATGGCATACCATCACGCAATGCAATCGCACTGGACTGCAAGGTGCAGCTCCGCCA	601
Oy	1522	TGCTCCCAAGCGTCACTGATTTGGGCTGGACTTTTGC	1557
Db	602	TGCTCCCAAGTGTCACTGATGGGCTGGATTTTTCG	637

Search completed: June 16, 2003, 09:06:28
Job time : 531 secs

Result	Query No.	Score	Length	DB	TD	Description
C	1	1677.6	70.9	2179	1	US-08-487-886-1
	2	1677.6	70.9	2179	2	US-08-531-070A-1
	3	1677.6	70.9	2179	3	US-08-482-855-1
	4	1677.6	70.9	2179	4	US-08-474-986-1
	5	818.8	34.6	1316	3	US-08-460-576-1
	6	799.8	33.8	1298	4	US-08-795-876-32
	7	799.8	33.8	1300	4	US-08-795-876-31
	8	799.8	33.8	1300	4	US-08-795-876-36
	9	799.8	33.8	1300	4	US-08-795-876-37
	10	799.8	33.8	1300	4	US-08-795-876-38
C	11	663	28.0	2987	4	US-07-757-343E-1
	12	447.8	18.9	4417	4	US-07-711-453A-2
	13	445.8	18.8	3710	4	US-08-232-463A-1
	14	72.2	3.1	1718	1	US-08-866-757-1
	15	64.6	2.7	4203	2	US-09-133-593-1
	16	64.6	2.7	4203	1	US-07-676-174A-1
	17	46.6	2.0	3335	1	US-08-194-338-1
	18	46.6	2.0	3335	1	US-09-182-024A-1
	19	42.2	1.8	5176	4	US-09-255-368-7
	20	40.8	1.7	1293	4	US-09-255-368-1
C	21	40.6	1.7	1410	4	US-09-255-368-1
	22	40.6	1.7	289	4	US-09-007-003-7
	23	40.4	1.7	792	1	US-08-446-823A-1
	24	39.2	1.7	792	1	US-09-138-114-14
	25	39.2	1.7	792	1	US-08-446-823A-1
	26	39.2	1.7	792	1	PCT-US91-12586-14
	27	39.2	1.7	1316	1	US-08-446-823-7
	28	39.2	1.7	1316	1	US-08-446-823-7
	29	39.2	1.7	1316	1	US-08-446-823-7
	30	39.2	1.7	1316	1	US-08-446-823-7

Db 981 CTGAAAAGCTGTGCGCCCTCATGGAAGCCAGCCTCACCTATCCAGCCATGCTGTGCC 1040
Oy 902 TTTCGAACCTTGAAGCGGCAATCTTGAACCTTCAATCAATTTGCACAAAGCTATTATTTA 961
Db 1041 TTTCGAACCTTGAAGCGGCAATCTTGAACCTTCAATCAATTTGCACAAAGCTATTATTTA 1100
Oy 962 AGGCAAGATATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1019
Db 1101 AGGCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1160
Oy 1020 -ATGAACCCAGTTATGGAAGAGATGATGATGATGATGATGATGATGATGATGATGATG 1078
Db 1161 AATGAGTCCAGCTACAGCAGAGGATTTGACATGACGATGACGATGACGATGACGATGAC 1220
Oy 1079 TGTAATGAAGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1138
Db 1221 TGCAATGAAGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1280
Oy 1139 GATATCATGGGTACAACATCCTCAG 1164
Db 1281 GATATCATGGGTACAACATCCTCAG 1306

RESULT 6

US-08-795-876-32/c

; Sequence 32, Application US/08795876

; Patent No. 6403305

; GENERAL INFORMATION:

; APPLICANT: Gershengorn, Marvin C.

; APPLICANT: Geras-Raaka, Elizabeth

; APPLICANT: Nussenzveig, Daniel R.

; TITLE OF INVENTION: STRATEGY TO CLONE DRUGS FOR G PROTEIN

; TITLE OF INVENTION: COUPLED RECEPTORS

; NUMBER OF SEQUENCES: 44

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: NIXON, HARGRAVE, DEVANS & DOYLE LLP

; STREET: Clinton Square, P.O. Box 1051

; CITY: Rochester

; STATE: New York

; COUNTRY: USA

; ZIP: 14603

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/795.876

; FILING DATE:

; CLASSIFICATION: 530

; ATTORNEY/AGENT INFORMATION:

; NAME: BRAMAN, SUSAN J.

; REGISTRATION NUMBER: 34,103

; REFERENCE/DOCKET NUMBER: 19603/1280

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 716-263-1636

; TELEFAX: 716-263-1600

; INFORMATION FOR SEQ ID NO: 32:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1298 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: double

; TOPOLOGY: linear

; MOLECULE TYPE: cDNA

US-08-795-876-32

; Query Match 33.8%; Score 799.8; DB 4; Length 1298;

; Best Local Similarity 87.4%; Pred. No. 1e-237;

Matches 889; Conservative 0; Mismatches 122; Indels 6; Gaps 1;

Oy 1139 GATATCATGGGTACAACATCCTCAGGCTTGTATGATGATGATGATGATGATGATGATG 1198

Db 1023 GGTACCTGGGTACAACTCCTCAGAGTCTGATATGGTTTATCAGCATCCTGGCCATC 964
Oy 1199 ACTGGGAACACCAGAGTGGTGGTCTGACCAACAGCCCAATACAAACTAACTTGTGCC 1258
Db 963 ACTGGGAACATCATAGTGTCTTAACTACCAAGCCCAATAAACTCAGACTGCC 904
Oy 1259 CGGTTCTTATGTGTAACCTCGCCTTCGCTGATCTCTGCATAGGCACTACTGCTACTT 1318
Db 903 AGGTTCTTATGTGCAACCTGGCCTTTGCTGATCTCTGCATTTGGAATCTACTGCTC 844
Oy 1319 ATAGCATCAGTTGACATCCATACCAAGAGCCAGTACCACAACTATGCCATTTGACTGG 1378
Db 843 ATTGCATCAGTTGATATCCATACCAAGAGCCCAATACCAACTATGCGATGCGCTG 784
Oy 1379 ACAGGACGAGCTGTGATGCTGGCTTTTCTACTGCTCTTGGCAGTGAAGTGTCACT 1438
Db 783 ACTGGGACGAGCTGTGATGCTGGCTTTTCTACTGCTCTTGGCAGTGAAGTGTCACT 724
Oy 1439 TACACATTTGACAGCCATCACCTAGAAAGTGGCATACCATCACACATGCTATGCAACTG 1498
Db 723 TACACTCTGACAGCTATCACCTTGGAAAGATGGGATACCATCAGCATGCCATGCGCTG 664
Oy 1499 GAATGCAAGTGTGAGCTCCGGCATGCTGCCAGCTCATGTTGGGCTGGACTTTTGGCC 1558
Db 663 GACTGCAAGTGTGAGCTCCGGCATGCTGCCAGTGTCTGTTGGCTGGATTTTGGCT 604
Oy 1559 TTGCGAGCTGCTCTCTTCCCATCTTTGGCATCAGTAGCTACATGAAAGTGAAGTGTG 1618
Db 603 TTGCGAGCTGCTCTCTTCCCATCTTTGGCATCAGTAGCTACATGAAAGTGAAGTGTG 544
Oy 1619 CTGCCCATGGATATCGACAGCCCTTTGTACAGCTGTATGTTATGGCCCTCTCTGCTC 1678
Db 543 CTGCCCATGGATATGACAGCCCTTTGTACAGCTGTATGTTATGGCCCTCTCTGCTC 484
Oy 1679 AATGCTCGGCTTTGTGGTCACTGTGGTGTCTATACCCACATCTACTCTCACAGTGG 1738
Db 483 AATGCTCGGCTTTGTGGTCACTGTGGTGTCTATACCCACATCTACTCTCACAGTGG 424
Oy 1739 AATCCTACCATTTGTCTCTCATCAAGGACACCAAGATTTGCCAAGCGCATGCCCACATC 1798
Db 423 AACCCCAACATCGTGTCTCTCTAGTACACCAAGATTTGCCAAGCGCATGCCCACATC 364
Oy 1799 ATCTTCACAGACTTTCTCTGCTATGCCCCCATTTTCATTTTGGCCATTTCTGCCCTC 1858
Db 363 ATCTTCACAGACTTTCTCTGCTATGCCCCCATTTTCATTTTGGCCATTTCTGCCCTC 304
Oy 1859 AAGTGGCGCTCATCATCTGTCTCAAGGCCAAGATTTCTCTAGTGTCTCTTACCCCATC 1918
Db 303 AAGTGGCGCTCATCATCTGTCTCAAGGCCAAGATTTCTCTAGTGTCTCTTACCCCATC 244
Oy 1919 AATCTTGTGCGCAATCTCTCTCTACGCCATTTTCACCAAGAACTTTCCGAGGAGCTC 1978
Db 243 AACTCTGTGCGCAACCTCTCTCTATGCCATTTTACCAAAACTTTTCGCGAGAGATTTC 184
Oy 1979 TTTCATCTCTGTGAGCAAGTTTGGCTGTATGAAATGCAAGCCCAAGATTTTACAGGACAG 2038
Db 183 TTTCATCTCTGTGAGCAAGTTTGGCTGTATGAAATGCAAGCCCAAGATTTTATAGGACAG 124
Oy 2039 ACCTCATCCGTACCCACAACTTCCATGCCGGAAGAGCCACTGCTCTCAGTCTCCAGAG 2098
Db 123 ACTTCATCCACTGTCCCAACACCCATCCGCGGAATGGCCACTGCTCTTACGCTCCAGAG 64
Oy 2099 CTCACCAAT-----AGTTAGTGTCTTGTCTCTCTTATCATCTTATCCAGAGACTAA 2149
Db 63 GTCACCAATGTTCCACTTACATCTTGTCTCTCTTATAGTCTTATAGCCCCAAACTAA 7

RESULT 7

US-08-795-876-31

; Sequence 31, Application US/08795876

; Patent No. 6403305

; GENERAL INFORMATION:

; APPLICANT: Gershengorn, Marvin C.

Query Match	33.8%	Score 799.8	DB 4	Length 1300
Best Local Similarity	87.4%	Pred. No. 1e-237		
Matches 889	Conservative 0	Mismatches 122	Indels 6	Gaps 1
Oy	1139	GATATCATGGGTACACATCTCGTAGGCTCTGATATGCTTTATTTAGCATCTGGCCATT	1198	
Db	282	GGTTACTTGGGGTACACATCTCGTAGGCTCTGATATGGTTTTTTCACATCTGGCCATC	341	
Oy	1199	ACTTGGGAACACACAGTCTGGTGGCTCTGACCACAGGCCAATACAACTACTCTGCCC	1258	
Db	342	ACTTGGGAACCATATAGTCTGATGCTCTACTACCAGGCCAATATAACTCATCAGTCCCC	401	
Oy	1259	CGGTTTTCTATCTGTAACTTGGCCCTTTCGGTGTATCTGTCATAGGCATCTACTTCTCACT	1318	
Db	402	AGGTTTCCTTTATGTGCACACCTGGCCCTTTCGTGTATCTGTCATTTGGAACTACTCTCGTCTC	461	
Oy	1319	ATAGCATCATGTTTGACATCCATCCACAGAGCCAGTACACAACTATGCCATTGACTGGCNA	1378	
Db	462	ATTGCATCATGTTGATATCCCATACCACAGAGCCAATATACAACTATGCGGATCGACTGGCNA	521	
Oy	1379	ACAGGACAGGCTGTGATGCTGTGGCTTTTTTCACTGTCTTTGGCCAGTGAATCTCAGTC	1438	
Db	522	ACTTGGGGAGGCTGTGATGCTGTGGCTTTTTTCACTGTCTTTGGCCAGTGAAGTCTCAGTC	581	
Oy	1439	TACACATTTGACAGGCCATCACCTCATAGAAAGATGGCATAGCATACACATGATGCAACGTG	1498	
Db	592	TACTCTGTACAGCTATCATCTGTGGAAAGATGAGTACCATCATGCAATGCCATGACCTG	641	
Oy	1499	GAATCGAAGTGCATCTCGGCGATCGGAGGCTCATGTTATGCGGCTGAGTCTTGGCC	1558	
Db	642	GACTCGAAGGTGCACTCTCGGCGATCTGCGAGTGTGTCATGCTGTGATGGCTGGATTTTTGCT	701	
Oy	1559	TTGCGACAGCTCTCTCTTCCCCCATCTTTTGGCATCAGTAGCTACATGAAAGTGAGCATCTGC	1618	
Db	702	TTTGCAGCTGCGCTCTTTTCCCATCTTTGGCATCAGTACAGTACATGAGTGAAGCATCTGC	761	

1619 GTGGCCATGGATATGACGACAGCCCTTTGTGCACAGCTGTATGTATTATGGCCCTCTCTGTGCTCTC 1678

762 GTCCCATGATATGACGACAGCCCTTTGTGCACAGCTGTATGTATTATGGCCCTCTCTGTGCTCTC 821

1679 AATGTCCTGGCCCTTTGGTGCATCTCTGGCTGCTATACCCACAGATCTACCTACAGCTGAGG 1738

822 AATGTCCTGGCCCTTTGGTGCATCTCTGGCTGCTATATCCACATCTACCTCACAAGTSCGG 881

1739 AATCTCATCAATTTGTCCTCATCAAGCCGACACCAAGATTTGCCAAGCGCATGGCCACACTC 1798

882 AACCACCAATCTGGTCTCTCTGTAGTGACACAGATGCGCCAAGCGCATGGCCACACTC 941

1799 ATCTTCACAGACTTCTCTGCATATGGCCGCCCATTTCACTCTTTGGCCATTTCTGCCCTCCCTC 1858

942 ATCTTCACAGACTTCTCTGCATATGGCCGCCCATTTCTCTTTGGCCATTTCTGCCCTCCCTC 1001

1859 AAGTCGCGCTCATCTATCTGCGACAGCCCAATCTTTCTTTGGCCATTTCTGCCCTCCCTC 1918

1002 AAGTGGCCCTCATCACTCTGTGTCCTCAAGCGCAAGATTTCTGCTGGTCTGTGTTTCAACCCCATC 1061

1919 AATCTGTGCGCAATCTCTTCTCTACGCGCAATTTTCACACAGAGCTTCGCCGAGGAGCTTC 1978

1062 AACTCTGTGCCACCCCTTCTCTATGCCATCTTTTACGAAAAGCTTTTCGACAGAGATTTTC 1121

1979 TTATCTCTGCTGAGCAAGTTTGGCTGTATGAATGCAAGCCCAAGATTTACAGACAGAA 2038

1122 TTATCTCTGCTGAGCAAGTTTGGCTGTATGAATGCAAGCCCAAGATTTACAGACAGAA 1181

2039 ACTCATCCCTAGCCACCAACTTCCATTCGCGCCGAAGAGCCACTGCTCTCAGCTGCCAG 2098

1182 ACTCATCCACTGTGCTGACACACACCCATCCGCGGATGGCCCTCTCTTCTGCTGCCGAG 1241

2099 GTACCAAT-----AGTTAGTGTGTTGCTCTCTTAATCATTTATCATATCCGACAGACTAA 2149

1242 GTCACCAATGGTTCACCTATACACTTGTCTCTCTTAAGTCAATTTAGCCCAAACTAA 1298

RESULT 8

US-08-795-876-36

: Sequence 36, Application US/08795876

: Patent No. 6403305

: GENERAL INFORMATION:

: APPLICANT: Gershenorn, Marvin C.

: APPLICANT: Geras-Raka, Elizabeth

: APPLICANT: Nixxon, Hargrave

: TITLE OF INVENTION: STRATEGY TO CLONE DRUGS FOR G PROTEIN

: TITLE OF INVENTION: COUPLED RECEPTORS

: NUMBER OF SEQUENCES: 44

: CORRESPONDENCE ADDRESS:

: ADDRESSEE: NIXON, HARGRAVE, DEVANS & DOYLE LLP

: STREET: Clinton Square, P.O. Box 1051

: CITY: Rochester

: STATE: New York

: COUNTRY: USA

: ZIP: 14603

: COMPUTER READABLE FORM:

: MEDIUM: 3 1/2 inch floppy disk

: COMPUTER: IBM PC compatible

: OPERATING SYSTEM: PC-DOS/MS-DOS

: SOFTWARE: PatentIn Release #1.0, Version #1.30

: CURRENT APPLICATION DATA:

: APPLICATION NUMBER: US/08/795.876

: FILING DATE:

: CLASSIFICATION: 530

: ATTORNEY/AGENT INFORMATION:

: NAME: BRAMAN, SUSAN J.

: REGISTRATION NUMBER: 34,103

: REFERENCE/DOCKET NUMBER: 19603/1280

: TELECOMMUNICATION INFORMATION:

: TELEPHONE: 716-2641636

: TELEFAX: 716-2641600

: INFORMATION FOR SEQ ID NO. 36:

: SEQUENCE CHARACTERISTICS:

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; LENGTH: 1300 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-795-876-36

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Query Match 33.8%; Score 799.8; DB 4; Length 1300;
Best Local Similarity 87.4%; Pred. No. 1e-237;
Matches 889; Conservative 0; Mismatches 122; Indels 6;

Qy	1139	GATATCATGGGGTACAAACATCTCAGGGCTTGATATGTTTATATAGCATCTCGGCCATT	1198
Db	282	GGTTACCTGGGGTACAAACATCTCAGAGTCTGATATGGTTTATCAGCATCTCGGCCATC	341
Qy	1199	ACTGGGAACACCAAGTGTGGTGGCTTGACCACAAGCCAATACAAACTTAACCTGNGCC	1258
Db	342	ACTGGGAACATCATAGTGTAGTGATCCCTAACCTACCAAGCCAATATAAATCAGCTGCC	401
Qy	1259	CGGTTCTTTATGTATAACCTCGCTTTCGGTGATCTCTGCATAGGCATCTACTTGTACTT	1318
Db	402	AGGTTCTCTTATGTCAACCTGGCTTTGCTGATCTCTGCATTTGGAATCACTTGTCTGC	461
Qy	1319	ATAGCATCTTGACATCCATACCAAGAGCCAGTACCACAACATATGCCATTGACTGGCAA	1378
Db	462	ATTGCATTCAGTTGATATCCATACCAAGAGCCAATATCAAACTATGCGATCGACTGGCAA	521
Qy	1379	ACAGGAGCAGGCTGTGATGCTGTGGCTTTTTCACATGTCTTTGCCAGTGAACGTGCAGTC	1438
Db	522	ACTGGGCGAGCTGTGATGCTGTGGCTTTTTCACATGTCTTTGCCAGTGAACGTGCAGTC	581
Qy	1439	TACACATTGACAGCCATCACCTTAGAAGAATGGCATACCATCACATGCTATGCAACTG	1498
Db	582	TACACTCTGACAGCTATCACCTTAGAAGAATGGCATACCATCACAGATGGCATCGAGCTG	641
Qy	1499	GAATGCAAGTGCAGCTCCGGSCATGCTGCCAGCGCTATGATTTGGCTGGACTTTTGGC	1558
Db	642	GACTGCAAGTGCAGCTCCGCCATGCTGCCAGTGTATGTTGATGGCTGGATTTTGGCT	701
Qy	1559	TTGCGAGCTGCTCTTCTCCCATCTTTTGGCATCAGTAGCTACATGAAGTGAAGTGTGCTG	1618
Db	702	TTTGCAGCTGCGCTCTTTTCCCATCTTTTGGCATCAGCAGCTACATGAAGTGAAGTGTG	761
Qy	1619	CTGCCCATGGATATCGACAGCCCTTTGTGCACAGCTGTATGTTATGGCCCTCTTGTCTC	1678
Db	762	CTGCCCATGGATATTTGACAGCCCTTTTGTGCACAGCTGTATGTTATGGCCCTCTTGTCTC	821
Qy	1679	AATGCTCCTGGCTTTGTGGTGCATCTGTGGCTGCTATACCCACATCATACCTCACAGTGAGG	1738
Db	822	ATGTCCTGGCTTTGTGGTGCATCTGTGGCTGCTATATCCACATCATACCTCACAGTGCGG	881
Qy	1739	AATCCTTACCATTGTGCTCTCATCAAGCGACACCAAGATTCGCCAAGCGCATGGCCACACT	1798
Db	882	AACCCCAACATCGTGTCTCTCTAGTGACACAGGATCGCCAAGCGCATGGCCATGCTC	941
Qy	1799	ATCTTTCACAGACTTCTCTGCATGGCCCCCATTTTCATTTCTTGGCCATTTCTGCTCCCTC	1858
Db	942	ATCTTTCAGTACTTCTCTGCATGGCCCCCATTTCTTCTTGGCCATTTCTGCTCCCTC	1901
Qy	1859	AAGTGCCGCTCATCACTGTGTCCAAGGCCAAGATTTCTCTAGTTCTTGTGTTTACCCCATC	1918
Db	1002	AAGTGCCCTCATCACTGTGTCCAAGCAAGATTTCTGCTGGTTCTGTTTTCACCCCATC	1961
Qy	1919	AATTTCTGTGCAATTCCTTCTCTAGCCATTTTTCACCAAGAACTTTCCCGCAGGACTTC	1978
Db	1062	AACCTCTGTGCAACCCCTCTCTATATGCCATCTTTTACCAAAAACCTTTCCGACAGATTTC	1121
Qy	1979	TTATCTCTGCTGACCAAGTTTGGCTGTATGAATGCAAGCCAGATTTTACAGACAGAA	2038
Db	1122	TTCAATCTGCTGACCAAGTGTGGCTGTATGAATGCAAGCCCAAAATTTTATAGACAGAA	1181
Qy	2039	ACCTCATCCCGTACCCCAACTTCCATGCGCCGAAAGACCACTGCTCTCAGCTGCCAGA	2098

Qy	904	TGCAAACTTGAAGCGGCAAACTCTCTGAACTTCATCCAAATTTGCAACAAAGTCTATTTTTAAG	963
Db	771	TAGAAATTTG--CCAACAAAAGAACAGAAATTTTTCACATTTCCATTTTCTGAAAACTTTTTC	828
Qy	964	GCAAGATTATGATGATATGACTCAATTTGGGGATCAGAGAGTCTCTGTGAATGATGATGA	1023
Db	829	AAACAATGTGAAAGCACAGTAAGGAAGTAGTACAGTAACAAACACATTTATTTCTCCATGCTT	888
Qy	1024	ACCAGTTATGGMAAAGGATCTGACATGATGTACAATGAATTTGATTATGACATTATGTAA	1083
Db	889	GCTGAGAGTGAAGTGAAGTGGCTGGGACTATGAATATGTTTCTGCTTACCCAGACACCC	948
Qy	1084	TGAAGTTGTTGATGTGACCTGCTCACCAAGCCAGATGSCATTTTAATCCATGTGAAGATAT	1143
Db	949	CGA-----TGTGCTCTGAAACAGATGCTTTTAATCCCTGTGAAGACAT	992
Qy	1144	CATGGGTACAACTCTCAGGTCTTGATATGGTTTATTAGCATCTGCGCCATCTAGTG	1203
Db	993	TATGGGTATGACTTCCTTAGGTCCTGATTTGGCTGATTAATAATTTAGCCATCATGCGG	1052
Qy	1204	GAACACACAGTGTGTGTGCTTGACCAACAGCCAAATACAAACTAACTGTGCCCGGTT	1263
Db	1053	AAACATGACTGTCTTTTGTCTCTGACAGTCTTTTCAAACTTACAGTGGCTCGGTT	1112
Qy	1264	TCCTATGTGAACCTCGCCCTTCGCTGATCTCTGCATAGGCATCTACTTGTACTTATAGC	1323
Db	1113	TCTCATGTGCAATCTCTCCTTTGACAGACTTTTGACATGGGCTCTATCTGCTGCTCATAGC	1172
Qy	1324	ATCAGTTGACATCCATACCAAGACCGAGTACACACAATATGCCANTGACITGGCAACAGG	1383
Db	1173	CTCAGTTGATTTCCCAACCAAGGSCCACTACTATAACCATGCCATGACACTGGCAGACAGG	1232
Qy	1384	AGCAGGCTGTGATGCTGCTGGCTTTTTCACCTGTCTTTGCCAGTGAACCTGTCAAGTCTACAC	1443
Db	1233	GAGTGGGTGCAGCACTGCTGGCTTTTTCACCTGTATTCGCAAGTGAACCTTTCTGTCTACAC	1292
Qy	1444	ATTGACAGCCATCACCTAGAAAGATGGCATACCATCACACATGCTATGCAACTGGAATG	1503
Db	1293	CCTCACCGTCTACTCTAGAAAGATGGCACACCATCACCTATGCTATTCACTGGGACCA	1352
Qy	1504	CAAGGTGCAGTCCGGCATGCTGCCAGCTCATGGTATTGGGCTGGAGCTTTTGGCTTCGC	1563
Db	1353	AAAGCTCGGATTAAAGACATGCCATCTCGATTATGCTTTGGAGGATGGCTCTTTTCTCTCT	1412
Qy	1564	AGCTGCTCTCTTCCCATCTTTGGCAGTCAGTAGCTACATGAAAGTAGAGCATCGCCGTC	1623
Db	1413	AAATGCTATGTTGCCCTTGTGGGTGTCAGCAATTACATGAAGGTGAGTATTGCTTTCCC	1472
Qy	1624	CATGGATATCGACAGCCCTTTGTGCAGCTGTATGTTATGGCCCTCCTTGTCTCAATGT	1683
Db	1473	CATGGATGTGMAAACCACTCTCACAAAGTCTATATATTAACCATCCTGATTTCTCAATGT	1532
Qy	1684	CTTGGCCCTTTGCTGTCATCTGTGGCTGCTATACCCACATCTACCTCACAGTAGGAATCC	1743
Db	1533	GGTGGCCCTCTCTCAATAATTTGTGCTGCTACATTAATAAATTTATTTTGCAGTTCGAAACCC	1592
Qy	1744	TACCATTGTGCTCATCAAGCGACACCAAGATTGCCAAGCATGCCACACCTCATCTT	1803
Db	1593	AGAATTAATGGCTACCATAATAGATACAAAGATTGCTAAGAAATGGCAATCCTCATCTT	1652
Qy	1804	CACAGACTTCTCTGCAATGCGCCCACTTTCATTTCTTTTGGCATTTCTGCTCCCTCAAGGT	1863
Db	1653	CACCGATTTCACTGCAATGCGACCTATCTCTTTTGGCCATCTCAAGTTCGCTTCAAGT	1712
Qy	1864	GCCTCATCATGTGTCCCAAGGCCAGATCTCCTAGTTCTGTTCTACCCCATCAATTC	1923
Db	1713	ACCTCTTATCACAGTAACCAACTCTAAAGTTTACTGGTTCTTTTTTATCCCATCAATTC	1772
Qy	1924	TTGTGCCAATCTTCTCTACGCCATTTTTCACCAAGAACTTCGCGAGGACATCTTTCAT	1983
Db	1773	TTGTGCCAATCCATTTCTGTATGCAATATTTCACTAAGACATTTCCAAAGAGATTTCTTTCT	1832
Qy	1984	CTGCTGAGCAAGTTTGGCTGTTATGAATGCAAGCCCAAGATTTTACAGGACAGAAACCTC	2043

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Db      1833 TTGCTCAGCAAAATTTGGCTGCTGTAAACGTCGGCTGAACCTTTATAGAAGAAAGATTT 1899
Qy      2044 ATCCGCT 2050
Db      1893 TTCAGCT 1899

RESULT 11
US-07-757-342D-1
; Sequence 1, Application US/07757342D
; Patent No. 6218509
; GENERAL INFORMATION:
; APPLICANT: IGARASHI, Masao
; MINEGISHI, Takashi
; NAKAMURA, Kazuto
; TITLE OF INVENTION: PROTEIN, DNA AND USE THEREOF
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DAVID G. COMLIN; DIKE, BRONSTEIN, ROBERTS & CUSHMAN
; STREET: 130 Water Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: US
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/757,342D
; FILING DATE: 10-Sep-1991
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: BUCKLEY, Landa M.
; REGISTRATION NUMBER: 31003
; REFERENCE/DOCKET NUMBER: 41226
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)523-3400
; TELEFAX: (617)523-6440
; TELEX: 200291 STRE UR
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2987 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..2097
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-07-757-342D-1

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	Query Match	28.0%;	Score 663;	DB 4;	Length 2987;	
	Best Local Similarity	61.8%;	Pred. No. 4.4e-195;			
	Matches 1116;	Conservative	0;	Mismatches 670;	Indels 21;	Gaps 3;
QY	247	AGTCATCCCGAAGGATCATTTCTGGATTGGAGACCTGGAGAAAATAAGAGATCTCTCA	306			
Db	186	AGTGATCCCCATCTCAAGCTTTCAGAGGACTTAATGAGGTCTATAAAAATTGAAATCTCTCA	245			
QY	307	GAATGATGTCCTTGGAAAGTAATAGAGGCAGATGTGTTCTCCAAGCTACCACAAGTTGGCATCA	366			
Db	246	GATTGATTCCTCGAAAGGATAGAAGCTAATGCCCTTTGACAACCTCCTCAATTTGTCTCA	305			
QY	367	AATTAGGATTGAAAGGCCAACAAATCTTCTGTACATCAACCCGGAGGCCTTCAGAAATCT	426			
Db	306	AATCTACTCCAGAACACCAAATAATCTGAGATCANTTTGAGCCGGGAGCATTTATAATAATCT	365			
QY	427	CCCAGTGCTCAGATATCTGTGTTAATATCCAAACACAGGCATTAAAGCACTTGCACGCTCTTCA	486			

Db		1428	AAMGCTGGGATTAAGACATGGCAATCTGTGATATAGCTTGGAGATGGCTCTTTTCTCTCTCT	1487
Qy		1564	ACCTGCTCTCTTCCGCAATCTTTGGCATACGACTACATGAAAGTAGACATCGCTGGCC	1623
Db		1488	AATTCATGCTTGGCCCTTCTGGGTGTCAGCAATATCATAGAGTCAGTATATGTTCCCC	1547
Qy		1624	CATGGATATCGACAGCCCTTTGTCCACAGCTGTATGTATGGCCCTCTCTCTCTCAATGCT	1683
Db		1548	CATGGATGTGGAACCACTCTCTCCACAGCTCATATATTAACCCATCTGATATCTCAATGCT	1607
Qy		1684	CTTGCCCTTTTGTGTCATCTGTGGCTGGCTATACCACATCTACCTACAGTCAGGAAGTCC	1743
Db		1608	GGTGGCCCTCTTCATTAATTTGTGCTTGCTGCTACATTAATAATTTATTTGGCGTTTGGAAACC	1667
Qy		1744	TACCAATTGTGCTCTCATCAAGCGACACCAAGATTTGCCAAGCGCATGGCCACACATCATCTTT	1803
Db		1668	AGAAATTAATGGCTACCAATAAAGATACAAAGATTTGCTAAGAAATGGCAATCTCATCTTT	1737
Qy		1804	CACAGACTTTTCTCTGCAATGGGCCCCCAATTTTCATCTTTTGCCATTTCTGCCTCCCTCAAGGT	1863
Db		1728	CACCGATTTTCACCTGCAATGGGCACCTATCTCTTTTTTGGCCATCTCAGCTGCCCTTCAAGGT	1787
Qy		1864	GGCGCTCATCACTGTGTCACAGGCCAAGATTTCTCTAGTTCTGTCTTACCCCATCAATTC	1923
Db		1788	ACCTCTATATACAGATAACCACTCTAAAGTTTACTTGGTGTCTTTTTTATCCCAACAATTC	1847
Qy		1924	TGTGGCAATCTTCTCTCTAGGCAATTTTTCACCAAGAACTTCCGCAAGGACTTCTTCTCAT	1983
Db		1848	TGTGCAATCCATTTCTGTATGCAATATTCATCAAGACATTTCCAAAGACATTTCTTTCT	1907
Qy		1984	CTGTGCGCAAGTTTGGCTGTATGAATTCGACGCCCAAGTTTTCAGGACAGAACCTTC	2043
Db		1908	TTTGTGTGCAAAATTTGGCTGCTTAAGCTGTGGGCTGACATCTTATAGAGGAAGAATTT	1967
Qy		2044	ATCCGCT 2050	
Db		1968	TTCACT 1974	

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1  RESULT 12
2  US-07-741-453A-57
3  : Sequence 57, Application US/07741453A
4  : Patent No. 6228557
5  : GENERAL INFORMATION:
6  : APPLICANT: PARMENTIER, MARC
7  : APPLICANT: LIBERT, FREDERIC
8  : APPLICANT: DUMONT, JACQUES
9  : APPLICANT: VASSART, GILBERT
10 : TITLE OF INVENTION: POLYPEPTIDES HAVING THYROTROPIN-RECEPTOR
11 : TITLE OF INVENTION: ACTIVITY, NUCLEIC ACID SEQUENCES CODING FOR SUCH RECEPTORS
12 : TITLE OF INVENTION: AND POLYPEPTIDES, AND APPLICATIONS OF THESE POLYPEPTIDES
13 : NUMBER OF SEQUENCES: 62
14 : CORRESPONDENCE ADDRESSES:
15 : RESSLER, ROSEMARY, DABRY & CUSHMAN
16 : STREET 1615 STREET, N.W.
17 : CITY, WASHINGTON, D.C.
18 : COUNTRY: U.S.A.
19 : ZIP: 20036
20 : COMPUTER READABLE FORM:
21 : MEDIUM TYPE: Disk
22 : COMPUTER: IBM PC compatible
23 : OPERATING SYSTEM: PC-DOS/MS-DOS
24 : SOFTWARE: PatentIn Release #1.0, Version #1.25
25 : CURRENT APPLICATION DATA:
26 : APPLICATION NUMBER: US/07/741,453A
27 : FILING DATE: 19911015
28 : CLASSIFICATION: 435
29 : ATTORNEY/AGENT INFORMATION:
30 : NAME: WILLIAM H. KIRK, JR.
31 : REGISTRATION NUMBER: 16673
32 : REFERENCE/DOCKET NUMBER: 91913/1107/US/ST
33 : TELECOMMUNICATION INFORMATION:
34 : TELEPHONE: (202) 861-3000

```

TELEFAX: (202) 822-0944
TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
LENGTH: 4417 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-07-741-453A-57

Query Match 18.9%; Score 447.8; DB 4; Length 4417;
Best Local Similarity 66.3%; Pred. No. 3e-128;
Matches 644; Conservative 0; Mismatches 327; Indels 0;

Matches	644; Conservative	0; Mismatches	327; Indels	0; Gaps	0
QY	1062	AATTGATATGACTTATGTAATGAAGTCTGTTGATGTGACCTGCTACCAAGCCAGATG	1121		
Db	1213	ATTATGACTACACTGTGTGGTGGCAATGAAGACACATGCTGTACTCTCAAGTCAGATG	1272		
QY	1122	CATTTAATCCATGTGAAGATATCATGGGTACAAACATCCTCAGGCTTCATGATGTTTA	1181		
Db	1273	AGTTCAACCCCTGTGAAGACATTAATGGCTTACAAGTTCCTTGAGGATGTGGTGTGGTTG	1332		
QY	1182	TTAGCATCTCGGCCATTACTGGGAACACCAACAGTGTGGTGGTCTTGACACCAAGCCAAT	1241		
Db	1333	TTAGTCTGTGGCTCTCTGGGCAATGCTTTGTCTGTGATCGTCTCTCTTACCAGTCACT	1392		
QY	1242	ACAACTAAGTGTGCCCCGGTTTCTTATGTGTAACTTGGCTTGGCTGTGATCTCTGCAATAG	1301		
Db	1393	ACAAATTGAGTGTCCCAACGCTTTCTCATGTGCAACTTGGCTTTTGCAGATTTCTGCATGG	1452		
QY	1302	GCATCTACTTGTCTACTTATAGCATCAGTTGCACATCCATACCAAGAGCCAGTACCACAACCT	1361		
Db	1453	GGATGTATCTGCTCTCTCTGCGCTCGGTAGACCTCTACACTCATTTGAGTACTACAAACC	1512		
QY	1362	ATGCCATTGACTGGCAAAACAGGACGGCTGTGATGCTGTGGCTTTTTCACCTGTCTTTTG	1421		
Db	1513	ATGCCATCGACTGGCAGACAGGCCCTGGGTGTAAACACAGCTGGTTCCTTCCACCTGTCTTG	1572		
QY	1422	CCAGTGAACCTCAGCTACACATATTGACACCCATACCCCTAGAAGATGGCATACCATCA	1481		
Db	1573	CCAGTGAATTTATCAGTGTATACACTGACATCTCATCCCTGGAGCGCTGGTATGCCAATTA	1632		
QY	1482	CACATGCTATGCAACTGGAAATGCAAGGTGCAGCTCCGGCATGTGCCAGCGTCTATGTAT	1541		
Db	1633	CCTTCCGCATGCGCCTGGACAGAGATCCGCTCAGGCATGATATGCCATCATGGTTG	1592		
QY	1542	TGGGCTGGACTTTTGGCTTCGCAAGCTGCTCTCTTCCCAATCTTTGGCATCAGTAGCTACA	1601		
Db	1693	GGGGCTGGGTTTGTGCTTCTGCTGCCCTGTCTCCCTCTGCTGGTGGGAATGAAGCAGCTATG	1752		
QY	1602	TGAAGTGTGACATCTGCTCGCCATGATATCGACAGCCCTTTGTGCACAGCTGTATGTTA	1661		
Db	1753	CCAAGTGCAGATCTGCTCGCCCATGGACACTGAGACACCTCTTGGCCCTGGCATATATTA	1812		
QY	1662	TGGCCCTCTCTGCTCAATGTCTCGCCCTTTGTGTCTCATCTGTGGCTGCTATACCCACA	1721		
Db	1813	TCCTTGTCTCTGTGCTCAACATAGTTGCCCTTTATCATTTGCTGCTCTGTTATGTGAAGA	1872		
QY	1722	TCFACCTCAGCTGAGGAATCTTACCAATTTGTGTCTCATCAAGGGACCAAGATGGCCA	1781		
Db	1873	TCFACATCAGATCCGAAATTCGCCAGTACAAACCCGGGGGACAAAGACCAAAATGGCCA	1932		
QY	1782	AGCGCATGGCCACACTCATCTTCACAGACATTTCTCTGCATGGCCCCCATTTTCATCTTTG	1841		
Db	1933	AAAGGATGGCTGTATTGATCTTCACTGACTTCATGTGCATGGCCCCCAATCTCATTTCTACG	1992		
QY	1842	CCATTTCTGCTCCCTCAAGGTCCGCTCATCACTGTGTCCAAGGCCAAGATTTCTCCCTAG	1901		
Db	1993	CTCTGTGAGCATTATGAACAAGCCTCTCATCACTGTTACCAACTCCAAANTCTTGCTGG	2052		
QY	1902	TTCTGTCTACCCGATCAATTTCTTGTGGCCAAATCCTTTTCTTACGCCATTTTTCACCAAGA	1961		

RESULT 13

US-07-741-453A-62
Sequence 62, Application US/07741453A
Patent No. 6228597
GENERAL INFORMATION:
APPLICANT: PARMENTIER, MARC
APPLICANT: LIBERT, FREDERIC
APPLICANT: DUMONT, JACQUES
APPLICANT: VASSART, GILBERT
TITLE OF INVENTION: POLYPEPTIDES HAVING THYROTROPIN-RECEPTOR
TITLE OF INVENTION: ACTIVITY, NUCLEIC ACID SEQUENCES CODING FOR SUCH RECEPTORS
TITLE OF INVENTION: AND POLYPEPTIDES, AND APPLICATIONS OF THESE POLYPEPTIDES
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHMAN DARBAY & CUSHMAN
STREET: 1615 L STREET, N.W.
CITY: WASHINGTON, D.C.
COUNTRY: U.S.A.
ZIP: 20036
COMPUTER READABLE FORM:
MEDIUM TYPE: Disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/741,453A
FILING DATE: 19911015
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: KOKULIS, PAUL N.
REGISTRATION NUMBER: 16773
REFERENCE/DOCKET NUMBER: 91913/1107/US/ST
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 861-3000
TELEFAX: (202) 822-0944
TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO: 62:
SEQUENCE CHARACTERISTICS:
LENGTH: 3710 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-07-741-453A-62

Query Match	18.8%	Score 445.8	DB 4	Length 3710
Best Local Similarity	66.0%	Pred. No. 1.1e+127		
Matches 645	Conservative 0	Mismatches 332	Indels 0	Gaps 0
QY	1056	ACAATCAATTGATTATGACTTATGTAATGAAGTTCTGTGATGTGACCTGCTCACCAAGC	1115	
Db	1477	ACAGCATTTATGACTACACCATATGTGGGACAGTCAAGACATGTGTGTACCCCCAAGT	1536	
QY	1116	CAGATGCATTTAATCCATGTGAAGATATCATGGGTACAACTCCAGGGTCTTGATAT	1175	
Db	1537	CCGATCAGATTCAACCGCTGTGAAGACATAATGGGTACAAGTTCTTGAGAATTTGTGCTGT	1596	
QY	1176	GGTTTATTAGCATCCGTGCCATTACTGGGAACACACAGTGTGGTGGTCCGTGACCACAA	1235	
Db	1597	GGTTCGTATGTCGTGGCTTCCTCTGGGCAATGCTTTGTCTGCTGTTATTCCTCTCACC	1656	
QY	1236	GCCAAATACAAACTAAGCTGCCCCGGTTCTTATGTGTAACTCGCCTTCGGTGTACTCT	1295	


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: TITLE OF INVENTION: NOVEL 7TM RECEPTOR (H2CAA71)
:
: NUMBER OF SEQUENCES: 4
:
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: RATNER & PRESTIA
: STREET: P.O. BOX 980
: CITY: VALLEY FORGE
: STATE: PA
:
: COUNTRY: USA
: ZIP: 19482
:
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette
:
: COMPUTER: IBM Compatible
:
: OPERATING SYSTEM: DOS
:
: SOFTWARE: FastSeq for Windows Version 2.0
:
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/866,757
: FILING DATE: 30-MAY-1997
:
: CLASSIFICATION: 536
:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER:
:
: FILING DATE:
:
: ATTORNEY/AGENT INFORMATION:
: NAME: PRESTIA, PAUL F
:
: REGISTRATION NUMBER: 23,031
:
: REFERENCE/DOCKET NUMBER: GH-70055
:
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 610-407-0700
:
: TELEFAX: 610-407-0701
:
: TELEX: 846169
:
: INFORMATION FOR SEQ ID NO: 1:
:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 4203 base pairs
:
: TYPE: nucleic acid
:
: STRANDEDNESS: single
:
: TOPOLOGY: linear
:
: MOLECULE TYPE: cDNA
:
: US-08-866-757-1

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	Query Match	2.78;	Score 64.6;	DB 2;	Length 4203;
	Best Local Similarity	43.08;	Pred. No. 1.9e-09;		
	Matches 371; Conservative	0;	Mismatches 489;	Indels	Gaps 1;
QY	1103	TGCTCACCAAGGCAGATGCATTAAATCCATGTGAAGATATCATGGGTACACAATCCTC	1162		
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Db	1126	TGTACACTTCAACAGGTGCTTTTAAGCCCTGTGAATATTTACTGGGAAGCTGGATGATT	1185		
QY	1163	AGGGTCCTTGATATGGTTTTATTAGCATCCTCGCCATTACTGGGAACACCACAGTGCCTGGTG	1222		
		JJ			
Db	1186	CGTCTTACTGTGGTTCAATTTCTGGTTGCCATTATTTTTCARCCCTGCTGTATTATTTA	1245		
QY	1223	GTCTTGACCACAGCCCAANTCAAACHTAACCTGTGCCCCGGTTCTTATGTGTAAACCTCGCC	1282		
		JJ			
Db	1246	ACAACATTTTCATCTTGTAGCATCACTGCCCTCGTCCAATTTGTTTATAGGCTTGATTTCT	1305		
QY	1283	TTGCTGCATCTCGCATAGGCATCTACTTCTACTTATACATCAAGTTGACATCCATAACC	1342		
		JJ			
Db	1306	GTGTCTAACTATTTCATGGGAATCTATFACCTGGCATCTCTAACTTTCTTGATGCTGTGTC	1365		
QY	1343	AAGAGCCAGTACCACAACTATGCCATTGACTTGGCAAACAGGAGCAGCTGTGATGCTGCT	1402		
		JJ			
Db	1366	TGGGGCAGATTCGCTGAATTTGGCAATTTGGTGGGAAGCTGGCAGTGCCTGCAAGTNACT	1425		
QY	1403	GGCTTTTTCAGTCTTTTGGCAGTGAAGCTGTCACTGTACACTTACAGCATTCACACCTA	1462		
		JJ			
Db	1426	GGGTTCCTTGCAGTTTTTCTCCTCAGAAGTGGCCATATTTTTTAAATGCTAGCAACTGTC	1485		
QY	1463	GAAGAATGGCATACCATCACATGCTATGCAACTGGAAATGCAAGSTGCAGCTCCGGSCAT	1522		
Db	1486	GAAGAAGCTTATCTGCAAAAAGATATAATCAAAAAATGGGAAGAGCAATCATCTCAACACAG	1545		
QY	1523	GCTGCCAGCGTCATGGTATTGGGCTGGACATTTTTCCTTCGACGTGCTCTTCCTCCCGCAT	1582		
		JJ			
Db	1546	TTCCGGGTGCTGCCCTTTTGGCTTTTCTTAGTGCTACAGTAAACAGGCTGTTTTTCCCCTT	1605		

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 16, 2003, 07:25:51 : Search time 2993 Seconds
(without alignments)
12802.714 Million cell updates/sec

Title: US-09-877-804-5

Perfect score: 2366

Sequence: 1 agagactctgggaattctgtg.....aaccaagcaaacaccgcaca 2366

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapert 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum Match 100%

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

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1:  em_estba:.*
2:  em_esthum:.*
3:  em_esthu:.*
4:  em_estov:.*
5:  em_estov:.*
6:  em_estpl:.*
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8:  em_hic:.*
9:  gb_est1:.*
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23: em_gss_nam:.*
24: em_gss_mus:.*
25: em_gss_other:.*
26: em_gss_pro:.*
27: em_gss_rod:.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2037.6	85.7	2360	11 AK016635	Mus musculus
2	619	26.2	703	17 BH029943	BH029943 RPCI-24-2
3	465.6	19.7	598	13 BM483278	BM483278 336539 MA
4	459.8	19.4	3015	11 AK014519	AK014519 Mus muscu
5	444	18.8	548	12 BF075894	BF075894 225322 MA
6	345.4	14.6	663	13 BM439989	BM439989 pgrin.pk0

7	306	12.9	591	13	BI186370	BI186370 UNL-P-FN-
8	305.4	12.9	711	13	BI185789	BI185789 UNL-P-FN-
9	282	12.1	253	10	AW558284	AW558284 42342 MAR
10	282	12.1	253	10	AW558284	AW558284 42342 MAR
11	228.2	9.6	1842	13	BM161409	BM161409 RCO-H7061
12	218.2	9.2	676	10	BM553437	BM553437 AGSCCORT
13	210.4	8.9	294	10	BM553437	BM553437 AGSCCORT
14	208.8	8.8	885	13	CNS03007	AL222734 Tetradon
15	181.4	7.7	1113	13	BM454054	BM454054 AGENCOURT
16	181.4	7.7	473	12	BF891227	BF891227 PM2-MT010
17	167.6	7.1	637	10	BM281564	BM281564 BB281564
18	161	6.8	392	17	AZ17827	AZ17827 RPCI-24-1
19	159.4	6.7	366	17	AZ17827	AZ17827 RPCI-24-1
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21	152.4	6.4	702	10	BB617484	BB617484 BB617484
22	141	6.0	181	13	BM484173	BM484173 537925 MA
23	134	5.7	302	17	AF455800	AF455800 AF455800
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26	106.2	4.5	303	17	AZ17827	AZ17827 RPCI-24-1
27	106.2	4.5	303	17	AZ17827	AZ17827 RPCI-24-1
28	100.2	4.2	1087	9	CNS0589Y	AL222734 Tetradon
29	98.6	4.2	568	13	BI508344	BI508344 RCI-24-1
30	96.2	4.1	427	12	BF523207	BF523207 UI-R-C3-8
31	89.4	3.8	437	12	BF523207	BF523207 UI-R-C3-8
32	87.6	3.7	761	12	BF036966	BF036966 601456712
33	84.8	3.6	913	17	CNS0404E	AL299543 Tetradon
34	83.2	3.5	628	13	BJ126800	BJ126800 BJ126800
35	82.2	3.5	932	11	AK021020	AK021020 Mus muscu
36	82	3.5	573	13	BI630907	BI630907 RH60250.5
37	82	3.5	610	13	BI628622	BI628622 RH57122.5
38	81.2	3.4	1101	17	CNS0181F	AL108765 Drosophila
39	80.6	3.4	397	10	AW174149	AW174149 FI39907.Y
40	79.8	3.3	515	9	AW177137	AW177137 EST220744
41	77.2	3.2	327	12	BE707642	BE707642 PM1-HF052
42	75.4	3.2	1891	17	CNS050AM	AL053719 Drosophila
43	75.4	3.2	1891	17	CNS050AM	AL053719 Drosophila
44	74.2	3.1	465	13	BI782833	BI782833 Tetradon
45	74	3.1	249	10	BB608621	BB608621 BB608621

ALIGNMENTS

RESULT 1	AK016635	2360 bp	linear	HTC 19-JAN-2002
LOCUS	Mus musculus adult male testis cDNA, RIKEN full-length enriched library, clone:4933403107:follicle stimulating hormone receptor, full insert sequence.			
DEFINITION	AK016635			
ACCESSION	AK016635	1	GI:12855479	
VERSION	AK016635			
KEYWORDS	HTC; CAP; trap; testis			
SOURCE	Mus musculus (strain:C57BL/6J) adult male testis cDNA to mRNA, clone:4933403107			
ORGANISM	Mus musculus			
REFERENCE	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.			
AUTHORS	Carninci, P. and Hayashizaki, Y.			
TITLE	High-efficiency full-length cDNA cloning			
JOURNAL	Meth. Enzymol. 303, 19-44 (1999)			
MEDLINE	99279253			
PUBLISHED	2	10349636		
REFERENCE	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, N., Kono, H., Ohtsuka, Y., Muramatsu, M. and Hayashizaki, Y.			
AUTHORS	Normalization and subtraction of cDNA libraries to generate full-length cDNA libraries for rapid discovery of new genes			
TITLE	Genome Res. 10 (10), 1617-1630 (2000)			
JOURNAL	20499374			
MEDLINE	11042159			
PUBLISHED				

Dh	242	TCATTCCAAAGGATCATTTTCTGGATTTCGGGACCTGGAGAAATAGAGATCTCTCA	301
Oy	309	ATGATGCTTTGGAGTAATAGAGGAGATGCTGCTCCAACTACCAAGTGGATGAA	368
Dh	302	ATGATGCTTTGGAGTAATAGAGGAGATGCTGCTCCAACTACCAAGTGGATGAA	361
Oy	369	TTAGGATGAAAGGCGCAACAACTTTCTGTACATCAACCGGAGGCTTCCGACTCC	428
Dh	362	TTAGGATGAAAGGCGCAACAACTTTCTGTACATCAACCGGAGGCTTCCGACTCC	421
Oy	429	CAAGTCTAGATCTGTAAATATCCAAACAGGCAATTAAGCACTTCCGAGCTGTCA	488
Dh	422	CAAGTCTAGATCTGTAAATATCCAAACAGGCAATTAAGCACTTCCGAGCTGTCA	481
Oy	489	AGATCCAGTCTCCAAAGGCTTCTAGACATCAAGATCAAGATCAAGATCAAGAT	548
Dh	482	AGATCCAGTCTCCAAAGGCTTCTAGACATCAAGATCAAGATCAAGATCAAGAT	541
Oy	549	TTGCCAGGAACTCTCATGAGGAGTGTGTTGAAGTGTGATTTATGGCTGACGA	608
Dh	542	TTGCCAGGAACTCTCATGAGGAGTGTGTTGAAGTGTGATTTATGGCTGACGA	601
Oy	609	ATGGATGAGAAATACAACTGTGCTTCAACGGAACAGCTAGATGAATGAATC	668
Dh	602	ATGGATGAGAAATACAACTGTGCTTCAACGGAACAGCTAGATGAATGAATC	661
Oy	669	TAAGGATACAAATATTTGGAAGATTTGCTTAATGACCTTTTCCAGGGAGCTCTGG	728
Dh	662	TAAGGATACAAATATTTGGAAGATTTGCTTAATGACCTTTTCCAGGGAGCTCTGG	721
Oy	729	CAGTCATTTAGATATCTCAGGCAAGAGGCTGCTTACCAACAGGCTGTTTGA	788
Dh	722	CAGTCATTTAGATATCTCAGGCAAGAGGCTTACCAACAGGCTGTTTGA	781
Oy	789	ATCTGAAGAGCTGAGGGCAGCTGACATACACCTGTTGAAAGCTCCCTAATCT	848
Dh	782	ATCTGAAGAGCTGAGGGCAGCTGACATACACCTGTTGAAAGCTCCCTAATCT	841
Oy	849	AGTTTGTCACTGAGGCGGAGCTGACATACACCTGAGGAGCTGCTGCTTTTGA	908
Dh	842	AGTTTGTCACTGAGGCGGAGCTGACATACACCTGAGGAGCTGCTGCTTTTGA	901
Oy	909	ACTGAGGCGCAATCTGCACTTCACTCAATTTCCCAAGTCTATTTAAGGCA	968
Dh	902	ACTGAGGCGCAATCTGCACTTCACTCAATTTCCCAAGTCTATTTAAGGCA	961
Oy	969	ATATTGATGATATGACTCAATTTGGGAGTCAAGAGTCTCTGATAGATGATGA	1028
Dh	962	ATATTGATGATATGACTCAATTTGGGAGTCAAGAGTCTCTGATAGATGATGA	1021
Oy	1029	GTTATGGAAGAGTCTGACATGATGATCAATTTGATTTATGACTTATGATGAG	1088
Dh	1022	GTTATGGAAGAGTCTGACATGATGATCAATTTGATTTATGACTTATGATGAG	1081
Oy	1089	TTGTTGATGACTGCTGCTCAACAAAGCCAGATGCAATTTAATCCATGTGAAGAT	1148
Dh	1082	TTGTTGATGACTGCTGCTCAACAAAGCCAGATGCAATTTAATCCATGTGAAGAT	1141
Oy	1149	GATACACATCTCAGGCTCTGATATGGTTTATAGCATCTGGCCATATCTGGGA	1208
Dh	1142	GATACACATCTCAGGCTCTGATATGGTTTATAGCATCTGGCCATATCTGGGA	1201
Oy	1209	CACAGTGTGCTGCTGCTCAGCAGCAAGCCATACCAACTGCTGGCGGTTTCTA	1268
Dh	1202	CACAGTGTGCTGCTGCTCAGCAGCAAGCCATACCAACTGCTGGCGGTTTCTA	1261
Oy	1269	TGTGTAACCTTCCGCTGCTGCTCAGCAGCAAGCCATACCAACTGCTGCTAT	1328
Dh	1262	TGTGTAACCTTCCGCTGCTGCTCAGCAGCAAGCCATACCAACTGCTGCTAT	1321
Oy	1329	TTGACATCCATACCAAGGCGGCTACCAACTATGCCATTTGACTGGCAACAGGAG	1388
Dh	1322	TTGATATCCATACCAAGGCGGCTACCAACTATGCCATTTGACTGGCAACAGGAG	1381

Oy	1389	GCTGTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1448
Dh	1382	GCTGTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1441
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Dh	1442	CAGCATTACCTTAGAAGATGGCATACATACATACATACATACATACATACATAC	1501
Oy	1509	TGAGCTCTGGGATGCTGCGGAGCTCATGTATTTGGGCTGGAGCTTTGCTTGG	1568
Dh	1502	TGAGCTCTGGGATGCTGCGGAGCTCATGTATTTGGGCTGGAGCTTTGCTTGG	1561
Oy	1569	CTCTCTTCCCATCTTTGGCATCAGTAGCTACATGAAGTGGAGCTGCTGCTGG	1628
Dh	1562	CTCTCTTCCCATCTTTGGCATCAGTAGCTACATGAAGTGGAGCTGCTGCTGG	1621
Oy	1629	ATATGAGAGGCTTTGTCAGAGCTGTATGTTATGGGCTCTTGTCTCAATGCTG	1688
Dh	1622	ATATGAGAGGCTTTGTCAGAGCTGTATGTTATGGGCTCTTGTCTCAATGCTG	1681
Oy	1689	CCTTTTGGTATCTCTGGGCTGTATACCCACATCTACCTACAGTAGGAGTCT	1748
Dh	1682	CCTTTTGGTATCTCTGGGCTGTATACCCACATCTACCTACAGTAGGAGTCT	1741
Oy	1749	TTGTGCTCTCATCAAGGAGCAACCAAGATTTGCCAAGGCGCATGGCCACAT	1808
Dh	1742	TTGTGCTCTCATCAAGGAGCAACCAAGATTTGCCAAGGCGCATGGCCACAT	1801
Oy	1809	ACTTCTCTGCAATGGGCGCCCATTTCTTTCATTTTGGCTTCTTCCAGGCTG	1868
Dh	1802	ACTTCTCTGCAATGGGCGCCCATTTCTTTCATTTTGGCTTCTTCCAGGCTG	1861
Oy	1869	TGATCACTCTGTGCGAGGCGAGATGCTGTAGTGTGTCTACGCCATCAATCT	1928
Dh	1862	TGATCACTCTGTGCGAGGCGAGATGCTGTAGTGTGTCTACGCCATCAATCT	1921
Oy	1929	CCATCTCTTCTCTAGGCGCATTTTCCAGGAGCTTCCGCGGAGCTTCTGCT	1988
Dh	1922	CCATCTCTTCTCTAGGCGCATTTTCCAGGAGCTTCCGCGGAGCTTCTGCT	1981
Oy	1989	TGAGCAAGTTTGGCTGTATGAATGCAAGCCAGATTTTACAGGAGCAAACT	2048
Dh	1982	TGAGCAAGTTTGGCTGTATGAAGTGCAGGCGGAGATTTTACAGGAGCAAACT	2041
Oy	2049	CTACCCAACTTCCATGCGGAGAGCCACTGCTCTCAGCTCCAGAGTCAACCA	2108
Dh	2042	CTACCCAACTTCCATGCGGAGAGCCACTGCTCTCAGCTCCAGAGTCAACCA	2101
Oy	2109	GTTAGGCTGTGCTGCTTAAATCAATTCATGCGAGAGCTTAAATCAATGCT	2168
Dh	2102	GTTAGGCTGTGCTGCTTAAATCAATTCATGCGAGAGCTTAAATCAATGCT	2161
Oy	2169	TCTTCACTTGAAGAGCAATTTATGAC-TCTTCTGAAGAGGAGGCGCTTAA	2227
Dh	2162	TCTTCACTTGAAGAGCAATTTATGAC-TCTTCTGAAGAGAGGCGCTTAA	2221
Oy	2228	AATCTCTGACATCTCATTAATTAATCTCTCTGGTCTCTGCTGCTGCTGCT	2287
Dh	2222	AGTGTCTGACATATTTATCTAATTAATCTCTCTGCTGCTGCTGCTGCTGCT	2281
Oy	2288	AGGAGCATTATCACCCCTTTGGCTCTCTCA-CATTAAATATGGTAAACGA	2346
Dh	2282	AGGAGCATTATATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	2341
Oy	2347	AAAGAGCAAAAGCCG	2363
Dh	2342	AAATAGTGAACACTGC	2358

RESULT 2
BH029943
LOCUS

BH029943 703 bp DNA linear GSS 17-JUL-2001

[5' GAGAGAGAAGAGATCCCAAGAGCTCTTTTTTTTTTNN 3'], cDNA was prepared by using trehalose tRNA-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 10.0 and subtraction to Rot = 100.0. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGAGAGAAGATTCGAGTAATTAATCCCTCCCCCCC 3']. cDNA was cleaved with BamHI and XhoI. cDNA of size comprised longer than 7 kb was selected before cloning. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I. Cloning sites, 5' end: SalI; 3' end: BamHI. Host: DH10B.

FEATURES

source

Location/Qualifiers

1. 3015

T. :3013
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1, 2017
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1. 3015

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92. .2386

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52. .2500
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evidence:ISS

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thyroid stimulating hormone

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799 c 652 a 754 t

ORIGIN

Query Match	19.4%	Score 459.8	DB 11	Length 3015
Best Local Similarity	67.2%	Pred. No. 9.7e-116		
Matches 650	Conservative 0	Mismatches 317	Indels 0	Gaps 0
QY	1062	AATTGTATTAGTACTTATGTGAATGAAGTTCTTCATGTGACCTGCTCACCACAAAGCCAGATG	1121	
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QY	1122	CATTTAATCCATGTGAAGATATCATGGGGPACAAACATCCTCAGGGCTTTTGATATGGTTTA	1181	
Db	1302	AGTTTAACCCCTGTGAAGATATCATGGCTACAGGTTCTTGAGAATCGTGGTGGTTTG	1361	
QY	1182	TTAGCATCTGTGGCCATTACTGGCAACACACATGCTGGTGGTCTGCACACACAGCCAA	1241	
Db	1362	TCAGTCTGTGGCTCTCTGGGGCAATATCTTCGTCTGCCTCATCTTGCATAACGAGCCACT	1421	
QY	1242	ACAACTAACTGTGCCCCGGTTTTCTTATGTGTAACCTCGCCTTCGTGTATCTCTGCATAG	1301	
Db	1422	ACAAATTGACCGTGGCGGGTTCTCATGTGCAACTTGGCCTTTGCAGATTTCTGCATGG	1481	
QY	1302	GCATCTACTTGGCTACTATATAGCATCAGTTGCATATCCATACCAAGAGCCAGTACCACT	1361	

316	TTAATAAGCAGTTAATACAAACTACTGTACCTCGTTTCTAATGCGAATCTTGCAATTT	375
1286	GCTGATCTCTGCATAGGCATCTACTTGCTACTTATAGCATCTAGTTGACATCCATACCAAG	1345
376	GCAGATCTCTGTATAGGTATCTCTGTTATTATTGTCATAGTAGATATCCAGACCATA	435
1346	AGCCAGTACCACAACTATGCCATTGACTGGCAACAGGAGCAGGCTGTGATGCTGTGGC	1405
436	AGCCGGTATTACAACCTATGCCATAGACTGGCAACCGGGCAGGATGCAATGCTGCAGGA	495
1406	TTTTTCACTGCTCTTGCCAGTGAACCTGTCAGTCTACACATTGCAGCCCATCACCCTAGAA	1465
496	TTTTTTACGTGTTTTGCAAGTGAACCTCTCAGTCTACACACTGACTCTGTATAACTCTCGAA	555
1466	AGATGGCATACCATCACACATGCTATGCAACTGGAATGCAAGTGCAGCTCCGGCATGCT	1525
556	AGGTGSCATACCATTACCTATGCCATGCAACTCAACCGCANNNNTCGACTTCGGCATGCT	615
1526	GCCAGGTCATGGTATTTGGCTGGAGCTTTTGGCTTCGCAGCTGCTCT	1572
616	GTGATCATATGGTTTTTGGCTGGATGTTTGCTTTTTCACGCTGGCACT	662

RESULT 7	LOCUS	BI186370	691 bp	mRNA	linear	EST 10-JUL-2001
BI186370	DEFINITION	UNL-P-FN-dd-b-11-0-UNL.s2	UNL-P-FN	Sus scrofa	cDNA clone	
		UNL-P-FN-dd-b-11-0-UNL.3			mRNA sequence.	

FEATURES
SOURCE

RESULT 8	
BI1185789	
LOCUS	B1185789 linear EST 10-JUL-2001
DEFINITION	UNL-P-FN-dd-b-11-0-UNL.s1 UNL-P-FN Sus scrofa cDNA clone
ACCESSION	BI1185789
VERSION	BI1185789.1 GI:14660198
KEYWORDS	EST.
SOURCE	pig.
ORGANISM	Sus scrofa
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS	Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
TITLE	1 (bases 1 to 711)
JOURNAL	Caetano,A.R., Johnson,R.K. and Pomp,D. Generation and sequence characterization of a normalized cDNA library from swine ovarian follicles
COMMENT	Unpublished (2001). Contact: Pomp, D Department of Animal Science University of Nebraska, Lincoln

Db 122 GAACCTTCCCAACCTCCGATATCTGTTAATATCCACACAGGTATTAAAGCACTTGCCAGC 181
 QY 481 TGTTCAAGATCCAGCTCTCTCCAAAGGTTCTACTAGACATTCAGATAAACAAT 540
 Db 182 TGTTCAAGATTCAGCTCTCTCCAAAGGTTTACTAGATATTCAGATAAATAAAT 241
 QY 541 CCACATCGTTGCGAGCAACTCTTCATGGGAGTGGTGTGAAAGTGGTATTTATGGCT 600
 Db 242 CCACACAGTTGAAGAAGATCTTCATGGGGCTAAGTTTGAAGATGACGTATGGCT 301
 QY 601 GAGTAGAGTGGAGTTGAAGAATACACAACTGTGCAATTCACGGGAACCTCA 651
 Db 302 GAGTAGAGTGGAGTTGAAGAATACACAACTGTGCAATTCACGGGAACCTCA 352

RESULT 10
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 LOCUS
 DEFINITION RCO-HT0613-200300-031-a10 HT0613 Homo sapiens cdna, mRNA sequence. EST 22-JUN-2000
 ACCESSION BE179105
 VERSION BE179105.1 GI:8658257
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 613)
 Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
 Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
 Goldman, G.H., Carvalho, A.F., Matsumura, A., Baia, G.S., Simpson, D.H.,
 Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare,
 M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
 Simpson, A.J.
 Shotgun sequencing of the human transcriptome with ORF expressed
 sequence tags

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
 MEDLINE 20202663
 COMMENT Contact: Simpson A.J.G.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
 Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br
 This sequence was derived from the FAPESP/LICR Human Cancer Genome
 Project. This entry can be seen in the following URL
 (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=st2-RCO-HT0613-200
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 Seq primer: puc 18 forward
 High quality sequence start: 19
 High quality sequence stop: 612.
 Location/Qualifiers
 1. 613
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_lib="HT0613"
 /dev_stage="Adult"
 /note="Organ: head_neck; Vector: puc18; Site1: SmaI;
 Site2: SmaI; A mini-library was made by cloning products
 derived from ORESTES PCR (U.S. Letters Patent application
 No. 196,716 - Ludwig Institute for Cancer Research)
 profiles into the puc 18 vector. Reverse transcription of
 tissue mRNA and cDNA amplification were performed under
 low stringency conditions."

FEATURES
 source
 BASE COUNT 168 a 132 c 178 g 135 t
 ORIGIN
 Query Match 10.2%; Score 242; DB 10; Length 613;
 Best Local Similarity 64.4%; Pred. No. 1.2e-55;
 Matches 362; Conservative 0; Mismatches 200; Indels 0; Gaps 0;
 QY 1471 GCATACCATCACATGCTATGCAACTGGAATGCAAGGTCCAGCTCCGGCATCTGCCAG 1530

Db 612 GTATGCCATCACCTTCGCCATCGGCTGGACGGAAGATCCGCTCAGGCACGCATGTGC 553
 QY 1531 COTCATGGTATTTGGGCTGGAGCTTTTGGCTTCGAGAGTCTCTCTCTCCCATCTTTGGCAT 1590
 Db 552 CATCATGGTGGGGCTGGTGTTCCTTCCTCGCCCTGCTTCTCTTGGTGGGAAT 493
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 Db 492 AAGTAGCTATGCAAGTCAGTATTCCTGCGCATGGACCGGAACCCCTCTTCTCT 433
 QY 1651 GCTGTATGTTATGGCCCTCTTGTCTCAATGTCTGGCTTTGTGGTCTATCTGTGGCTG 1710
 Db 432 GCATATATTTGTTTGTCTGACGCTCAACATAGTTGCTTCGTCATCTGCTGCTG 373
 QY 1711 CTATACCCACATCTACCTCACAGTGAAGAACTCTACCATTTGTCTCTCATCAAGCACAC 1770
 Db 372 TTATGTGAAGATCTACATCACAGTCCGAAATCCGAGTACAACCCAGGGGACAAGATAC 313
 QY 1771 CAAGATTGCCAAGCGCATGCCACACTCATCTTCACAGACTTCTCTGTCATGCCCCCAT 1830
 Db 312 CAAATTTGCCAAGAGATGGCTGTGTGATCTTCACCGACTTCATATGTCATGCCCCCAT 253
 QY 1831 TTCAATTTTGGCATTTCCTCCCTCAAGGTGGCTCATCACTGTGTCTCAAGGCCAA 1890
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 Db 192 AATCTTCTGCTGCTCTCTATCCACTTAACCTCTCTGCAATCCATCTCTCTATGCTAT 133
 QY 1951 TTTCACCAAGAACTTCCGAGGAGCTTCTTCATCTCTGCTGACCAAGTTTGGCTGTTATGA 2010
 Db 132 TTTCACCAAGGCTTCCAGGGGATGTGTTCTCTACTCAGCAAGTTTGGCATCTGTAT 73
 QY 2011 AATGCAAGCCACAGTTTACAGG 2032
 Db 72 ACGCCAGGCTCAGGCATACCGG 51
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 AGENCOURT_6419913 NCI_CGAP_Ov44 Mus musculus CDNA clone
 IMAGE:5503889 5', mRNA sequence.
 ACCESSION BM461149
 VERSION BM461149.1 GI:18510189
 KEYWORDS EST.
 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 NIH-MGC http://mgc.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgapus-remail.nih.gov
 Tissue Procurement: Aaron Haueh
 CDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLAM12144 row: f column: 18
 High quality sequence start: 16
 High quality sequence stop: 685.
 Location/Qualifiers
 1. 1142
 /organism="Mus musculus"
 /db_xref="taxon:10090"
 /clone="IMAGE:5503889"

XX Examples; Fig 12; 103pp; English.

PS This sequence represents the N-terminal of a novel protein having a

CC binding affinity for human chorionic gonadotropin (hCG), luteinising

CC hormone (LH), and follicle stimulating hormone (FSH). The protein

CC itself is a chimera having residues from both the FSH receptor,

CC and LH receptor. The receptor analogues can be used in bioimmunoassays

CC for the simultaneous detection of both LH (or hCG) and FSH as

CC well as their ratio of biological activities. The analogues can also

CC be used for raising, purifying and assaying antibodies to the

CC analogues. Coding sequence for the chimera was produced by two step

CC PCR.

XX Sequence 695 AA;

XX

Query Match 99.9%; Score 3589; DB 14; Length 695;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 691; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MALLVSLAFGLTSGCHHLCNSNRVFLCQDSKVTEIPTDLPRNAIELRVLTCLR 60

Db 1 MALLVSLAFGLTSGCHHLCNSNRVFLCQDSKVTEIPTDLPRNAIELRVLTCLR 60

Qy 61 IPKGSFAGFGLDKIEISQNDVLEADVFSNPKLHEIRIEKANNLLYINPEAFQNL 120

Db 61 IPKGSFAGFGLDKIEISQNDVLEADVFSNPKLHEIRIEKANNLLYINPEAFQNL 120

Qy 121 SLRYLLISNTGIKHLPVAVHKIQSLQKVLDDIODNINIHIVARNFMSGLSFESVILWLSKN 180

Db 121 SLRYLLISNTGIKHLPVAVHKIQSLQKVLDDIODNINIHIVARNFMSGLSFESVILWLSKN 180

Qy 181 GIEIHNCAFNGTQDLNLSNNLEELPNDVFGASGVPVLDISTRTKVSHPNHGLEN 240

Db 181 GIEIHNCAFNGTQDLNLSNNLEELPNDVFGASGVPVLDISTRTKVSHPNHGLEN 240

Qy 241 LKLRARSTYRLKLPNDKFPVTLMEASLYTPSHCCAFANLKRQISELHPICNKILROD 300

Db 241 LKLRARSTYRLKLPNDKFPVTLMEASLYTPSHCCAFANLKRQISELHPICNKILROD 300

Qy 301 IDDMTQIGDQVRSLIDDEPSYKSGSDMMYNEFDYDLCEVVDVTCSPKPAFNPCEIDMG 360

Db 301 IDDMTQIGDQVRSLIDDEPSYKSGSDMMYNEFDYDLCEVVDVTCSPKPAFNPCEIDMG 360

Qy 421 DIHTKSOYHNYAIDWQTGAGDAAGFTVFASLSVYTLTAITLERWHTITHAMOLECKV 480

Db 421 DIHTKSOYHNYAIDWQTGAGDAAGFTVFASLSVYTLTAITLERWHTITHAMOLECKV 480

Qy 481 QLRHAASVMVLGWTFAFAALFPFIFGISSYMKVSIQCLPMDIDSPLSQLYNALLVNLVA 540

Db 481 QLRHAASVMVLGWTFAFAALFPFIFGISSYMKVSIQCLPMDIDSPLSQLYNALLVNLVA 540

Qy 541 FWTCGCTHYLYLVRNPTIVSSSDTKIAKRMATLIFTDFLCMAPISFFAISLKVPL 600

Db 541 FWTCGCTHYLYLVRNPTIVSSSDTKIAKRMATLIFTDFLCMAPISFFAISLKVPL 600

Qy 601 ITVSKAKILLVFPINSCANPFLYAIPTKFRDRDFILLSKFCGYEMQAOIYRTETSSA 660

Db 601 ITVSKAKILLVFPINSCANPFLYAIPTKFRDRDFILLSKFCGYEMQAOIYRTETSSA 660

Qy 661 THNFHARKSHCSSAPRVNTSYVLPLNHSQN 692

Db 661 THNFHARKSHCSSAPRVNTSYVLPLNHSQN 692

RESULT 2

AAR08038

ID AAR08038 standard; protein; 692 AA.

XX

AC AAR08038;

XX

DT 26-FEB-1991 (first entry)

XX

DE Rat testicular luteinising hormone/choriogonadotropin receptor.

XX

KW LH/CG receptor; FSH receptor; TSH receptor; fertility; breast cancer;

KW prostate cancer; thyroid cancer; osteoporosis; Graves disease;

KW polycystic ovarian disease; vasomotor instability.

XX

OS Rattus rattus.

XX

PN WO9013643-A.

XX

PD 15-NOV-1990.

XX

PF 04-MAY-1990; 90WO-US02488.

XX

PR 05-MAY-1989; 89US-0347683.

XX

PA (GETH) GENENTECH INC.

XX

PI Nikolics K, McFarland KC, Segaloff DL, Seeburg PH;

XX

DR WPI; 1990-361478/48.

XX

DR N-PSDB; AAQ06634.

XX

XX Pharmaceutical compsn. contg. hormone receptor mol - used for

PT treating fertility, breast-and prostate-cancer and osteoporosis,

PT etc.

XX

XX Disclosure; fig 6; 78pp; English.

XX

CC This rat testicular follicle-stimulating hormone (FSH) receptor.

CC This receptor is useful in a pharmaceutical compsn. for treating

CC e.g. breast-, prostate- and thyroid cancer, fertility, osteopor-

CC ois, vasomotor instability and polycystic ovarian disease.

CC LH/CG- or TSH-receptors can also be used, to treat e.g. Graves

CC disease. Abs can be used to inhibit receptor binding and for imag-

CC ing and therapy. See also AAR08015-23, AAR08035-36 and AAQ06633.

XX

SQ Sequence 692 AA;

Query Match 99.7%; Score 3585; DB 11; Length 692;

Best Local Similarity 99.7%; Pred. No. 0;

Matches 690; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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Db 1 MALLVSLAFGLTSGCHHLCNSNRVFLCQDSKVTEIPTDLPRNAIELRVLTCLR 60

Qy 61 IPKGSFAGFGLDKIEISQNDVLEADVFSNPKLHEIRIEKANNLLYINPEAFQNL 120

Db 61 IPKGSFAGFGLDKIEISQNDVLEADVFSNPKLHEIRIEKANNLLYINPEAFQNL 120

Qy 121 SLRYLLISNTGIKHLPVAVHKIQSLQKVLDDIODNINIHIVARNFMSGLSFESVILWLSKN 180

Db 121 SLRYLLISNTGIKHLPVAVHKIQSLQKVLDDIODNINIHIVARNFMSGLSFESVILWLSKN 180

Qy 181 GIEIHNCAFNGTQDLNLSNNLEELPNDVFGASGVPVLDISTRTKVSHPNHGLEN 240

Db 181 GIEIHNCAFNGTQDLNLSNNLEELPNDVFGASGVPVLDISTRTKVSHPNHGLEN 240

Qy 241 LKLRARSTYRLKLPNDKFPVTLMEASLYTPSHCCAFANLKRQISELHPICNKILROD 300

Db 241 LKLRARSTYRLKLPNDKFPVTLMEASLYTPSHCCAFANLKRQISELHPICNKILROD 300

Qy 301 IDDMTQIGDQVRSLIDDEPSYKSGSDMMYNEFDYDLCEVVDVTCSPKPAFNPCEIDMG 360

Db 301 IDDMTQIGDQVRSLIDDEPSYKSGSDMMYNEFDYDLCEVVDVTCSPKPAFNPCEIDMG 360

Qy 361 YNLRVLIWFISILAITGNTTVLVLTTSOYKLVTPRFLMCNLAFAADLCIGYLLLIASV 420

Db 361 YNLRVLIWFISILAITGNTTVLVLTTSOYKLVTPRFLMCNLAFAADLCIGYLLLIASV 420

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Db 361 YNLRVLNFIATIGTNTVLVLTTSQYKLTVPFLMCLAFADLCIGIYLLIASV 420
QY 421 DIHTKSOYHNTAIDMOTGACGDAAGFTTFVASELSVYTLTAITLERHHTITHAMOLECKV 480
Db 421 DIHTKSOYHNTAIDMOTGACGDAAGFTTFVASELSVYTLTAITLERHHTITHAMOLECKV 480
QY 481 QLRHAASVWLGHTFAFAALPPIFGISSYKVSICLPMDIDSPLSQLYMALLVNLVLA 540
Db 481 QLRHAASVWLGHTFAFAALPPIFGISSYKVSICLPMDIDSPLSQLYMALLVNLVLA 540
QY 541 FVVICGCTHYIYLVNPTIVSSSDTKIAKPMATLIPTDFLCMAPISFFAISASLKVPL 600
Db 541 FVVICGCTHYIYLVNPTIVSSSDTKIAKPMATLIPTDFLCMAPISFFAISASLKVPL 600
QY 601 ITVSKAKILLVLYPINSKANPELYAIFTKNFRDRFFILLSKGTCYENQAIYRTETSSA 660
Db 601 ITVSKAKILLVLYPINSKANPELYAIFTKNFRDRFFILLSKGTCYENQAIYRTETSSA 660
QY 661 TINFHARKSHCSSAPRVNTSVLYVPLNHSQN 692
Db 661 TINFHARKSHCSSAPRVNTSVLYVPLNHSQN 692

RESULT 3
AAR30524
ID AAR30524 standard; protein; 695 AA.
AC AAR30524;
XX
XX 10-MAY-1993 (first entry)
DE N-terminal of LH receptor/FSH receptor chimera #33.
KW Follicle stimulating hormone receptor; luteinising hormone receptor;
KW human chorionic gonadotrophin; glycoprotein hormone receptor;
XX chimera; chimera.
OS Chimaeric; homo sapiens.
XX
XX W09222667-A.
XX
XX 23-DEC-1992.
XX 12-JUN-1992; 92MO-US04987.
XX 14-JUN-1991; 91US-0715911.
XX (UYNE-) UNIV NEW JERSEY.
PA Bernard M, Moyle WR, Myera R;
PI
XX
XX MPI; 1993-018150/02.
XX
XX Glyco:protein hormone receptor analogues - having binding
XX affinity to human chorionic gonadotrophin, luteinising and
XX follicle stimulating hormones, useful in bio:immunoassays
XX
XX Examples; Fig 12: 103pp: English.
XX
XX This sequence represents the N-terminal of a novel protein having a
XX binding affinity for human chorionic gonadotrophin (hCG), luteinising
XX hormone (LH), and follicle stimulating hormone (FSH). The protein
XX itself contains residues from both the FSH receptor,
XX and LH receptor. The detection of both LH (or hCG) and FSH
XX for the simultaneous detection of both LH (or hCG) and FSH
XX as well as their ratio of biological activities. The analogues can also
XX be used for raising, purifying and assaying antibodies to the
XX analogues. Coding sequence for the chimera was produced by two step
XX PCR.
XX
XX Sequence 695 AA;

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Query Match 98.3%; Score 3532; DB 14; Length 695;

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Best Local Similarity 98.1%; Pred. No. 0;
Matches 679; Conservative 6; Mismatches 7; Indels 0; Caps 0;
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Db 1 MALLVSLALPLATGTCGCHHLCCHSRVFLCQDSKVTETPTDLPNNAIELRFVLTJLAV 60
QY 61 IPKGSFAGCDLEKTEISONDVLEVIEADVFSNLPKLHEIRIEKANNLLYINPEAFONLP 120
Db 61 IPKGSFAGCDLEKTEISONDVLEVIEADVFSNLPKLHEIRIEKANNLLYINPEAFONLP 120
QY 121 SLRYLLISMTGIXKHPAYKHQKVLQVLLDIDNNINIHIVARNSPMGSPESVILMSKN 180
Db 121 SLRYLLISMTGIXKHPAYKHQKVLQVLLDIDNNINIHIVARNSPMGSPESVILMSKN 180
QY 181 GIEZIHNCNFTQDDELNLSNNNLELPELNDVPOGASPVILDISRTKVHSLPMHLEN 240
Db 181 GIEZIHNCNFTQDDELNLSNNNLELPELNDVPOGASPVILDISRTKVHSLPMHLEN 240
QY 241 LKKLRARSTYRLKLLPNLDKFTVLTWEASLTYPSSHCCAFANLKROISELHPICNKLROD 300
Db 241 LKKLRARSTYRLKLLPNLDKFTVLTWEASLTYPSSHCCAFANLKROISELHPICNKLROD 300
QY 301 IDDMTOIGDQVSLIDDEPSYKSGSDMYNEFDYDLCNEVYDVTCSPKPDAPNCDING 360
Db 301 IDDMTOIGDQVSLIDDEPSYKSGSDMYNEFDYDLCNEVYDVTCSPKPDAPNCDING 360
QY 361 YNLRVLNFIATIGTNTVLVLTTSQYKLTVPFLMCLAFADLCIGIYLLIASV 420
Db 361 YNLRVLNFIATIGTNTVLVLTTSQYKLTVPFLMCLAFADLCIGIYLLIASV 420
QY 421 DIHTKSOYHNTAIDMOTGACGDAAGFTTFVASELSVYTLTAITLERHHTITHAMOLECKV 480
Db 421 DIHTKSOYHNTAIDMOTGACGDAAGFTTFVASELSVYTLTAITLERHHTITHAMOLECKV 480
QY 481 QLRHAASVWLGHTFAFAALPPIFGISSYKVSICLPMDIDSPLSQLYMALLVNLVLA 540
Db 481 QLRHAASVWLGHTFAFAALPPIFGISSYKVSICLPMDIDSPLSQLYMALLVNLVLA 540
QY 541 FVVICGCTHYIYLVNPTIVSSSDTKIAKPMATLIPTDFLCMAPISFFAISASLKVPL 600
Db 541 FVVICGCTHYIYLVNPTIVSSSDTKIAKPMATLIPTDFLCMAPISFFAISASLKVPL 600
QY 601 ITVSKAKILLVLYPINSKANPELYAIFTKNFRDRFFILLSKGTCYENQAIYRTETSSA 660
Db 601 ITVSKAKILLVLYPINSKANPELYAIFTKNFRDRFFILLSKGTCYENQAIYRTETSSA 660
QY 661 TINFHARKSHCSSAPRVNTSVLYVPLNHSQN 692
Db 661 TINFHARKSHCSSAPRVNTSVLYVPLNHSQN 692

RESULT 4
AAR30525
ID AAR30525 standard; protein; 695 AA.
AC AAR30525;
XX
XX 10-MAY-1993 (first entry)
DE N-terminal of LH receptor/FSH receptor chimera #34.
KW Follicle stimulating hormone receptor; luteinising hormone receptor;
KW human chorionic gonadotrophin; glycoprotein hormone receptor;
XX chimera; chimera.
OS Chimaeric; homo sapiens.
XX
XX W09222667-A.
XX
XX 23-DEC-1992.
XX 12-JUN-1992; 92MO-US04987.

```

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XX PR 14-JUN-1991: 91US-0715911.
XX PA (UYNE-) UNIV NEW JERSEY.
XX PI Bernard M, Moyle WR, Myers R;
XX DR WPI; 1993-018150/02.
XX PT Glyco:protein hormone receptor analogues - having binding
XX PT affinity to human chorionic gonadotrophin, luteinising and
XX PS follicle stimulating hormones, useful in bio:immunoassays
XX PS Examples; Fig 12; 103pp; English.
XX CC This sequence represents the N-terminal of a novel protein having a
XX CC binding affinity for human chorionic gonadotrophin (hCG), luteinising
XX CC hormone (LH), and follicle stimulating hormone (FSH). The protein
XX CC itself is a chimera having residues from both the FSH receptor,
XX CC and LH receptor. The receptor analogues can be used in bioimmunoassays
XX CC for the simultaneous detection of both LH (or hCG) and FSH as
XX CC well as their ratio of biological activities. The analogues can also
XX CC be used for raising, purifying and assaying antibodies to the
XX CC analogues. Coding sequence for the chimera was produced by two step
XX CC PCR.
XX SQ Sequence 695 AA;

Query Match 98.0%; Score 3523; DB 14; Length 695;
Best Local Similarity 98.4%; Pred. NO. 0;
Matches 681; Conservative 2; Mismatches 9; Indels 0; Gaps 0;

QY 1 MALLVSLAFLGTCGCHHLCCHSNRVFLCQDSKVTEIPTDLPRAIELRFLVTLKRV 60
DB 1 MALLVSLAFLGTCGCHHLCCHSNRVFLCQDSKVTEIPTDLPRAIELRFLVTLKRV 60
QY 61 IPKGSFAGFGDLEKIEISQNDVLEIADVFSNLPKLEIRIEKANNLLYNPEAFQNL 120
DB 61 IPKGSFAGFGDLEKIEISQNDVLEIADVFSNLPKLEIRIEKANNLLYNPEAFQNL 120
QY 121 SLRYLLISNTGKHLPAVHKQTSQKVLQDQNNINIHIVARNFPMGLSFESVILWLSK 180
DB 121 SLRYLLISNTGKHLPAVHKQTSQKVLQDQNNINIHIVARNFPMGLSFESVILWLSK 180
QY 181 GIEETHNCAFNGTOLDNLSDNNLELPNDVFGAGSPVILDSIRKTVHSLNPHGLE 240
DB 181 GIEETHNCAFNGTOLDNLSDNNLELPNDVFGAGSPVILDSIRKTVHSLNPHGLE 240
QY 181 GFEEVSHAFNGTQDENLSDNNLELPNDVFGAGSPVILDSIRKTVHSLNPHGLE 240
DB 181 GFEEVSHAFNGTQDENLSDNNLELPNDVFGAGSPVILDSIRKTVHSLNPHGLE 240
QY 241 LKLLRARSTYRLKLPNLDKFTVLMASLTYPSCCAPANLKROISELHPICNKSILROD 300
DB 241 LKLLRARSTYRLKLPNLDKFTVLMASLTYPSCCAPANLKROISELHPICNKSILROD 300
QY 301 IDMTQIGDQVSLIDDEPSYKSGSDMMYNEFDYDLNCEVVDVTCSPKPDAPNCPEDIMG 360
DB 301 IDMTQIGDQVSLIDDEPSYKSGSDMMYNEFDYDLNCEVVDVTCSPKPDAPNCPEDIMG 360
QY 361 YNLRVLWFLTSLAITNTVLLVLTTSQYKLVTPRELMLNLAFAADLCIGYLLLTASV 420
DB 361 YNLRVLWFLTSLAITNTVLLVLTTSQYKLVTPRELMLNLAFAADLCIGYLLLTASV 420
QY 421 DIHTKSOYHNYAIDMQTGAGDAAGFTVFASLSVYTLTATLERWHITTHAMOLECKV 480
DB 421 DIHTKSOYHNYAIDMQTGAGDAAGFTVFASLSVYTLTATLERWHITTHAMOLECKV 480
QY 481 QLRHAASVWLGWTFAPAAALFPFPGISSYKWSVICLPMIDSPLSQLYVALLVNLVLA 540
DB 481 QLRHAASVWLGWTFAPAAALFPFPGISSYKWSVICLPMIDSPLSQLYVALLVNLVLA 540
QY 541 FWIGCGYTHLYTVRNPTIVSSSDTKIARMTLIFTDFLCNAPISFFAISLKVPL 600
DB 541 FWIGCGYTHLYTVRNPTIVSSSDTKIARMTLIFTDFLCNAPISFFAISLKVPL 600
QY 601 ITVSKAKILLVLFYPINSCANPFLYAIFTKNRRDFFILLSKFCGYEMQAQIYRTETSSA 660
DB 601 ITVSKAKILLVLFYPINSCANPFLYAIFTKNRRDFFILLSKFCGYEMQAQIYRTETSSA 660

RESULT 5
AAR30523.
ID AAR30523 standard; protein: 696 AA.
XX AC AAR30523;
XX DT 10-MAY-1993 (first entry)
XX DE N-terminal of LH receptor/FSH receptor chimera #32.
XX KW Follicle stimulating hormone receptor; luteinising hormone receptor;
XX KW human chorionic gonadotrophin; glycoprotein hormone receptor;
XX KW chimera; chimera.
XX OS Chimeraic; homo sapiens.
XX PN WO9222667-A.
XX PD 23-DEC-1992.
XX PF 12-JUN-1992; 92WO-US04987.
XX PR 14-JUN-1991; 91US-0715911.
XX PA (UYNE-) UNIV NEW JERSEY.
XX PI Bernard M, Moyle WR, Myers R;
XX DR WPI; 1993-018150/02.
XX PT Glyco:protein hormone receptor analogues - having binding
XX PT affinity to human chorionic gonadotrophin, luteinising and
XX PT follicle stimulating hormones, useful in bio:immunoassays
XX PS Examples; Fig 12; 103pp; English.
XX CC This sequence represents the N-terminal of a novel protein having a
XX CC binding affinity for human chorionic gonadotrophin (hCG), luteinising
XX CC hormone (LH), and follicle stimulating hormone (FSH). The protein
XX CC itself is a chimera having residues from both the FSH receptor,
XX CC and LH receptor. The receptor analogues can be used in bioimmunoassays
XX CC for the simultaneous detection of both LH (or hCG) and FSH as
XX CC well as their ratio of biological activities. The analogues can also
XX CC be used for raising, purifying and assaying antibodies to the
XX CC analogues. Coding sequence for the chimera was produced by two step
XX CC PCR.
XX SQ Sequence 696 AA;

Query Match 97.9%; Score 3519.5; DB 14; Length 696;
Best Local Similarity 98.1%; Pred. NO. 0;
Matches 680; Conservative 4; Mismatches 8; Indels 1; Gaps 1;

QY 1 MALLVSLAFLGTCGCHHLCCHSNRVFLCQDSKVTEIPTDLPRAIELRFLVTLKRV 60
DB 1 MALLVSLAFLGTCGCHHLCCHSNRVFLCQDSKVTEIPTDLPRAIELRFLVTLKRV 60
QY 61 IPKGSFAGFGDLEKIEISQNDVLEIADVFSNLPKLEIRIEKANNLLYNPEAFQNL 120
DB 61 IPKGSFAGFGDLEKIEISQNDVLEIADVFSNLPKLEIRIEKANNLLYNPEAFQNL 120
QY 121 SLRYLLISNTGKHLPAVHKQTSQKVLQDQNNINIHIVARNFPMGLSFESVILWLSK 179
DB 121 SLRYLLISNTGKHLPAVHKQTSQKVLQDQNNINIHIVARNFPMGLSFESVILWLSK 180
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OY 180 NGIEEIHNCFAWGTQDELNLSDNNLEELPNDFVQAGSGPVILDI SRTKVHSLPNHGLE 239
 DB 181 NGIEEIHNCFAWGTQDELNLSDNNLEELPNDFVQAGSGPVILDI SRTKVHSLPNHGLE 240
 OY 240 NLKLRARSTTRALKLPNDKPVTLMEASITYPSCCAPANLKRQISELHPICNKSLRQ 299
 DB 241 NLKLRARSTTRALKLPNDKPVTLMEASITYPSCCAPANLKRQISELHPICNKSLRQ 300
 OY 300 DIDDMTQIGDQVSLIDDEPSYKSGSDMNTNEFDYDLCHNEVDVTCSPKDFAPNCPEDIM 359
 DB 301 DIDDMTQIGDQVSLIDDEPSYKSGSDMNTNEFDYDLCHNEVDVTCSPKDFAPNCPEDIM 360
 OY 360 GYNILRVLWPFISLAI TGNVTYVLTTSQYKLTVPRLMCLNAPADLCIGYILLIAS 419
 DB 361 GYNILRVLWPFISLAI TGNVTYVLTTSQYKLTVPRLMCLNAPADLCIGYILLIAS 420
 OY 420 VOIHTKSOYHNTAIDMOTGACDAAGFTVPFASLSVYTLTATLERHHTITHAMOLECK 479
 DB 421 VOIHTKSOYHNTAIDMOTGACDAAGFTVPFASLSVYTLTATLERHHTITHAMOLECK 480
 OY 480 VOLRHAASVWVGLWTFAPAAALPPIFGISYKVSICLPMIDISPLSOLYVALLVNL 539
 DB 481 VOLRHAASVWVGLWTFAPAAALPPIFGISYKVSICLPMIDISPLSOLYVALLVNL 540
 OY 540 AFVVICGCTTHILTVRNPTIVSSSDTKIAKRNATLIFTDFLCHAPISFFAISASLKV 599
 DB 541 AFVVICGCTTHILTVRNPTIVSSSDTKIAKRNATLIFTDFLCHAPISFFAISASLKV 600
 OY 600 LITVSKAKILLVLPYINSCANPFLYAIPTKFNRRDFFILLSKFCGYEMOAOIYRTETSS 659
 DB 601 LITVSKAKILLVLPYINSCANPFLYAIPTKFNRRDFFILLSKFCGYEMOAOIYRTETSS 660
 OY 660 ATNHFHAKSHCSSAPRVNTSNVYVLPJNHISSON 692
 DB 661 ATNHFHAKSHCSSAPRVNTSNVYVLPJNHISSON 693

RESULT 6

AAR30519
 ID AAR30519 standard; protein: 696 AA.

AC AAR30519;

DT 10-MAY-1993 (first entry)

DE N-terminal of LH receptor/FSH receptor chimera #28.

XX Follicle stimulating hormone receptor; luteinizing hormone receptor;

KW human chorionic gonadotropin; glycoprotein hormone receptor;

XX chimera; chimera.

OS Chimeraic; homo sapiens.

XX MO9222667-A.

XX 23-DEC-1992.

XX 12-JUN-1992; 92MO-US04987.

XX 14-JUN-1991; 91US-0715911.

XX (UTNE-) UNIV NEW JERSEY.

XX Bernard M. Moyle WR, Myers R;

XX WPI; 1993-018150/02.

XX Glyco:protein hormone receptor analogues - having binding

PT affinity to human chorionic gonadotropin, luteinizing and

PT follicle stimulating hormones, useful in bio:immunoassays

PS Examples: Fig 12; 103pp: English.

XX

CC This sequence represents the N-terminal of a novel protein having a
 CC binding affinity for human chorionic gonadotropin (hCG), luteinizing
 CC hormone (LH), and follicle stimulating hormone (FSH). The protein
 CC itself is a chimera having residues from both the FSH receptor,
 CC and LH receptor. The receptor analogues can be used in immunoassays
 CC for the simultaneous detection of both LH (or hCG) and FSH as
 CC well as for the detection of biological activities. The analogues can also
 CC be used for raising antibodies against the chimera. The chimera
 CC analogues. Coding sequence for the chimera was produced by two step
 CC PCR.

XX Sequence 696 AA;

SQ Query Match 93.1%; Score 3346.5; DB 14; Length 696;
 Best Local Similarity 93.8%; Pred. No. 7.5e-316;
 Matches 650; Conservative 13; Mismatches 29; Indels 1; Gaps 1;

OY 1 MALLVLSLAFATGSGCHHMLCHSNNRVFLCQDSKVTETPTDLPNNAIELRPFVTLKRV 60
 DB 1 MALLVLSLAFATGSGCHHMLCHSNNRVFLCQDSKVTETPTDLPNNAIELRPFVTLKRV 60
 OY 61 KPSGSPAGSGOLEKTEISONDVLEVLEIVADVFNPLKHEIRIEKANLLYIMPAPONLP 120
 DB 61 KPSGSPAGSGOLEKTEISONDVLEVLEIVADVFNPLKHEIRIEKANLLYIMPAPONLP 120
 OY 121 SURYLLISNTGIKHLPVAVHKIQSLQ-KVLLDIQDNINITHIVARNSPGLCSFESVILWSK 179
 DB 121 RUKYLSICNTGIRTPDVTIKISSSEFNILEICDNLHRTTIPGNAFOCMNNEVTLALYG 180
 OY 180 NGIEEIHNCFAWGTQDELNLSDNNLEELPNDFVQAGSGPVILDI SRTKVHSLPNHGLE 239
 DB 181 NGIEEIHNCFAWGTQDELNLSDNNLEELPNDFVQAGSGPVILDI SRTKVHSLPNHGLE 240
 OY 240 NLKLRARSTTRALKLPNDKPVTLMEASITYPSCCAPANLKRQISELHPICNKSLRQ 299
 DB 241 NLKLRARSTTRALKLPNDKPVTLMEASITYPSCCAPANLKRQISELHPICNKSLRQ 300
 OY 300 DIDDMTQIGDQVSLIDDEPSYKSGSDMNTNEFDYDLCHNEVDVTCSPKDFAPNCPEDIM 359
 DB 301 DIDDMTQIGDQVSLIDDEPSYKSGSDMNTNEFDYDLCHNEVDVTCSPKDFAPNCPEDIM 360
 OY 360 GYNILRVLWPFISLAI TGNVTYVLTTSQYKLTVPRLMCLNAPADLCIGYILLIAS 419
 DB 361 GYNILRVLWPFISLAI TGNVTYVLTTSQYKLTVPRLMCLNAPADLCIGYILLIAS 420
 OY 420 VOIHTKSOYHNTAIDMOTGACDAAGFTVPFASLSVYTLTATLERHHTITHAMOLECK 479
 DB 421 VOIHTKSOYHNTAIDMOTGACDAAGFTVPFASLSVYTLTATLERHHTITHAMOLECK 480
 OY 480 VOLRHAASVWVGLWTFAPAAALPPIFGISYKVSICLPMIDISPLSOLYVALLVNL 539
 DB 481 VOLRHAASVWVGLWTFAPAAALPPIFGISYKVSICLPMIDISPLSOLYVALLVNL 540
 OY 540 AFVVICGCTTHILTVRNPTIVSSSDTKIAKRNATLIFTDFLCHAPISFFAISASLKV 599
 DB 541 AFVVICGCTTHILTVRNPTIVSSSDTKIAKRNATLIFTDFLCHAPISFFAISASLKV 600
 OY 600 LITVSKAKILLVLPYINSCANPFLYAIPTKFNRRDFFILLSKFCGYEMOAOIYRTETSS 659
 DB 601 LITVSKAKILLVLPYINSCANPFLYAIPTKFNRRDFFILLSKFCGYEMOAOIYRTETSS 660
 OY 660 ATNHFHAKSHCSSAPRVNTSNVYVLPJNHISSON 692
 DB 661 ATNHFHAKSHCSSAPRVNTSNVYVLPJNHISSON 693

RESULT 7

AAR30526
 ID AAR30526 standard; protein: 696 AA.

AC AAR30526;

DT 10-MAY-1993 (first entry)

XX N-terminal of LH receptor/FSH receptor chimera #35.
 XX Follicle stimulating hormone receptor; luteinising hormone receptor;
 KW human chorionic gonadotrophin; glycoprotein hormone receptor;
 KW chimera; chimera.
 XX Chimeraic; homo sapiens.
 XX W09222667-A.
 XX 23-DEC-1992.
 XX 12-JUN-1992; 92WO-US04987.
 XX 14-JUN-1991; 91US-0715911.
 XX (UYNE-) UNIV NEW JERSEY.
 XX Bernard M, Moyle WR, Myers R;
 XX WPI; 1993-018150/02.
 XX Glyco:protein hormone receptor analogues - having binding
 PT affinity to human chorionic gonadotrophin, luteinising and
 PT follicle stimulating hormones, useful in bio:immunoassays
 XX Examples; Fig 12; 103pp; English.
 XX This sequence represents the N-terminal of a novel protein having a
 CC binding affinity for human chorionic gonadotrophin (hCG), luteinising
 CC hormone (LH), and follicle stimulating hormone (FSH). The protein
 CC itself is a chimera having residues from both the FSH receptor,
 CC and LH receptor. The receptor analogues can be used in bio:immunoassays
 CC for the simultaneous detection of both LH (or hCG) and FSH as
 CC well as their ratio of biological activities. The analogues can also
 CC be used for raising, purifying and assaying antibodies to the
 CC analogues. Coding sequence for the chimera was produced by two step
 CC PCR.
 XX Sequence 696 AA;

Query Match 91.1%; Score 3272.5; DB 14; Length 696;
 Best Local Similarity 91.8%; Pred. No. 1.2e-308;
 Matches 636; Conservative 17; Mismatches 39; Indels 1; Gaps 1;

QY 1 MALLVSLAFGLTSGSCHHNLCHSNRVFLCQDSKVTEIPTDLPRNAIELRFLVTLKRV 60
 DB 1 MALLVSLAFGLTSGSCHHNLCHSNRVFLCQDSKVTEIPTDLPRNAIELRFLVTLKRV 60
 QY 61 IPKGSFAGFGLKIEISQNDVLEIADYVSNLPKLHEIRIEKANNLLYNPFAONLP 120
 DB 61 IPKGSFAGFGLKIEISQNDVLEIADYVSNLPKLHEIRIEKANNLLYNPFAONLP 120
 QY 121 SLRYLLSNTGKIKLPAHVHTQSLQ-KVLIDIONINIHIVARNSEFGLSFESVILWSK 179
 DB 121 RLKYLSCNTGIRLPDVTKISSEFNFLEICDNLHITIPGAFQGMNVESTLYKG 180
 QY 180 NGIEEINCAPNGTQDLNLSNDNNLEELPNDFVQASGFPVLDISRTKVHSLPNHGLE 239
 DB 181 NGFEEVOSHAFNGTQDLNLSNDNNLEELPNDFVQASGFPVLDISRTKVHSLPNHGLE 240
 QY 240 NLKRLARSTYRLAKLNLDFVTLMEASLTYPHSCCAFANLKRQISELHPICKNSILRQ 299
 DB 241 NLKRLARSTYRLAKLNLDFVTLMEASLTYPHSCCAFANLKRQISELHPICKNSILRQ 300
 QY 300 DIDDMTQIGQVRSLIDDEPSYGGSDMWNNEFDYDLNCEVVDVTCSPKDPANPCEDIM 359
 DB 301 DIDDMTQIGQVRSLIDDEPSYGGSDMWNNEFDYDLNCEVVDVTCSPKDPANPCEDIM 360
 QY 360 GYNILRVLIWFISTAILTGNTTVLVLTTSQYKLTVPFRLMCNLAFLADLCIGIYLLIAS 419
 DB 361 GYNILRVLIWFISTAILTGNTTVLVLTTSQYKLTVPFRLMCNLAFLADLCIGIYLLIAS 420

QY 420 VDLHTKSOYHNYAIDWQTGAGCDAAGFTTFVASELSVYTLTAITLERWHHTITHAMQLECK 479
 DB 421 VDLHTKSOYHNYAIDWQTGAGCDAAGFTTFVASELSVYTLTAITLERWHHTITHAMQLECK 480
 QY 480 VOLRHAASVNLGWTFAFAAALPFIIGISSYMKVSYICLPMIDISPLSOLYVMALLVNLV 539
 DB 481 VOLRHAASVNLGWTFAFAAALPFIIGISSYMKVSYICLPMIDISPLSOLYVMALLVNLV 540
 QY 540 AFVVICGCTHYIYLVNPTIVSSSDTKIAKRMATLIPTDFLCMAPISFAISASLKV 599
 DB 541 AFVVICGCTHYIYLVNPTIVSSSDTKIAKRMATLIPTDFLCMAPISFAISASLKV 600
 QY 600 LITVSKAKILLVLPYIPINSCANPFLYAIFTKNRRDRFFILLSKFCGYEMOAIYRTETSS 659
 DB 601 LITVSKAKILLVLPYIPINSCANPFLYAIFTKNRRDRFFILLSKFCGYEMOAIYRTETSS 660
 QY 660 ATHNFHARKSHCSSAPRVNTNSYVLVPLNHSSQN 692
 DB 661 ATHNFHARKSHCSSAPRVNTNSYVLVPLNHSSQN 693

RESULT 8

AAR42082

ID AAR42082 standard; Protein; 695 AA.

AC AAR42082;

DT 05-MAY-1994 (first entry)

DE FSH receptor.

XX FSH; receptor; follicle stimulating hormone; GST;
 KW glutathione-S-transferase; primer; PCR; amplification;
 KW polymerase chain reaction; probe; antibody; overstimulation.

OS Homo sapiens.

XX W09320199-A.

XX 14-OCT-1993.

XX 29-MAR-1993; 93WO-EP00780.

XX 30-MAR-1992; 92EP-0200886.

XX (ALKU) AKZO NV.

XX De Leeuw R, Dijkema R;

XX WPI; 1993-336907/42.

XX N-PSDB; AAQ50013.

PT New follicle stimulating hormone receptor - and derived
 PT antibodies, anti-idiotypic antibodies, and transfected cells,
 PT useful e.g. in diagnosis and as antidote for FSH overstimulation

PS Claim 7; Page 20-23; 42pp; English.

XX The primers given in AAQ50029-34 were used in the cloning of GST-FSH-
 CC R1, GST-FSH-R2 and GST-FSH-R3 fusion protein constructs.
 CC Screening of the human testis cDNA library with a hFSH-R specific
 CC probe resulted in five recombinant phages positive in hybridisation.
 CC Sequence analysis was performed of the 2222 bp fragment of pGEM3Zc1
 CC (AAQ50013).

XX Sequence 695 AA;

Query Match 90.0%; Score 3235.5; DB 14; Length 695;

Best Local Similarity 89.5%; Pred. No. 4.6e-305;

Matches 622; Conservative 31; Mismatches 39; Indels 3; Gaps 2;

QY 1 MALLVSLAFGLTSGSCHHNLCHSNRVFLCQDSKVTEIPTDLPRNAIELRFLVTLKRV 60

```
Db 1 MALLVSLAFSLGSGCHRRICHSNRVFLCQSKVTEIPSDLPNAIELRVLTCLR 60
Oy 61 IPKGSFAGDLEKIEISONDVLEIADVFNPLKHEIRIEKANNLLYINPEAFONLP 120
Db 61 IQKGFSGDLEKIEISONDVLEIADVFNPLKHEIRIEKANNLLYINPEAFONLP 120
Oy 121 SLRYLLISMTGIRKLPVAVHKIOSLOKVLIDQDNIHIVARNSPFGLSFESVILWLSKN 180
Db 121 NLYQLLSMTGIRKLPVAVHKIOSLOKVLIDQDNIHIVARNSPFGLSFESVILWLSKN 180
Oy 181 GIEETHKAFNGTOLDLNLSDNNLEELPNDVFGAGSPVILDISRTKVSHPNHLN 240
Db 181 GIEETHKAFNGTOLDLNLSDNNLEELPNDVFGAGSPVILDISRTKVSHPNHLN 240
Oy 241 LKKLRARSTYRLKLPNDKPYTLMEASLTPSHCCAFANLKRQISELHPICNKSILROD 300
Db 241 LKKLRARSTYRLKLPNDKPYTLMEASLTPSHCCAFANLKRQISELHPICNKSILROD 300
Oy 301 IDDMTOIGDQVSLIDD-EPYSGKSDMKNYNEFDYDLCEVVDVTCSPKDAFNPCEIDM 359
Db 301 IDDMTOIGDQVSLIDD-EPYSGKSDMKNYNEFDYDLCEVVDVTCSPKDAFNPCEIDM 359
Oy 360 GYNILRVLWFIISLAIITGNTTVLVLTTSQTKLTPRFLMCLNAPADLCIGIYLLIAS 419
Db 360 GYNILRVLWFIISLAIITGNTTVLVLTTSQTKLTPRFLMCLNAPADLCIGIYLLIAS 419
Oy 420 VOLHRAASVYVLGWTFAAALPFIPIGSSYMKVSYICLPMDIDPSLSQLYVALLVNLV 539
Db 420 VOLHRAASVYVLGWTFAAALPFIPIGSSYMKVSYICLPMDIDPSLSQLYVALLVNLV 539
Oy 540 AFVVICGCTHYITLVYRNPTVSSSDTKIAKRMATLIFTDFLCHAPISFFAISAKVP 599
Db 540 AFVVICGCTHYITLVYRNPTVSSSDTKIAKRMATLIFTDFLCHAPISFFAISAKVP 599
Oy 600 LITVSKAKILLVLPYINSCANPFLYALFTKMFRRDFFILLSKFCGYEMOQIYRTTSS 659
Db 600 LITVSKAKILLVLPYINSCANPFLYALFTKMFRRDFFILLSKFCGYEMOQIYRTTSS 659
Oy 660 ATNHFAKSHCSAPRVN--SYVLVPLNHSSON 692
Db 660 ATNHFAKSHCSAPRVN--SYVLVPLNHSSON 692
Oy 661 TVMTHPRNGHCSSAPRVN--SYVLVPLNHSSON 692
Db 661 TVMTHPRNGHCSSAPRVN--SYVLVPLNHSSON 692

RESULT 9
AAW14782
ID AAW14782 standard; Protein; 695 AA.
AC AAW14782;
DE 20-JUN-1997 (first entry)
Oy FSH receptor.
KW Follicle stimulating hormone receptor; FSH receptor;
OS ovariian dysgenesis; hypogonadotropic hypogonadism; diagnosis.
XX Homo sapiens.
XX W09711194-A1.
XX 27-MAR-1997.
XX 20-SEP-1996; 96NO-F100501.
XX 20-SEP-1995; 95US-0531070.
XX (UYHE-) UNIV HELSINKI LICENSING LTD Oy.
XX
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PI Alttomaeki K, De La Chapelle A, Huhtaniemi I;
DR WPI: 1997-202900/18.
N-PSDB: AAT6181.
XX Diagnosis of ovarian dysgenesis and carriers from DNA abnormalities
XX by amplifying DNA and adding follicle stimulating hormone receptor
XX allele(s), i.e. codon 189, cleaving fragments, and examination
XX Disclosure: Page 18-21; 43pp; English.
XX The human follicle stimulating hormone (FSH) receptor (AAW14782)
XX is a G-protein coupled transmembrane receptor. A mutation in the
XX fshr gene (see also AAT6181) is associated with ovarian dysgenesis,
XX and methods for provided for the diagnosis of this disorder.
XX Sequence 695 AA:
SQ
Query Match 90.0%; Score 3235.5; DB 18; Length 695;
Best Local Similarity 95.5%; Pred. No. 4.6e-305;
Matches 622; Conservative 31; Mismatches 39; Indels 3; Gaps 2;
Oy 1 MALLVSLAFSLGSGCHRRICHSNRVFLCQSKVTEIPSDLPNAIELRVLTCLR 60
Db 1 MALLVSLAFSLGSGCHRRICHSNRVFLCQSKVTEIPSDLPNAIELRVLTCLR 60
Oy 61 IPKGSFAGDLEKIEISONDVLEIADVFNPLKHEIRIEKANNLLYINPEAFONLP 120
Db 61 IQKGFSGDLEKIEISONDVLEIADVFNPLKHEIRIEKANNLLYINPEAFONLP 120
Oy 121 SLRYLLISMTGIRKLPVAVHKIOSLOKVLIDQDNIHIVARNSPFGLSFESVILWLSKN 180
Db 121 NLYQLLSMTGIRKLPVAVHKIOSLOKVLIDQDNIHIVARNSPFGLSFESVILWLSKN 180
Oy 181 GIEETHKAFNGTOLDLNLSDNNLEELPNDVFGAGSPVILDISRTKVSHPNHLN 240
Db 181 GIEETHKAFNGTOLDLNLSDNNLEELPNDVFGAGSPVILDISRTKVSHPNHLN 240
Oy 241 LKKLRARSTYRLKLPNDKPYTLMEASLTPSHCCAFANLKRQISELHPICNKSILROD 300
Db 241 LKKLRARSTYRLKLPNDKPYTLMEASLTPSHCCAFANLKRQISELHPICNKSILROD 300
Oy 301 IDDMTOIGDQVSLIDD-EPYSGKSDMKNYNEFDYDLCEVVDVTCSPKDAFNPCEIDM 359
Db 301 IDDMTOIGDQVSLIDD-EPYSGKSDMKNYNEFDYDLCEVVDVTCSPKDAFNPCEIDM 359
Oy 360 GYNILRVLWFIISLAIITGNTTVLVLTTSQTKLTPRFLMCLNAPADLCIGIYLLIAS 419
Db 360 GYNILRVLWFIISLAIITGNTTVLVLTTSQTKLTPRFLMCLNAPADLCIGIYLLIAS 419
Oy 420 VOLHRAASVYVLGWTFAAALPFIPIGSSYMKVSYICLPMDIDPSLSQLYVALLVNLV 539
Db 420 VOLHRAASVYVLGWTFAAALPFIPIGSSYMKVSYICLPMDIDPSLSQLYVALLVNLV 539
Oy 540 AFVVICGCTHYITLVYRNPTVSSSDTKIAKRMATLIFTDFLCHAPISFFAISAKVP 599
Db 540 AFVVICGCTHYITLVYRNPTVSSSDTKIAKRMATLIFTDFLCHAPISFFAISAKVP 599
Oy 600 LITVSKAKILLVLPYINSCANPFLYALFTKMFRRDFFILLSKFCGYEMOQIYRTTSS 659
Db 600 LITVSKAKILLVLPYINSCANPFLYALFTKMFRRDFFILLSKFCGYEMOQIYRTTSS 659
Oy 660 ATNHFAKSHCSAPRVN--SYVLVPLNHSSON 692
Db 660 ATNHFAKSHCSAPRVN--SYVLVPLNHSSON 692
Oy 661 TVMTHPRNGHCSSAPRVN--SYVLVPLNHSSON 692
Db 661 TVMTHPRNGHCSSAPRVN--SYVLVPLNHSSON 692

RESULT 10
AAW27558
```

ID XX AAR27558 standard; Protein; 695 AA.
AC XX AAR27558;
DT XX 04-MAR-1993 (first entry)
DE XX FSHR.
KW Human; follicle stimulating hormone receptor; maturation;
KW spermatogenesis; birth control.
OS Homo sapiens.
PH Key Location/Qualifiers
FT Peptide 1..17
FT Protein /note= "signal peptide"
FT Domain 18..695
FT Domain /note= "mature hFSHR"
FT Domain 18..366
FT Domain /note= "N-terminal extracellular domain"
FT Domain 367..620
FT Domain /note= "transmembrane domain"
FT Domain 367..387
FT Domain /note= "transmembrane region I"
FT Domain 399..421
FT Domain /note= "transmembrane region II"
FT Domain 444..465
FT Domain /note= "transmembrane region III"
FT Domain 486..508
FT Domain /note= "transmembrane region IV"
FT Domain 529..550
FT Domain /note= "transmembrane region V"
FT Domain 574..597
FT Domain /note= "transmembrane region VI"
FT Domain 609..630
FT Domain /note= "transmembrane region VII"
FT Domain 631..695
FT Domain /note= "C-terminal intracellular domain"
PN WO9216620-A.
XX
XX
PD 01-OCT-1992.
XX
PF 02-JAN-1992; 92WO-US00122.
XX
PR 15-MAR-1991; 91US-0670085.
XX
PA (ISTF) ARS APPL RES SYST HOLDING NV.
XX
PI Cheng SVY, Kelton CA, Nugent NP, Schweickhardt RL;
XX WPI; 1992-349206/42.
DR N-PSDB; AAQ29377.
XX
PT Pure human FSH receptor, fragments and mutants - for preventing
PT follicle growth, maturation and spermatogenesis, also for use of
PT appropriate cell lines for bio-assays of FSH
XX
PS Claim 2; Page 25; 48pp; English.
XX
CC The protein sequence of human follicle stimulating hormone receptor
CC (FSHR) was deduced from the DNA sequence obtd. by screening a lambda
CC gtl1 cDNA library constructed from RNA extracted from human testis
CC with a rat FSHR cDNA clone as a probe. hFSHR binds to FSH to reduce
CC endogenous FSH bioactivity, in females to prevent follicle growth and
CC maturation and in males to prevent spermatogenesis, i.e. as a birth
CC control agent. hFSHR may be used in assays for detection of FSH
CC bioactivity and in x-ray crystallographic analysis to develop molecular
CC models useful in defining the tertiary structure of the hormone binding
CC domains of hFSHR. This will aid the design of peptides with FSH
CC (ant)agonist activity.
XX
XX Sequence 695 AA;
SQ

Query Match 89.9%; Score 3230.5; DB 13; Length 695;
Best Local Similarity 89.4%; Pred. No. 1.4e-304;
Matches 621; Conservative 32; Mismatches 39; Indels 3; Gaps 2;
QY 1 MALLVSLAFLGTGSGCHHLCNSNRVFLCQDSKYVTEPTDLPRAIELRFLVTLKRV 60
DB 1 MALLVSLAFLSLGSGCHHLCNSNRVFLCQDSKYVTEPTDLPRAIELRFLVTLKRV 60
QY 61 IPKSGPAGFGDLEKIEISQNDVLEIADVPFSLPKLHEIRIEKANNLLYINPEAFQNP 120
DB 61 IQKGFSGFGDLEKIEISQNNVLEIADVPFSLPKLHEIRIEKANNLLYINPEAFQNP 120
QY 121 SLRYLLISNTGIRKHPAVHKIQSLQKVLLODQNNINITHIVARNFSGMGLSPESVILWLSKN 180
DB 121 NLQYLLISNTGIRKHPDVHKIHSQKVLLODQNNINITHIVARNFSGMGLSPESVILWLSKN 180
QY 181 GIEIHNCAFNGTQDELNLSDNNBELPNDVFGASGPVILDISRTIRHSLPSYGLN 240
DB 181 GIEIHNCAFNGTQDELNLSDNNBELPNDVFGASGPVILDISRTIRHSLPSYGLN 240
QY 241 LKLRARSTYRLKKLPNDKRVTLMEASLYTPSHCCAFANLKRQISELHPICNKSILRQD 300
DB 241 LKLRARSTYRLKKLPNDKRVTLMEASLYTPSHCCAFANLKRQISELHPICNKSILRQD 300
QY 301 IDDMTOIGDQSVLIDD-EPYSGKSDMYNEFDYDLCNEVVDVTCSPKPAFNPCEBIM 359
DB 301 IDDMTOIGDQSVLIDD-EPYSGKSDMYNEFDYDLCNEVVDVTCSPKPAFNPCEBIM 359
QY 360 GYNILRVLIWIFISILAITGNTTVLVLTTSQYKLTVPFRLMCLNLAFAADLCIGIYLLIAS 419
DB 360 GYNILRVLIWIFISILAITGNTTVLVLTTSQYKLTVPFRLMCLNLAFAADLCIGIYLLIAS 419
QY 420 VDIHTKSOYHNYAIDWOTGACDAGPFTVPASELSVYTLTAITLERWHTITHAMQLECK 479
DB 420 VDIHTKSOYHNYAIDWOTGACDAGPFTVPASELSVYTLTAITLERWHTITHAMQLECK 479
QY 480 VOLRHAASVMVLGWTFAFAAALFPFIFGISSYKMYKVICLPMDIDSPSLQYVALLVNLV 539
DB 480 VOLRHAASVMVLGWTFAFAAALFPFIFGISSYKMYKVICLPMDIDSPSLQYVALLVNLV 539
QY 540 AFVVICGYTHIYLTVRNPTIVSSSDTKIAKRMATLIFTDFLCNAPISFFAISASLKV 599
DB 540 AFVVICGYTHIYLTVRNPTIVSSSDTKIAKRMATLIFTDFLCNAPISFFAISASLKV 599
QY 600 LITVSKAKILLVLPFINSKANPFLYAITFNFRDRDFFILLKFCGCEYKQAIYRTETSS 659
DB 600 LITVSKAKILLVLPFINSKANPFLYAITFNFRDRDFFILLKFCGCEYKQAIYRTETSS 659
QY 660 ATHNPFARKSHCSSAPRYTN--SYVLVPLNHSSQN 692
DB 660 TVNTHPRNGHSCSSAPRYTN--SYVLVPLNHSSQN 692
RESULT 11
AAR30520
ID AAR30520 standard; protein; 634 AA.
XX
AC AAR30520;
XX
DT 10-MAY-1993 (first entry)
DE N-terminal of LH receptor/FSH receptor chimera #29.
KW Follicle stimulating hormone receptor; luteinising hormone receptor;
KW human chorionic gonadotrophin; glycoprotein hormone receptor;
KW chimera; chimera.
XX
OS Chimaeric; homo sapiens.
XX
PN WO9222667-A.
XX
PD 23-DEC-1992.

XX 12-JUN-1992: 92WO-US04987.
 XX 14-JUN-1991: 91US-0715911.
 XX (UYNE-) UNIV NEW JERSEY.
 XX Bernard M. Moyle WR. Myers R;
 XX WPI: 1993-018150/02.
 XX Glyco:protein hormone receptor analogues - having binding
 PT affinity to human chorionic gonadotrophin, luteinising and
 PT follicle stimulating hormones, useful in bio:immunoassays
 XX Examples; Fig 12: 103pp: English.
 XX This sequence represents the N-terminal of a novel protein having a
 CC binding affinity for human chorionic gonadotrophin (hCG), luteinising
 CC hormone (LH), and follicle stimulating hormone (FSH). The protein
 CC itself is a chimera having residues from both their FSH receptor,
 CC and LH receptor. The receptor analogues can be used in bio:immunoassays
 CC for the simultaneous detection of both LH (or hCG) and FSH as
 CC well as their ratio of biological activities. The analogues can also
 CC be used for raising, purifying and assaying antibodies to the
 CC analogues. Coding sequence for the chimera was produced by two step
 CC PCR.
 XX Sequence 634 AA:
 XX Query Match 89.9%; Score 3229.5; DB 14; Length 634;
 XX Best Local Similarity 91.0%; Pred. No. 1.5e-304;
 XX Matches 630; Conservative 0; Mismatches 1; Indels 61; Gaps 1;
 OY 1 MALLVSLAFVLTGSGCHHMLCHCSNRVFLCQDSKYTEIPTDLPNNAIELRVLTCLR 60
 DB 1 MALLVSLAFVLTGSGCHHMLCHCSNRVFLCQDSKYTEIPTDLPNNAIELRVLTCLR 60
 OY 61 IPKGFAGFDLEKIEISONDVLEADVFNLSNPKLHEIREKANLLYINPEAFONLP 120
 DB 61 IPKGFAGFDLEKIEISONDVLEADVFNLSNPKLHEIREKANLLYINPEAFONLP 120
 OY 61 IPKGFAGFDLEKIEISONDVLEADVFNLSNPKLHEIREKANLLYINPEAFONLP 120
 DB 61 IPKGFAGFDLEKIEISONDVLEADVFNLSNPKLHEIREKANLLYINPEAFONLP 120
 OY 121 SLRYLLSNTGKHLPAVHTKIOSLQKVLDDIODNINHIHIVARNFSGLSFESVYLWLSKN 180
 DB 121 SLRYLLSNTGKHLPAVHTKIOSLQKVLDDIODNINHIHIVARNFSGLSFESVYLWLSKN 180
 OY 181 GIEZHNCAPNGTQDELNLSDNNNLELNDVDFGASGVVILDIERTKVHSLPHNGLEN 240
 DB 181 GIEZHNCAPNGTQDELNLSDNNNLELNDVDFGASGVVILDIERTKVHSLPHNGLEN 240
 OY 241 LKLRASSTYLLKLPNLRKLVTLWEASLTYPSCCAPANLKRQISELHPYCHKSILROD 300
 DB 241 LKLRASSTYLLKLPNLRKLVTLWEASLTYPSCCAPANLKRQISELHPYCHKSILROD 300
 OY 301 IDDMTOIGDQVSLIDDEPSYKGSMDMYNEFDVLCNEVDVTCSPKPAFNPCEIDMG 360
 DB 301 IDDMTOIGDQVSLIDDEPSYKGSMDMYNEFDVLCNEVDVTCSPKPAFNPCEIDMG 360
 OY 361 YNLRVLNPFISILATGNTVLVLTTSQKLTVPFLMCLNFAFADLCIGYLLLIASV 420
 DB 361 YNLRVLNPFISILATGNTVLVLTTSQKLTVPFLMCLNFAFADLCIGYLLLIASV 420
 OY 421 DIHTSOTHTNATDNGTACGDAAGFTTVPASLSVYTLTATLERMHTITHAWOLECKV 480
 DB 421 DIHTSOTHTNATDNGTACGDAAGFTTVPASLSVYTLTATLERMHTITHAWOLECKV 480
 OY 481 QLRHAASVYVLTGTPAALPPIFGISYKVSVCPLPMDISPSQLYVALLVLYLA 540
 DB 481 QLRHAASVYVLTGTPAALPPIFGISYKVSVCPLPMDISPSQLYVALLVLYLA 540
 OY 541 FVVICCTTHYLVTRNPTIVSSSDTIKARMATLIFTDFLCMAPIGFAISASIKVPL 600
 DB 541 FVVICCTTHYLVTRNPTIVSSSDTIKARMATLIFTDFLCMAPIGFAISASIKVPL 600
 OY 600 FVVICCTTHYLVTRNPTIVSSSDTIKARMATLIFTDFLCMAPIGFAISASIKVPL 600
 DB 600 FVVICCTTHYLVTRNPTIVSSSDTIKARMATLIFTDFLCMAPIGFAISASIKVPL 600

OY 601 ITVSKAKILLVFPYFINSKANPELYAIFTKNFRDRDFILLSSKFGCYEQAIYRTETSSA 660
 DB 540 ITVSKAKILLVFPYFINSKANPELYAIFTKNFRDRDFILLSSKFGCYEQAIYRTETSSA 599
 OY 661 TINFHARKSKSSAPRYNSVYVLPJHSSON 692
 DB 600 TINFHARKSKSSAPRYNSVYVLPJHSSON 631
 RESULT 12
 AAR30513
 ID AAR30513 standard; protein; 696 AA.
 XX AAR30513:
 XX AC AAR30513:
 XX DT 10-MAY-1993 (first entry)
 XX N-terminal of LH receptor/FSH receptor chimera #22.
 KW Follicle stimulating hormone receptor; luteinising hormone receptor;
 KW human chorionic gonadotrophin; glycoprotein hormone receptor;
 XX chimera; chimera.
 OS Chimeraic; homo sapiens.
 PN WO9222667-A.
 PD 23-DEC-1992.
 PF 12-JUN-1992: 92WO-US04987.
 PR 14-JUN-1991: 91US-0715911.
 XX (UYNE-) UNIV NEW JERSEY.
 XX Bernard M. Moyle WR. Myers R;
 XX WPI: 1993-018150/02.
 XX Glyco:protein hormone receptor analogues - having binding
 PT affinity to human chorionic gonadotrophin, luteinising and
 PT follicle stimulating hormones, useful in bio:immunoassays
 XX Examples; Fig 12: 103pp: English.
 XX This sequence represents the N-terminal of a novel protein having a
 CC binding affinity for human chorionic gonadotrophin (hCG), luteinising
 CC hormone (LH), and follicle stimulating hormone (FSH). The protein
 CC itself is a chimera having residues from both their FSH receptor,
 CC and LH receptor. The receptor analogues can be used in bio:immunoassays
 CC for the simultaneous detection of both LH (or hCG) and FSH as
 CC well as their ratio of biological activities. The analogues can also
 CC be used for raising and assaying antibodies to the
 CC analogues. Coding sequence for the chimera was produced by two step
 CC PCR.
 XX Sequence 696 AA:
 XX Query Match 88.7%; Score 3187.5; DB 14; Length 696;
 XX Best Local Similarity 89.6%; Pred. No. 2.1e-300;
 XX Matches 621; Conservative 22; Mismatches 49; Indels 1; Gaps 1;
 OY 1 MALLVSLAFVLTGSGCHHMLCHCSNRVFLCQDSKYTEIPTDLPNNAIELRVLTCLR 60
 DB 1 MALLVSLAFVLTGSGCHHMLCHCSNRVFLCQDSKYTEIPTDLPNNAIELRVLTCLR 60
 OY 61 IPKGFAGFDLEKIEISONDVLEADVFNLSNPKLHEIREKANLLYINPEAFONLP 120
 DB 61 IPKGFAGFDLEKIEISONDVLEADVFNLSNPKLHEIREKANLLYINPEAFONLP 120
 OY 121 SLRYLLSNTGKHLPAVHTKIOSLQKVLDDIODNINHIHIVARNFSGLSFESVYLWLSKN 179
 DB 121 SLRYLLSNTGKHLPAVHTKIOSLQKVLDDIODNINHIHIVARNFSGLSFESVYLWLSKN 179

Db 121 RLKYLSTGNTGIRTPDVTKISSEFNFIIEICDNLHITTPGNAFOGMNNESTVLKLYG 180
 Qy 180 NGIEEIHNCFAFGTQDLDELNSDNNLELNDVFOGASGVILDSRTKVSHPNHLG 239
 Db 181 NGFEVQSHAFNGCTTSLSEKENIYLEKHSNGAFQATGPVILDSRTKVSHPNHLG 240
 Qy 240 NLKRLARSTYRLKLLPNLDFVTLMEASLTYPSCCAFANLKRQISELHPICNKSILRQ 299
 Db 241 NLKRLARSTYRLKLLPNLDFVTLMEASLTYPSCCAFANLKRQISELHPICNKSILRQ 300
 Qy 300 DIDDMTOIGDORVSLIDDEPSYKSGSDMYNEFDYDLCNEVDVTCSPKDFAFNCPEDIM 359
 Db 301 DIDDMTOIGDORVSLIDDEPSYKSGSDMYNEFDYDLCNEVDVTCSPKDFAFNCPEDIM 360
 Qy 360 GYNILRLVLIWFISITLAIKNTVTLVLTTSQYKLTVPFRLMCLNLAFAADLCIGIYLLIAS 419
 Db 361 GYNILRLVLIWFISITLAIKNTVTLVLTTSQYKLTVPFRLMCLNLAFAADLCIGIYLLIAS 420
 Qy 420 VDIHTKSOYHNYAIDWOTGAGCDAAAGFTTFVASELSVYTLTAITLERWHTITHAMQLECK 479
 Db 421 VDIHTKSOYHNYAIDWOTGAGCDAAAGFTTFVASELSVYTLTAITLERWHTITHAMQLECK 480
 Qy 480 VOLRHAASVMVLGWTFAFAALPFIPIGSISSYMKVSIICLPMDIDSPLSQLYMALLVNLV 539
 Db 481 VOLRHAASVMVLGWTFAFAALPFIPIGSISSYMKVSIICLPMDIDSPLSQLYMALLVNLV 540
 Qy 540 AFVVICGCTHYILTVRNPTIVSSSDTKIAKRMATLIFTDFLCMAPISFPAISASLKVP 599
 Db 541 AFVVICGCTHYILTVRNPTIVSSSDTKIAKRMATLIFTDFLCMAPISFPAISASLKVP 600
 Qy 600 LITVSKAKILLVLPYINSCANPELYAIFTKNFRDRFFILLSKFGCYEMOQAIYRTETSS 659
 Db 601 LITVSKAKILLVLPYINSCANPELYAIFTKNFRDRFFILLSKFGCYEMOQAIYRTETSS 660
 Qy 660 ATHNFHARKSHCSSAPRVNTSYVLVPLNHSQN 692
 Db 661 ATHNFHARKSHCSSAPRVNTSYVLVPLNHSQN 693

RESULT 13

AAR30521

ID AAR30521 standard; protein: 696 AA;

XX AC AAR30521;

XX DT 10-MAY-1993 (first entry)

XX DE N-terminal of LH receptor/FSH receptor chimaera #30.

XX KW Follicle stimulating hormone receptor; luteinising hormone receptor;

XX KW human chorionic gonadotrophin; glycoprotein hormone receptor;

XX KW chimaera; chimera.

XX OS Chimaeric; homo sapiens.

XX PN WO9222667-A.

XX PD 23-DEC-1992.

XX PF 12-JUN-1992; 92WO-US04987.

XX PR 14-JUN-1991; 91US-0715911.

XX PA (UYNE-) UNIV NEW JERSEY.

XX PI Bernard M, Moyle WR, Myers R;

XX DR WPI; 1993-018150/02.

XX PT Glyco:protein hormone receptor analogues - having binding

XX PT affinity to human chorionic gonadotrophin, luteinising and

XX PT follicle stimulating hormones, useful in bio:immunoassays

PS Examples; Fig 12; 103pp; English.

XX This sequence represents the N-terminal of a novel protein having a
 CC binding affinity for human chorionic gonadotrophin (hCG), luteinising
 CC hormone (LH), and follicle stimulating hormone (FSH). The protein
 CC itself is a chimaera having residues from both the FSH receptor,
 CC and LH receptor. The receptor analogues can be used in bio:immunoassays
 CC for the simultaneous detection of both LH (or hCG) and FSH as
 CC well as their ratio of biological activities. The analogues can also
 CC be used for raising, purifying and assaying antibodies to the
 CC analogues. Coding sequence for the chimaera was produced by two step
 CC PCR.

SQ Sequence 696 AA;

Query Match 88.7%; Score 3187.5; DB 14; Length 696;
 Best Local Similarity 89.6%; Pred. No. 2,1e-300;
 Matches 621; Conservative 22; Mismatches 49; Indels 1; Gaps 1;

Qy 1 MALLLVSLAFLGSGCHHWLCHCSNRVFLCQDSKVTETPTDLPRNAIELRFLVTKLV 60
 Db 1 MALLLVSLAFLGSGCHHWLCHCSNRVFLCQDSKVTETPTDLPRNAIELRFLVTKLV 60
 Qy 61 IPKGSFAGFGLKIEISQNDVLEIVADVFENLPKLHIEIRKANNLLIYNPEAFQNL 120
 Db 61 IPKGSFAGFGLKIEISQSDSLERIEANAFDNLNLSSELLIQNTKLLIYEPGAFNLP 120
 Qy 121 SLRYLLSNTGKIKLPAVHKIQSLQ-KVLLDIOQNIHIVARNFSFGLSPESVILWSK 179
 Db 121 RLKYLSTGNTGIRTPDVTKISSEFNFIIEICDNLHITTPGNAFOGMNNESTVLKLYG 180
 Qy 180 NGIEEIHNCFAFGTQDLDELNSDNNLELNDVFOGASGVILDSRTKVSHPNHLG 239
 Db 181 NGFEVQSHAFNGCTTSLSEKENIYLEKHSNGAFQATGPVILDSRTKVSHPNHLG 240
 Qy 240 NLKRLARSTYRLKLLPNLDFVTLMEASLTYPSCCAFANLKRQISELHPICNKSILRQ 299
 Db 241 NLKRLARSTYRLKLLPNLDFVTLMEASLTYPSCCAFANLKRQISELHPICNKSILRQ 300
 Qy 300 DIDDMTOIGDORVSLIDDEPSYKSGSDMYNEFDYDLCNEVDVTCSPKDFAFNCPEDIM 359
 Db 301 DIDDMTOIGDORVSLIDDEPSYKSGSDMYNEFDYDLCNEVDVTCSPKDFAFNCPEDIM 360
 Qy 360 GYNILRLVLIWFISITLAIKNTVTLVLTTSQYKLTVPFRLMCLNLAFAADLCIGIYLLIAS 419
 Db 361 GYNILRLVLIWFISITLAIKNTVTLVLTTSQYKLTVPFRLMCLNLAFAADLCIGIYLLIAS 420
 Qy 420 VDIHTKSOYHNYAIDWOTGAGCDAAAGFTTFVASELSVYTLTAITLERWHTITHAMQLECK 479
 Db 421 VDIHTKSOYHNYAIDWOTGAGCDAAAGFTTFVASELSVYTLTAITLERWHTITHAMQLECK 480
 Qy 480 VOLRHAASVMVLGWTFAFAALPFIPIGSISSYMKVSIICLPMDIDSPLSQLYMALLVNLV 539
 Db 481 VOLRHAASVMVLGWTFAFAALPFIPIGSISSYMKVSIICLPMDIDSPLSQLYMALLVNLV 540
 Qy 540 AFVVICGCTHYILTVRNPTIVSSSDTKIAKRMATLIFTDFLCMAPISFPAISASLKVP 599
 Db 541 AFVVICGCTHYILTVRNPTIVSSSDTKIAKRMATLIFTDFLCMAPISFPAISASLKVP 600
 Qy 600 LITVSKAKILLVLPYINSCANPELYAIFTKNFRDRFFILLSKFGCYEMOQAIYRTETSS 659
 Db 601 LITVSKAKILLVLPYINSCANPELYAIFTKNFRDRFFILLSKFGCYEMOQAIYRTETSS 660
 Qy 660 ATHNFHARKSHCSSAPRVNTSYVLVPLNHSQN 692
 Db 661 ATHNFHARKSHCSSAPRVNTSYVLVPLNHSQN 693

RESULT 14

AAR30522

ID AAR30522 standard; protein: 620 AA.

XX AC AAR30522;

	Dd	286	VNIRLVYWFISLTATGNTVTVLVLTTSQYKLTVPRTFACNLAFADLCIGTYLLLSASV	345
	Oy	421	DIHTKSQYHNYAIDMOTGAGCDAAGFTVFASELSVYTLTAITLERWHITTHANOLECKV	480
	Dd	346	DIHTKSQYHNYAIDMOTGAGCDAAGFTVFASELSVYTLTAITLERWHITTHANOLECKV	405
	Oy	481	QRMAASVWVLGWTFAPAAALPFIPTGISYMKYSICLPMOIDSPLSOLTVNALLVNLVA	540
	Dd	406	QRMAASVWVLGWTFAPAAALPFIPTGISYMKYSICLPMOIDSPLSOLTVNALLVNLVA	465
	Oy	541	PWVICGCYTHIYLTVRNPITVSSSSDTKIAKNMATLIPTDFLCNAPISPFAISASLKVPL	600
	Dd	466	PWVICGCYTHIYLTVRNPITVSSSSDTKIAKNMATLIPTDFLCNAPISPFAISASLKVPL	525
	Oy	601	ITSVKAKILLVLFPYINSCANPFYAIFTKNFRDFFILLSKFCGYEMQAQIYRTETSSA	660
	Dd	526	ITSVKAKILLVLFPYINSCANPFYAIFTKNFRDFFILLSKFCGYEMQAQIYRTETSSA	585
	Oy	661	TINPHARKSCHSSAPRVINSYVLYPLMHSSON	692
	Dd	586	TINPHARKSCHSSAPRVINSYVLYPLMHSSON	617
		RESULT 15		
		AAR30509		
	ID	AAR30509 standard; protein: 689 AA.		
	AC	AAR30509:		
	CC			
	DD			
	DT			
	DE	10-MAY-1993 (first entry)		
	DK	N-terminal of LH receptor/FSH receptor chimera #18.		
	DJ	Follicle stimulating hormone receptor; lutetising hormone receptor;		
	KW	human chorionic gonadotrophin; glycoprotein hormone receptor;		
	KV	chimera; chimera.		
	XX	Chimaeric: homo sapiens.		
	OS			
	PN	HO9222667-A.		
	XX			
	PD	23-DEC-1992.		
	PZ			
	PR	12-JUN-1992: 92WO-US04987.		
	PP			
	PR	14-JUN-1991: 91US-0715911.		
	PA	(UYNE-) UNIV NEW JERSEY.		
	PI	Bernard M, Moyle WR, Myers R;		
	PI	WPI: 1993-018150/02.		
	DR			
	XX	Glyco:protein hormone receptor analogues - having binding		
	TT	affinity to human chorionic gonadotrophin, lutetinsing and		
	PT	follicle stimulating hormones, useful in bio:immunoassays		
	PS	Examples: Fig 12: 103pp: English.		
	XX			
	CC	This sequence represents the N-terminal of a novel protein having a		
	CC	binding affinity for human chorionic gonadotrophin (hCG), lutetinsig		
	CC	hormone (LH), and follicle stimulating hormone (FSH). The protein		
	CC	itself is a chimera having residues from both the FSH receptor,		
	CC	LH receptor. The receptor analogues can be used in bio:immunoassays		
	CC	for the simultaneous detection of both LH (or hCG) and FSH as		
	CC	well as their ratio of biological activities. The analogues can also		
	CC	be used for testing, purifying and assaying antibodies to the		
	CC	analogues. Coding sequence for the chimera was produced by two step		
	CC	PCR.		
	XX			
	SO	Sequence 689 AA:		

Query Match		86.6%	Score 3112	DB 14	Length 689
Best Local Similarity		87.3%	Pred. No. 4	6e-293	
Matches 607		Conservative 32	Mismatches 44	Indels 12	Gaps 3
Qy	1	MALLVSLAFLAGTGGCHHLCNSNRVFLCQDSKVTEIPTDLPRNAIELRFLVLTCLR	60		
Db	1	MALLVSLAFLAGTGGCHHLCNSNRVFLCQDSKVTEIPTDLPRNAIELRFLVLTCLR	60		
Qy	61	IPKGSFAGFGLKIEISONDVLEIVADVFSNLPKLHEIRIEKANNLLYINPEAFONLP	120		
Db	61	IPKGSFAGFGLKIEISONDVLEIVADVFSNLPKLHEIRIEKANNLLYINPEAFONLP	120		
Qy	121	SLRYLLISNTGIRKHPAVHKIQSLQKVLDDIQDNINIHIVARNSEFGLSFESVILWLSKN	180		
Db	121	SLRYLLISNTGIRKHPAVHKIQSLQKVLDDIQDNINIHIVARNSEFGLSFESVILWLSKN	180		
Qy	181	GIEIHNCAFNGTQDELNLSNNDNLEELPNDVFOGASGPVILDISRTKVHSLPNHGLE	240		
Db	181	GIEIHNCAFNGTQDELNLSNNDNLEELPNDVFOGASGPVILDISRTKVHSLPNHGLE	240		
Qy	241	LKLLRABSTYRLKLPNLDKFTVLMASLTYPHSCCAFANLKROISELHPICHNKSILRQD	300		
Db	241	IQTIALUSSYSLTKLPSEKFTSLLVATLTPSHCCAFRLPKK-----EQNFSESI	292		
Qy	301	IDDMTOIGDQVRSLIDDEPSYG---KGSMDMYNEFDYDLNCEVVDVTCSPKPDAPNCPED	357		
Db	293	FENFSKQCESTVRKADNETLYSAIFEENELSGWDYDYGFCSPKT-LOCAPEPDAPNCPED	351		
Qy	358	IMGYNLRVLWIFTSILAITGNTTVLVLTTSQYKLTVPRLMCNLAFAADLCIGIYLLI	417		
Db	352	IMGYAFLRVLWIFTSILAITGNTTVLVLTTSQYKLTVPRLMCNLAFAADLCIGIYLLI	411		
Qy	418	ASVDIHTKSOYHNVAIDWQTGAGCDAAGFTVFASLSVYTLTAITLERWHTITHAMQLE	477		
Db	412	ASVDIHTKSOYHNVAIDWQTGAGCDAAGFTVFASLSVYTLTAITLERWHTITHAMQLE	471		
Qy	478	CKVOLRHAASVMVLGWTFAFAALFPIFGISSYMKVSIKLPMDIDSPLSQLYVMALLVLN	537		
Db	472	CKVOLRHAASVMVLGWTFAFAALFPIFGISSYMKVSIKLPMDIDSPLSQLYVMALLVLN	531		
Qy	538	VLAFVWICGCTHYIYLVNRNPTIVSSSDTKIAKRMATLIFTDFLCMAPISFFAISASLK	597		
Db	532	VLAFVWICGCTHYIYLVNRNPTIVSSSDTKIAKRMATLIFTDFLCMAPISFFAISASLK	591		
Qy	598	VPLITVSKAKILLVFLYPINSCANPFLYAIFTKNFRDFFILLSKFCGYEMQAOIYRTET	657		
Db	592	VPLITVSKAKILLVFLYPINSCANPFLYAIFTKNFRDFFILLSKFCGYEMQAOIYRTET	651		
Qy	658	SSATHNFARKSHCSCSAPRVNTSNVYVPLNHSQN	692		
Db	652	SSATHNFARKSHCSCSAPRVNTSNVYVPLNHSQN	686		

Search completed: June 16, 2003, 13:33:19
Job time : 49.5845 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 16, 2003, 13:31:41 : Search time 21.7674 Seconds
(without alignments)
935.375 Million cell updates/sec

Title: US-09-877-804-6

Perfect score: 359.4

Sequence: 1 MALLVSLAPLTGSGCHH.....SAPRTNSVLYPLNHSQSN 692

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_AA.*
1: /cgn2_6/ptodata/2/las/5A.COMB.pep.*
2: /cgn2_6/ptodata/2/las/5A.COMB.pep.*
3: /cgn2_6/ptodata/2/las/5A.COMB.pep.*
4: /cgn2_6/ptodata/2/las/5A.COMB.pep.*
5: /cgn2_6/ptodata/2/las/5A.COMB.pep.*
6: /cgn2_6/ptodata/2/las/5A.COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	359.4	100.0	682	US-07-757-342D-6
2	3235.5	90.0	681	US-08-497-886-2
3	3235.5	90.0	685	US-08-492-885-2
4	3235.5	90.0	684	US-08-474-986-2
5	1817.5	50.6	764	US-07-741-453A-60
6	1807.5	50.3	696	US-07-757-342D-3
7	1797	50.0	700	US-07-757-342D-3
8	1776	49.4	674	US-07-757-342D-10
9	1776	49.4	699	US-07-757-342D-2
10	1674	46.6	764	US-07-741-453A-61
11	1673.5	46.6	764	US-07-741-453A-54
12	1670	46.5	792	US-07-741-453A-56
13	1659	46.2	764	US-07-741-453A-59
14	1658	46.1	764	US-07-757-342D-5
15	1632.5	46.0	795	US-07-741-453A-55
16	1628.5	44.8	390	US-08-460-576-2
17	1628.5	44.8	423	US-08-752-876-33
18	1598	44.5	436	US-08-735-876-2
19	1598	44.5	436	US-07-757-342D-8
20	1567.5	43.6	611	US-07-757-342D-7
21	1542	42.9	764	US-07-741-453A-29
22	1474.5	41.0	337	US-08-118-270-55
23	1474.5	41.0	337	PCT-US93-08528-55
24	1027.5	28.6	336	US-08-118-270-54
25	1027.5	28.6	336	PCT-US93-08528-54
26	983.5	27.4	332	US-08-118-270-53
27	983.5	27.4	332	US-08-118-270-53

Sequence 53, Appl
Sequence 2, Appl
Sequence 2, Appl
Sequence 2, Appl
Sequence 58, Appl
Sequence 35, Appl
Sequence 4, Appl
Sequence 6, Appl
Sequence 4, Appl
Sequence 6, Appl
Sequence 2, Appl
Sequence 16, Appl
Sequence 2, Appl
Sequence 2, Appl
Sequence 2, Appl
Sequence 2, Appl

ALIGNMENTS

RESULT 1
US-07-757-342D-6
: Sequence 6, Application US/07757342D
: Patent No. 6218509
: GENERAL INFORMATION:
: APPLICANT: IGARASHI, Masao
: MINEGISHI, Takashi
: NAKAMURA, Kazuto
: TITLE OF INVENTION: PROTEIN, DNA AND USE THEREOF
: NUMBER OF SEQUENCES: 10
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &
: USHMAN
: STREET: 130 Water Street
: CITY: Boston
: STATE: Massachusetts
: COUNTRY: US
: ZIP: 02109
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/07/757,342D
: FILING DATE: 10-Sep-1991
: CLASSIFICATION: <Unknown>
: ATTORNEY/AGENT INFORMATION:
: NAME/ADDRESS:
: REGISTRATION NUMBER: 51003
: REFERENCE/DOCKET NUMBER: 41226
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (617)523-3400
: TELEFAX: (617)523-6440
: TELEX: 200291 STRE UR
: INFORMATION FOR SEQ ID NO: 6:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 692 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-07-757-342D-6

Query Match 100.0%; Score 359.4; DB 4; Length 692;
Best Local Similarity 100.0%; Prod. No. 8e-284; 0;
Matches 692; Conservative 0; Mismatches 0; Gaps 0;
OY 1 MALLVSLAPLTGSGCHHCHSRVFLCQDSKVTPTDLPRLNLEPLVTLKLV 60
|||||

Db 1 MALLVSLAFLGTSGCHHLCNSNRVFLQDQSKVTEIPTOLPRNAIELRVFLTKLRV 60
Qy 61 IPKGSFAGDLEKIEISQNDVLEIADVFSLNPKLHEIRIEKANNLLYINPEAFONLP 120
Db 61 IPKGSFAGDLEKIEISQNDVLEIADVFSLNPKLHEIRIEKANNLLYINPEAFONLP 120
Qy 121 SLRYLLISNTGIKHLPVAVHKIQSLQKVLDDIQDNNIHIIVARNFMSFESVILWLSKN 180
Db 121 SLRYLLISNTGIKHLPVAVHKIQSLQKVLDDIQDNNIHIIVARNFMSFESVILWLSKN 180
Qy 181 GIEIHNCAGNGTQDELNLSDDNNLEELPNVFGASGVPVILDISRTKVHSLPNHGLEN 240
Db 181 GIEIHNCAGNGTQDELNLSDDNNLEELPNVFGASGVPVILDISRTKVHSLPNHGLEN 240
Qy 241 LKLRARSTYRLKLPNLDKFTVLTMEASLTYPSCCAFANLKRQISELHPCTCNKSIILROD 300
Db 241 LKLRARSTYRLKLPNLDKFTVLTMEASLTYPSCCAFANLKRQISELHPCTCNKSIILROD 300
Qy 301 IDDMTOIGDQVSLIDDEPSYKSGSDMMYNEFDYDLNCEVVDVTCSPKPAFNPCEDIMG 360
Db 301 IDDMTOIGDQVSLIDDEPSYKSGSDMMYNEFDYDLNCEVVDVTCSPKPAFNPCEDIMG 360
Qy 361 YNILRVLIWFISILAITGNTTVLVLTTSQYKLVPRFLMCNLAFAADLCIGIYLLIASV 420
Db 361 YNILRVLIWFISILAITGNTTVLVLTTSQYKLVPRFLMCNLAFAADLCIGIYLLIASV 420
Qy 421 DIHTKSOYHVAIDWOTGAGDAGFTVFASLSVYTLTAITLERWHTITHAMOLECKV 480
Db 421 DIHTKSOYHVAIDWOTGAGDAGFTVFASLSVYTLTAITLERWHTITHAMOLECKV 480
Qy 481 QLRHAASVMVLGTFVFAAALFPFIFGISSYKMSVICLPMDDSPLSQLYVMAILLVNLVA 540
Db 481 QLRHAASVMVLGTFVFAAALFPFIFGISSYKMSVICLPMDDSPLSQLYVMAILLVNLVA 540
Qy 541 FWICGCTHYLYVRNPVTVSSSDTKIAKRMATLIFTDFLCMAPISFFAISASLKVPL 600
Db 541 FWICGCTHYLYVRNPVTVSSSDTKIAKRMATLIFTDFLCMAPISFFAISASLKVPL 600
Qy 601 ITVSKAKILLVLPINSCANPFLYAIFTKFRDRDFILLSKFCYEMQAOIYRTETSSA 660
Db 601 ITVSKAKILLVLPINSCANPFLYAIFTKFRDRDFILLSKFCYEMQAOIYRTETSSA 660
Qy 661 THNPHARKSHCSSAPRVNTSYLVPLNHSQN 692
Db 661 THNPHARKSHCSSAPRVNTSYLVPLNHSQN 692

RESULT 2

US-08-487-886-2
; Sequence 2, Application US/08487886
; Patent No. 5744448
; GENERAL INFORMATION:
; APPLICANT: Kelton, Christie Ann
; APPLICANT: Schweickhardt, Rene Lynn
; APPLICANT: Cheng, Shirley Vui Yen
; APPLICANT: Nugent, No. 5744448een Patrice
; TITLE OF INVENTION: Human Follicle Stimulating
; TITLE OF INVENTION: Hormone Receptor
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Stephan P. Williams,
; ADDRESSEE: Ares-serono, Inc.
; STREET: Exchange Place, 37th floor
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" diskette, 1.44 MB, high density
; COMPUTER: IBM PS/2, model 55 SX
; OPERATING SYSTEM: MS-DOS version 4.0
; SOFTWARE: VAX/VMS Massall via Kermit to IBM MS-DOS
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/487,886
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA: 07/670,085
; APPLICATION NUMBER: 15-MAR-1991
; FILING DATE: 15-MAR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Williams, Stephan P.
; REGISTRATION NUMBER: 28546
; REFERENCE/DOCKET NUMBER: US/252
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 723-1300
; TELEFAX: (617) 723-8923
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 695
; TYPE: Amino acid
; TOPOLOGY: Linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: signal sequence
; LOCATION: -17 to -1
; IDENTIFICATION METHOD: hydrophobic
; FEATURE:
; NAME/KEY: putative amino-terminal extracellular domain
; LOCATION: 1 to 349
; IDENTIFICATION METHOD: similarity with other
; IDENTIFICATION METHOD: dimeric glycoprotein receptor extracellular
; IDENTIFICATION METHOD: domains, hydrophilic
; FEATURE:
; NAME/KEY: transmembrane domain
; LOCATION: 350 to 613
; IDENTIFICATION METHOD: similarity to other G
; IDENTIFICATION METHOD: protein-coupled receptor transmembrane domains
; FEATURE:
; NAME/KEY: putative transmembrane region I
; LOCATION: 350 to 370
; IDENTIFICATION METHOD: similarity to other G
; IDENTIFICATION METHOD: protein-coupled receptor transmembrane regions,
; IDENTIFICATION METHOD: hydrophobic, about 20-23 amino acids in length
; FEATURE:
; NAME/KEY: putative transmembrane region II
; LOCATION: 382 to 404
; IDENTIFICATION METHOD: similarity to other G
; IDENTIFICATION METHOD: protein-coupled receptor transmembrane regions,
; IDENTIFICATION METHOD: hydrophobic, about 20-23 amino acids in length
; FEATURE:
; NAME/KEY: putative transmembrane region III
; LOCATION: 427 to 448
; IDENTIFICATION METHOD: similarity to other G
; IDENTIFICATION METHOD: protein-coupled receptor transmembrane regions,
; IDENTIFICATION METHOD: hydrophobic, about 20-23 amino acids in length
; FEATURE:
; NAME/KEY: putative transmembrane region IV
; LOCATION: 469 to 491
; IDENTIFICATION METHOD: similarity to other G
; IDENTIFICATION METHOD: protein-coupled receptor transmembrane regions,
; IDENTIFICATION METHOD: hydrophobic, about 20-23 amino acids in length
; FEATURE:
; NAME/KEY: putative transmembrane region V
; LOCATION: 512 to 533
; IDENTIFICATION METHOD: similarity to other G
; IDENTIFICATION METHOD: protein-coupled receptor transmembrane regions,
; IDENTIFICATION METHOD: hydrophobic, about 20-23 amino acids in length
; FEATURE:
; NAME/KEY: putative transmembrane region VI
; LOCATION: 557 to 580
; IDENTIFICATION METHOD: similarity to other G
; IDENTIFICATION METHOD: protein-coupled receptor transmembrane regions,
; IDENTIFICATION METHOD: hydrophobic, about 20-23 amino acids in length
; FEATURE:
; NAME/KEY: putative transmembrane region VII
; LOCATION: 592 to 613

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IDENTIFICATION METHOD: similarity to other G
IDENTIFICATION METHOD: protein-coupled receptor transmembrane regions,
IDENTIFICATION METHOD: hydrophobic, about 20-23 amino acids in length
FEATURE:
NAME/KEY: putative carboxy-terminal intracellular
NAME/KEY: domain
LOCATION: 614 to 678
US-08-487-886-2

Query Match          90.0%  Score 3235.5; DB 1; Length 695;
Best Local Similarity 89.5%  Pred. No. 1.1e-254;
Matches 622; Conservative 31; Mismatches 30; Indels 3; Gaps 2;

OY 1 MALLVSLLAFLATGSGCHRLCHGSRVFCDSKVEITPDLPRNRIELRFLVTKLRV 60
DB 1 MALLVSLLAFLSLGSGCHRLCHGSRVFCDSKVEITPDLPRNRIELRFLVTKLRV 60
OY 61 IKGSPAGPDLKRIEISONDVLEIENDVSNLPLKHEIRIEKANLLYINPEAFONCP 120
DB 61 IKGSPAGPDLKRIEISONDVLEIENDVSNLPLKHEIRIEKANLLYINPEAFONCP 120
OY 121 SLRYLLSNGTGKHPANVKGLOKVLQDQNNINIRIVARISPMGLSPESVILWLN 180
DB 121 SLRYLLSNGTGKHPANVKGLOKVLQDQNNINIRIVARISPMGLSPESVILWLN 180
OY 121 NLOVLLISNGIKHLPDVHKLHSLQKVLQDQNNINIRIVARISPMGLSPESVILWLN 180
DB 121 NLOVLLISNGIKHLPDVHKLHSLQKVLQDQNNINIRIVARISPMGLSPESVILWLN 180
OY 181 GIEEIHNCFAFGTQDLDELNLSDNNHLELNDPFGAGSPVILDIRTKVHSLPHGLN 240
DB 181 GIEEIHNCFAFGTQDLDELNLSDNNHLELNDPFGAGSPVILDIRTKVHSLPHGLN 240
OY 241 LKKURASTYRLKLPDLKRLVFLMEASLTYPSCCAFANLKRQISELHPICNKSILROD 300
DB 241 LKKURASTYRLKLPDLKRLVFLMEASLTYPSCCAFANLKRQISELHPICNKSILROE 300
OY 301 IDMTQIGQORVSLIDD-EPYSGKSGDMYNEFYDLCNEVDVTCSPKPDAPNCPEDIM 359
DB 301 VDTMTQIGQORVSLIDD-EPYSGKSGDMYNEFYDLCNEVDVTCSPKPDAPNCPEDIM 360
OY 360 GYNILRLVLIWISTLAITGNTVVLVLTGNTVLPFLNCLAPADLCIGVILLIAS 419
DB 360 GYNILRLVLIWISTLAITGNTVVLVLTGNTVLPFLNCLAPADLCIGVILLIAS 419
OY 420 VDIHTKSOYHNATIDMOTGAGCDAAGFTVPASELSVYLTATILRHHTITHAMOLCK 479
DB 420 VDIHTKSOYHNATIDMOTGAGCDAAGFTVPASELSVYLTATILRHHTITHAMOLCK 480
OY 480 VOLRRAASVYVGLYTFAPAAALPFIIGISYMYKSYICLDPIDSPLSQLYMALLVNLVYL 539
DB 480 VOLRRAASVYVGLYTFAPAAALPFIIGISYMYKSYICLDPIDSPLSQLYMALLVNLVYL 540
OY 540 APVVICGCTHILKLYVNPVTVSSSDTKIAKRNATLIPTOFICHAPISSFAISKLVP 599
DB 540 APVVICGCTHILKLYVNPVTVSSSDTKIAKRNATLIPTOFICHAPISSFAISKLVP 599
OY 600 LITVSKAKILLVLPYINSCANPFLYALPTKRNFRDPTLLSKFCGYEMOAOIYRTTSS 659
DB 600 LITVSKAKILLVLPYINSCANPFLYALPTKRNFRDPTLLSKFCGYEMOAOIYRTTSS 660
OY 660 ATHNPHARKSCSAPRVYN--SYVLPLHSSQN 692
DB 661 TVNTHPHRNGHSCSAPRVYNGSYVLPLSHLAON 695
```

RESULT 3

US-08-482-855-2

Sequence 2, Application US/08482855

Patent No. 6121016

GENERAL INFORMATION:

APPLICANT: Kelton, Christie Ann

APPLICANT: Schweickhardt, Rene Lynn

APPLICANT: Cheng, Shirley Vui Yen

APPLICANT: Nugent, No. 6121016een Patrice

TITLE OF INVENTION: Human Follicle Stimulating

TITLE OF INVENTION: Hormone Receptor

```
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Stephen P. Williams,
ADDRESS: Area-Serono, Inc.,
CITY: Exchange Place, 37th floor
STATE: Boston
CITY: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" diskette, 1.44 MB, high density
COMPUTER: IBM PS/2, model 55 SX
OPERATING SYSTEM: MS-DOS version 4.0
SOFTWARE: VAX/VMS Massill via Kermit to IBM MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482.855
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA: 07/670,085
APPLICATION NUMBER: 8-1991
ATTORNEY/AGENT INFORMATION:
NAME: Williams, Stephen P.
REGISTRATION NUMBER: 28546
REFERENCE/DOCKET NUMBER: US/252
TELEPHONE: (617) 723-1300
TELEFAX: (617) 723-8923
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 695
TYPE: Amino acid
TOPOLOGY: Linear
FEATURE:
NAME/KEY: signal sequence
LOCATION: 1 to 10
IDENTIFICATION METHOD: hydrophobic
FEATURE:
NAME/KEY: putative amino-terminal extracellular domain
LOCATION: 1 to 349
IDENTIFICATION METHOD: similarity with other
IDENTIFICATION METHOD: dimeric glycoprotein receptor extracellular
IDENTIFICATION METHOD: domains, hydrophilic
FEATURE:
NAME/KEY: transmembrane domain
LOCATION: 350 to 613
IDENTIFICATION METHOD: similarity to other G
IDENTIFICATION METHOD: protein-coupled receptor transmembrane domains
FEATURE:
NAME/KEY: putative transmembrane region I
LOCATION: 350 to 404
IDENTIFICATION METHOD: similarity to other G
IDENTIFICATION METHOD: protein-coupled receptor transmembrane regions,
IDENTIFICATION METHOD: hydrophobic, about 20-23 amino acids in length
FEATURE:
NAME/KEY: putative transmembrane region II
LOCATION: 382 to 404
IDENTIFICATION METHOD: similarity to other G
IDENTIFICATION METHOD: protein-coupled receptor transmembrane regions,
IDENTIFICATION METHOD: hydrophobic, about 20-23 amino acids in length
FEATURE:
NAME/KEY: putative transmembrane region III
LOCATION: 427 to 448
IDENTIFICATION METHOD: similarity to other G
IDENTIFICATION METHOD: protein-coupled receptor transmembrane regions,
IDENTIFICATION METHOD: hydrophobic, about 20-23 amino acids in length
FEATURE:
NAME/KEY: putative transmembrane region IV
LOCATION: 469 to 491
IDENTIFICATION METHOD: similarity to other G
IDENTIFICATION METHOD: protein-coupled receptor transmembrane regions,
IDENTIFICATION METHOD: hydrophobic, about 20-23 amino acids in length
```

```

FEATURE:
NAME/KEY: putative transmembrane region V
LOCATION: 512 to 533
IDENTIFICATION METHOD: similarity to other G
IDENTIFICATION METHOD: protein-coupled receptor transmembrane regions,
IDENTIFICATION METHOD: hydrophobic, about 20-23 amino acids in length
FEATURE:
NAME/KEY: putative transmembrane region VI
LOCATION: 557 to 580
IDENTIFICATION METHOD: similarity to other G
IDENTIFICATION METHOD: protein-coupled receptor transmembrane regions,
IDENTIFICATION METHOD: hydrophobic, about 20-23 amino acids in length
FEATURE:
NAME/KEY: putative transmembrane region VII
LOCATION: 592 to 613
IDENTIFICATION METHOD: similarity to other G
IDENTIFICATION METHOD: protein-coupled receptor transmembrane regions,
IDENTIFICATION METHOD: hydrophobic, about 20-23 amino acids in length
FEATURE:
NAME/KEY: putative carboxy-terminal intracellular
NAME/KEY: domain
LOCATION: 614 to 678
US-08-482-855-2

```

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Query Match 90.0%; Score 3235.5; DB 3; Length 695;
Best Local Similarity 89.5%; Pred. No. 1.1e-254;
Matches 622; Conservative 31; Mismatches 39; Indels 3; Gaps 2;

Qy 1 MALLVSLAFLGTSGCHHLCNSNRVFLCQSKVTEIPDLPRNAIELRFLVTLKRV 60
Db 1 MALLVSLAFLGTSGCHHLCNSNRVFLCQSKVTEIPDLPRNAIELRFLVTLKRV 60
Qy 61 IPKSGFAGFGLKIEISQNDVLEIADVFNLPKLHEIRKANNLLYINPEAFQNL 120
Db 1 IQKAFSGFGLKIEISQNDVLEIADVFNLPKLHEIRKANNLLYINPEAFQNL 120
Qy 121 SLRYLLISNTGKILPAVHKIQSLQKVLDDQDNIHIVARNSPFGLSFESVILWLSKN 180
Db 121 NLYQLLISNTGKILPAVHKIQSLQKVLDDQDNIHIVARNSPFGLSFESVILWLSKN 180
Qy 181 GIEIHCNCFNGTQDELNDLSDNNLELNDVFGAGSPVILDSIRTKVHSLPHNGLEN 240
Db 181 GIOEIHNCNCFNGTQDELNDLSDNNLELNDVFGAGSPVILDSIRTKVHSLPHNGLEN 240
Qy 181 GIOEIHNCNCFNGTQDELNDLSDNNLELNDVFGAGSPVILDSIRTKVHSLPHNGLEN 240
Db 181 GIOEIHNCNCFNGTQDELNDLSDNNLELNDVFGAGSPVILDSIRTKVHSLPHNGLEN 240
Qy 241 LKLLRARSTYRLKLLPNDKFTVLEASLTYPSCCAFANLKRQISELHPTCNKILRQD 300
Db 241 LKLLRARSTYRLKLLPNDKFTVLEASLTYPSCCAFANLKRQISELHPTCNKILRQD 300
Qy 301 IDDMTQIGDQVSLDD--EPSYKSGSDMMYNEFDYDLCNEVVDVTCSPKPAFNPCE 359
Db 301 VDYMTQTRGQRSSLAEDNESSYRGFDMTYTEFDYDLCNEVVDVTCSPKPAFNPCE 359
Qy 301 VDYMTQTRGQRSSLAEDNESSYRGFDMTYTEFDYDLCNEVVDVTCSPKPAFNPCE 359
Db 301 VDYMTQTRGQRSSLAEDNESSYRGFDMTYTEFDYDLCNEVVDVTCSPKPAFNPCE 359
Qy 660 ATHNFARKSHCSSAPRVNT--SYVLVPLNHSQN 692

```

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Db 661 TVNTHPRNGHCSSAPRVNTGNTGTYLPLSLAON 695
US-08-474-986-2
RESULT 4
GENERAL INFORMATION:
APPLICANT: Kelton, Christie Ann
Schweickhardt, Rene Lynn
Cheng, Shirley Vui Yen
Nugent, No. 637271leen Patrice
TITLE OF INVENTION: Human Follicle Stimulating
Hormone Receptor
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Stephan P. Williams,
Ares-Serono, Inc.
STREET: Exchange Place, 37th floor
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" diskette, 1.44 MB, high density
COMPUTER: IBM PS/2, model 55 SX
OPERATING SYSTEM: MS-DOS version 4.0
SOFTWARE: VAX/VMS Massll via Kermit to IBM MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/474,986
FILING DATE: 07-Jun-1995
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/670,085
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Williams, Stephan P.
REGISTRATION NUMBER: 28546
REFERENCE/DOCKET NUMBER: US/252
TELEPHONE: (617) 723-1300
TELEFAX: (617) 723-8923
LOCATION: 614 to 678
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-08-474-986-2

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Query Match 90.0%; Score 3235.5; DB 4; Length 695;
Best Local Similarity 89.5%; Pred. No. 1.1e-254;
Matches 622; Conservative 31; Mismatches 39; Indels 3; Gaps 2;

Qy 1 MALLVSLAFLGTSGCHHLCNSNRVFLCQSKVTEIPDLPRNAIELRFLVTLKRV 60
Db 1 MALLVSLAFLGTSGCHHLCNSNRVFLCQSKVTEIPDLPRNAIELRFLVTLKRV 60
Qy 61 IPKSGFAGFGLKIEISQNDVLEIADVFNLPKLHEIRKANNLLYINPEAFQNL 120
Db 1 IQKAFSGFGLKIEISQNDVLEIADVFNLPKLHEIRKANNLLYINPEAFQNL 120
Qy 121 SLRYLLISNTGKILPAVHKIQSLQKVLDDQDNIHIVARNSPFGLSFESVILWLSKN 180
Db 121 NLYQLLISNTGKILPAVHKIQSLQKVLDDQDNIHIVARNSPFGLSFESVILWLSKN 180
Qy 181 GIEIHCNCFNGTQDELNDLSDNNLELNDVFGAGSPVILDSIRTKVHSLPHNGLEN 240
Db 181 GIOEIHNCNCFNGTQDELNDLSDNNLELNDVFGAGSPVILDSIRTKVHSLPHNGLEN 240
Qy 241 LKLLRARSTYRLKLLPNDKFTVLEASLTYPSCCAFANLKRQISELHPTCNKILRQD 300
Db 241 LKLLRARSTYRLKLLPNDKFTVLEASLTYPSCCAFANLKRQISELHPTCNKILRQD 300
Qy 301 IDDMTQIGDQVSLDD--EPSYKSGSDMMYNEFDYDLCNEVVDVTCSPKPAFNPCE 359
Db 301 VDYMTQTRGQRSSLAEDNESSYRGFDMTYTEFDYDLCNEVVDVTCSPKPAFNPCE 359
Qy 301 VDYMTQTRGQRSSLAEDNESSYRGFDMTYTEFDYDLCNEVVDVTCSPKPAFNPCE 359
Db 301 VDYMTQTRGQRSSLAEDNESSYRGFDMTYTEFDYDLCNEVVDVTCSPKPAFNPCE 359

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QY 360 GYNLVLNFIPTSLAIGTNTVLTSTQYVLPVREFMLCNLAFADLCIGIYLLILAS 419
DB 361 GYNLVLNFIPTSLAIGTNTVLTSTQYVLPVREFMLCNLAFADLCIGIYLLILAS 420
QY 420 VDIRTSQYHFAIDMTGAGCDAAGFTVPASELSVYLTATLTHRHHTITHAMQLECK 479
DB 421 VDIRTSQYHFAIDMTGAGCDAAGFTVPASELSVYLTATLTHRHHTITHAMQLECK 480
QY 480 VOLRHAASVWVGMFTFAFAALFFPFGISSTVMKVSICLPHDIDSPLSOLYVMAVLLVNL 539
DB 481 VOLRHAASVWVGMFTFAFAALFFPFGISSTVMKVSICLPHDIDSPLSOLYVMAVLLVNL 540
QY 540 APVYICCGTTHYLVVNPVTVSSSDTKIAKRNATLFTDFLCHAPISFPFASISLKP 599
DB 541 APVYICCGTTHYLVVNPVTVSSSDTKIAKRNATLFTDFLCHAPISFPFASISLKP 600
QY 600 LTVSKAKILLVLPYVINSKANPELTAFTKRNEDFTFLLSKGCGYEMQAQYRTETSS 659
DB 601 LTVSKAKILLVLPYVINSKANPELTAFTKRNEDFTFLLSKGCGYEMQAQYRTETSS 660
QY 660 ATHFHARKSCSSAPRVN--SYVLVPLNHSN 692
DB 661 TVMTHPRNGHSCSSAPRVN--SYVLVPLNHSN 695

RESULT 5
US-07-741-453A-60
; Sequence 60
; Patent No. 621859
; GENERAL INFORMATION:
; APPLICANT: PARMENTIER, MARC
; APPLICANT: LIBERT, FREDERIC
; APPLICANT: DUMONT, JACQUES
; APPLICANT: VASSART, GILBERT
; TITLE OF INVENTION: POLYPEPTIDES HAVING THYROTROPIN-RECEPTOR
; TITLE OF INVENTION: ACTIVITY, NUCLEIC ACID SEQUENCES CODING FOR SUCH RECEPTORS
; TITLE OF INVENTION: AND, POLYPEPTIDES, AND APPLICATIONS OF THESE POLYPEPTIDES
; NUMBER OF SEQUENCES: 62
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN DABRY & CUSHMAN
; STREET: 1615 L STREET, N.W.
; CITY: WASHINGTON, D.C.
; COUNTRY: U.S.A.
; ZIP: 20036
; COMPUTER READABLE FORM:
; FILE NAME: 1615L.DAT
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release 1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: 19911015
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: KOKULIS, PAUL N.
; REGISTRATION NUMBER: 16773
; REFERENCE/DOCKET NUMBER: 91913/1107/US/ST
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 861-3000
; TELEFAX: (202) 861-0944
; TELEMAIL: 6714527
; INFORMATION FOR SEQ ID NO: 60:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 764 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-741-453A-60

Query Match 50.6% Score 1817.5; DB 4; Length 764;
Best Local Similarity 51.7%; Pred. No. 2.le-139;
Matches 385; Conservative 94; Mismatches 205; Indels 61; Gaps 11;

QY 4 LVLSLAFIQTGSCGHHWCHCSN-----RVFLCQDSKVTEIPTDLPNRAIELRFLVTKLR 59
DB 11 LVLSLAFIQTGSCGHHWCHCSN-----RVFLCQDSKVTEIPTDLPNRAIELRFLVTKLR 65
QY 60 VIPKSGFAGGQLEKLEISONDVLEVEADVSFNKLEHEIRIEKANULLYINPFAONL 119
DB 66 TIPSRAFSLNPNLSRIVLSIDATLORLESHPNLSKRWTHIEIRWTSLSIOPDAKEL 125
QY 120 PSURLISHTGKIKHLPVAKIOSQK--VLLDIDONINITHIVARNSPMGLSFSFVILWLS 178
DB 126 PLKFLGIPGTGLVFPVDTKVSTDFVFILEITDNPMASIPANAFQCLNETLTALKY 185
QY 179 KNGIEITHINCAFNSTOLDLNNLNNLEELPNDFQGA--SGPVILDISRTKVSILPHNG 237
DB 186 NNGFTSTOGHAFNGTKLDAYLVKNNKYLISAIDKADAPGVYSGPTLLDVSYSVTALPSKG 245
QY 238 LBNLKKARSTYRIKKLPNDKAPVTLMEASLTYPSSHCCAPANKRQISELHP1-CNKSI 296
DB 246 LBNLKKARSTYRIKKLPNDKAPVTLMEASLTYPSSHCCAPANKRQISELHP1-CNKSI 305
QY 297 LRQ-----DIDDMTOIGDOOVSLLIDDEPSYKGSOMWY----- 329
DB 306 IRSLRQRKSVNTLPPDQVEEYVLCDSHAGYKDNQSQFQDTSNHSYVYVPEEQEDELG 365
QY 330 -----NEFDYDLNCEVVDVTCSPKPAFNPCEDIMGYNILRLVLFIS 372
DB 366 FGOELKNPOEETLAQFDSHYDYTVCGNEDMWCTPKSDEFNCPEDIMGYKFLRVVNEVS 425
QY 373 ILAIGNTVTVLVLTSTQYVLPVREFMLCNLAFADLCIGIYLLILASVDIHTKSQYHFA 432
DB 426 LLALGNFVLLVLTSTQYVLPVREFMLCNLAFADLCIGIYLLILASVDIHTKSQYHFA 485
QY 433 IDQGTGAGCDAAGFTVPASELSVYLTATLTHRHHTITHAMQLECKVOLRHAASVWVVLG 492
DB 486 IDQGTGAGCDAAGFTVPASELSVYLTATLTHRHHTITHAMQLECKVOLRHAASVWVVLG 545
QY 493 WTEFAAALFPFGISSTVMKVSICLPHDIDSPLSOLYVMAVLLVNLVLPVYICGCTHYI 552
DB 546 WTEFAAALFPFGISSTVMKVSICLPHDIDSPLSOLYVMAVLLVNLVLPVYICGCTHYI 605
QY 553 LTVRNPTVSSSDTKIAKRNATLFTDFLCHAPISFPFASISLKPVLYTSKAKILLVL 612
DB 606 LTVRNPTVSSSDTKIAKRNATLFTDFLCHAPISFPFASISLKPVLYTSKAKILLVL 665
QY 613 FYPINSCANPFLYAIETKRNFRDFFLLSKGCGYEMQAQYRTETSSATHNF-----HAR 667
DB 666 FYPINSCANPFLYAIETKRNFRDFFLLSKGCGYEMQAQYRTETSSATHNF-----HAR 725
QY 668 KSHCSAPRVTVNSVYVPLNHSN 692
DB 726 RDMRSLPNHQDETLLENRLTFN 750

RESULT 6
US-07-757-342D-4
; Sequence 4, Application US/07757342D
; Patent No. 6218509
; GENERAL INFORMATION:
; APPLICANT: IGARASHI, Masao
; INVENTOR: MINEGISHI, Takashi
; NAKAMURA, Kazuo
; TITLE OF INVENTION: PROTEIN, DNA AND USE THEREOF
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &
; CUSHMAN
; STREET: 130 Water Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: US
; ZIP: 02109
; COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA: US/07/757,342D
APPLICATION NUMBER: US/07/757,342D
FILING DATE: 10-Sep-1991
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: BUCKLEY, Linda M.
REGISTRATION NUMBER: 31003
REFERENCE/DOCKET NUMBER: 41226
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)523-3400
TELEFAX: (617)523-6440
TELEX: 200291 STRE UR
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 696 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-07-757-342D-4

Query Match 50.3%; Score 1807.5; DB 4; Length 696;
Best Local Similarity 55.1%; Pred. No. 1.2e-138;
Matches 373; Conservative 103; Mismatches 154; Indels 47; Gaps 13;
QY 1 MALLV-----SLAFLGTGSGCHHWHCHSNRVFLQDSKVTEIPTDLPNAIELRV 54
DB 12 LALLLPPLPOTLL-----GAPCE---PCS-----CRPDGALCPG--PRAGLS-RLS 55
QY 55 LTKL--RVIPKSGFAGDLEKIEISONDVLEIVADVFNLPKLEHRIEKANLLYIN 112
DB 56 LYLTKVPSQAFGLNEVVKIEISQSDSEKIEANAFDNLNLSEILQNTKNLYIE 115
QY 113 PEAFNLRLYLLISNTGKIKHLPVHKIQSLQ-KVLLDIQDNIHIVARNSEFGLSPE 171
DB 116 PGFTNLPRLKYLSCITGIRLPDVKIFSEFNFLEICDNLHTTVPANAFQGMNE 175
QY 172 SVILMSKNGIEIHNCAPGOLDENLSDNNLEELPNVFGASGVILDISRTKVH 231
DB 176 SITLKYNGFEEIOSHAFNGTLLISLEKNAHLKMHNDAPRGARGPSILDISTKLQ 235
QY 232 SLPNHGLENLKLRARSTYRLAKLNLDFVILMEASLYPSHCCAFANL--KQ----- 284
DB 236 ALPSYGLSIEQTLIATSSYSLKPLSREKFTNLLDNLATLYPSHCCAFANLPTKEQNFSS 295
QY 285 -ISELHPICNKSILRODIDDMTQIGDQVSLDIDDEPSYKSGSDMMYNEFDYDLCEVVDV 343
DB 296 IFKNFSKQCESTARPNNETL-----YSAFAE-----SELSWDYDYGFCSPKT-L 341
QY 344 TCSKPKDAPNCPEDINGYNILRVLIWFISILAITGNTVVLVLTTSQYKLTVPRLMCLN 403
DB 342 QCAPEPAENCPEDINGYDLRVLIWILINILAIMGNVTLFVLLTSHYKLTVPRLMCLN 401
QY 404 AFADLCIGYLLLIASVDIHTKSOVHNYAIDNQTGAGCDAAAGFTTFVASELSYTLTAT 463
DB 402 SFADFCMGYLLLIASVDAQTGGQYNNHAIQNTGNGCSVAGFTTFVASELSYTLTAT 461
QY 464 LERWHTTHAMOLECKVQLRHAASVNLGWTAFAAALPPIFGISYMKVSLCLPMDIDS 523
DB 462 LERWHTTAYIQDLRLRHAIPIMLGWLSTLIAMLPVGVSYMKVSLCLPMDVET 521
QY 524 PLSQYVMALLVNLVAFVYICGYYHTYVRNPTIVSSSDSTIAKRMATLIETDFLC 583
DB 522 TISQVYLTILNLVVAFTIICACYIKIYFQVNPENLMATNKDKTKAKMVAVLIFTDFC 581
QY 584 MAPISFAISAKVPLITVNSKAILLVLFYVNSCANPFLYAITKFNRRDFILLSKF 643
DB 582 MAPISFAISAKVPLITVNSKAILLVLFYVNSCANPFLYAITKFNRRDFILLSKS 641

QY 644 GYEMQAQIYRTETSSA 660
DB 642 GCKKHOAELYRRKDFSA 658
RESULT 7
US-07-757-342D-3
Sequence 3, Application US/07757342D
Patent No. 6218509
GENERAL INFORMATION:
APPLICANT: IGARASHI, Masao
MINEGISHI, Takashi
NAKAMURA, Kazuto
TITLE OF INVENTION: PROTEIN, DNA AND USE THEREOF
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &
CUSHMAN
STREET: 130 Water Street
CITY: Boston
STATE: Massachusetts
COUNTRY: US
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/757,342D
FILING DATE: 10-Sep-1991
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: BUCKLEY, Linda M.
REGISTRATION NUMBER: 31003
REFERENCE/DOCKET NUMBER: 41226
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)523-3400
TELEFAX: (617)523-6440
TELEX: 200291 STRE UR
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 700 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-07-757-342D-3

Query Match 50.0%; Score 1797; DB 4; Length 700;
Best Local Similarity 56.5%; Pred. No. 8.5e-138;
Matches 359; Conservative 105; Mismatches 149; Indels 22; Gaps 7;
QY 45 PRNAIELREVLTKL--RVIPKSGFAGDLEKIEISONDVLEIVADVFNLPKLEHRI 102
DB 51 PRAGL-ARLSLTVLPVKVPSQAFGLNEVVKIEISQSDSEKIEANAFDNLNLSELLI 109
QY 103 EKANNLLYNPAFQNLPSRLYLLISNTGKIKHLPVHKIQSLQ-KVLLDIQDNIHIVA 161
DB 110 QNTKNLYTEPGAFTNLPRLKYLSCITGIRLPDVKIFSEFNFLEICDNLHTTIP 169
QY 162 RNSFMGLSPESVILMSKNGIEIHNCAPGOLDENLSDNNLEELPNVFGASGPV 221
DB 170 GNAFQGMNESVTLYKLYNGFEEVOSHAFNGTLLISLEKNIYLEKMHSGAFQGTGPS 229
QY 222 ILDISRTKVHSLPNHGLENLKLRARSTYRLAKLNLDFVILMEASLYPSHCCAFANL 281
DB 230 ILDISRTKVHSLPNHGLENLKLRARSTYRLAKLNLDFVILMEASLYPSHCCAFANL 289
QY 282 KQISELHPICNKSILRODIDDMTQIGDQVSLDIDDEPSYKSGSDMMYNEFDYDLCE 338
DB 290 PKK-----EQNFSSIFENFSKQCESTARPNNETLYSAFAE-----SELSWDYDYGFC 341

QY 339 EVVDYTCSPKPAFPCDINGNYLRLVLPFISLAIQTGNTVLVLTTSYKLTVPF 398
DB 342 PNT-LOCAPDAFPCDINGNYLRLVLPFISLAIQTGNTVLVLTTSYKLTVPF 400
QY 399 LACNLAPADLCIGYLLIYLLASVDIHTKSOYHNYAIDMOTGAGCDAAGFTTFVASELSVYT 458
DB 401 LACNLSPAFPCDINGNYLRLVLPFISLAIQTGNTVLVLTTSYKLTVPF 460
QY 459 LTAITLERHRTTHAMOLECKVOLRHAASVYVLTGTFAPFAALFPFIFGSISSYKYSICLIP 518
DB 461 LVITLERHRTTHAMOLECKVOLRHAASVYVLTGTFAPFAALFPFIFGSISSYKYSICLIP 520
QY 519 MOIDPSOLYVLLVLPFISLAIQTGNTVLVLTTSYKLTVPF 578
DB 521 MOIDPSOLYVLLVLPFISLAIQTGNTVLVLTTSYKLTVPF 580
QY 579 TQPCMAPISPAISASKVLPLTVTSKAKILLVLPYINSCANPFLYAIETKFNRFDEFL 638
DB 581 TQPCMAPISPAISASKVLPLTVTSKAKILLVLPYINSCANPFLYAIETKFNRFDEFL 640
QY 639 LLSAFPCYEQMAQIYETTSATHNFHAKSHCS 673
DB 641 LLSAFPCYEQMAQIYETTSATHNFHAKSHCS 673

RESULT 8
US-07-757-3420-10
Sequence 10, Application US/077573420
Patent No. 6218509
GENERAL INFORMATION:
APPLICANT: IGARASHI, Masao
INVENTOR: IGARASHI, Masao
NAKAMURA, Kazuo
TITLE OF INVENTION: PROTEIN, DNA AND USE THEREOF
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSER: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &
CUSHMAN
STREET: 130 Water Street
CITY: Boston
STATE: Massachusetts
COUNTRY: US
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM SIZE: 5.25 inch
OPERATING SYSTEM: PC compatible
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07757,3420
FILING DATE: 10-Sep-1991
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: BUCKLEY, Linda M.
REGISTRATION NUMBER: 31003
REFERENCE/DOCKET NUMBER: 41226
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)523-3400
TELEFAX: (617)523-6440
FAX: 00251 STRE OR
INFORMATION FOR SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
LENGTH: 674 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 10:

US-07-757-3420-10
Query Match 49.4%; Score 1776; DB 4; Length 674;
Best Local Similarity 55.4%; Pred. No. 4.1e-136;
Matches 349; Conservative 107; Mismatches 148; Indels 26; Gaps 6;

QY 55 LTKL-----RVIPKSGFAGFGDLEKIEISQNDVLEIVADVFNPLKLEIREKANN 107
DB 26 LTKL-----RVIPKSGFAGFGDLEKIEISQNDVLEIVADVFNPLKLEIREKANN 85
QY 108 LLYINPAPONLRYLLYLLSNTGKILPAVKTI-OSLQKVLDDIOTNINIHIVARNSPM 166
DB 86 LRYTEPCAFINLPLGLYLSICNTGIRKFPDVTKVPSSESNFLEICDNLHITTPGNAFO 145
QY 167 GLSPESVILWLSKNGIEIHNKCAFNGTQDDELNLSDNNNLEELPNDVDFQAGSGPVLDIS 226
DB 146 GNNNESVTKLYNGFEEVQSHAFNGTTLTSLLEKNVHLEKMHGAPGATGPKTLDIS 205
QY 227 RPKVHSLPHGLNKLKLRARSTYKRLKLPNDKPFVTLMEASUTYPSHCCAFANLKRQIS 286
DB 206 STKQALPSTGLSISQRIATISYSLAKLPSTRETFYNLEATUTYPSHCCAFANL----- 260
QY 287 ELHPCNKSLRDDIDDMTOIGDQVSLIDDEPSYCK---GSDMYNEFDYDLCNEVDV 343
DB 261 ---PYKDFNSHSISENSKQESTVTKVSNITLYSSMLAESLSCMDTETGCLPKTP- 316
QY 344 TCSKPKDAPNCPEDINGNYLRLVLPFISLAIQTGNTVLVLTTSYKLTVPF 403
DB 317 RCAPEAPNCPEDINGNYLRLVLPFISLAIQTGNTVLVLTTSYKLTVPF 376
QY 404 AFADLCIGYLLIYLLASVDIHTKSOYHNYAIDMOTGAGCDAAGFTTFVASELSVYT 463
DB 377 SFADFCMGLYLLIYLLASVDIHTKSOYHNYAIDMOTGAGCDAAGFTTFVASELSVYT 436
QY 464 LERHRTTHAMOLECKVOLRHAASVYVLTGTFAPFAALFPFIFGSISSYKYSICLIP 523
DB 437 LERHRTTHAMOLECKVOLRHAASVYVLTGTFAPFAALFPFIFGSISSYKYSICLIP 496
QY 524 PLSOLYVLLVLPFISLAIQTGNTVLVLTTSYKLTVPF 583
DB 497 TQPCMAPISPAISASKVLPLTVTSKAKILLVLPYINSCANPFLYAIETKFNRFDEFL 556
QY 584 MAPISPAISASKVLPLTVTSKAKILLVLPYINSCANPFLYAIETKFNRFDEFL 643
DB 557 MAPISPAISASKVLPLTVTSKAKILLVLPYINSCANPFLYAIETKFNRFDEFL 616
QY 644 GYEQMAQIYETTSATHNFHAKSHCS 673
DB 617 GCKKRAELRYRK-----DFSAYTSNCKN 640

RESULT 9
US-07-757-3420-2
Sequence 2, Application US/077573420
Patent No. 6218509
GENERAL INFORMATION:
APPLICANT: IGARASHI, Masao
INVENTOR: IGARASHI, Masao
NAKAMURA, Kazuo
TITLE OF INVENTION: PROTEIN, DNA AND USE THEREOF
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSER: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &
CUSHMAN
STREET: 130 Water Street
CITY: Boston
STATE: Massachusetts
COUNTRY: US
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM SIZE: 5.25 inch
OPERATING SYSTEM: PC compatible
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07757,3420
FILING DATE: 10-Sep-1991
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:

NAME: BUCKLEY, Linda M.
REGISTRATION NUMBER: 31003
REFERENCE/DOCKET NUMBER: 41226
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)523-3400
TELEFAX: (617)523-6440
TELEX: 200291 STRE UR
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 699 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-07-757-342D-2

Query Match 49.4%; Score 1776; DB 4; Length 699;
Best Local Similarity 55.4%; Pred. No. 4.3e-136;
Matches 349; Conservative 107; Mismatches 148; Indels 26; Gaps 6;

Qy 55 LTKL-----RVIPKGFAGFGDLEKIEISQNDVLEIADVFESNPKLHEIRKANN 107
Db 51 LTRLAYLPVKVPSQAFRLNEVIEKIEISQDSLEKIEANAFDNLNLSEILQNTKN 110
Qy 108 LLYINPEAFONPLSLRYLLISNTGKIKHLPVHKI-QSLQKVLDDIODNINIHVARNSEFM 166
Db 111 LRYIEPGAFINPLGLKYLSCITGIRKFPDVKYFSSSENFLEICDNLHTTIPGNFQ 170
Qy 167 GLSFESVILWLSKNGIEIHNCAENGQOLDELNLSDNNLEELPNDVFGASGVILDIS 226
Db 171 GNNESVTLKLYNGFEEVQSHAFNGTTLTSLKENVHLEKMGHNGAFRGATGPKTLDIS 230
Qy 227 RTKVHSLPNHGLENLKRLARSTYRLKLPNLFVTLMEASLYPSHCCAFANLKRQIS 286
Db 231 STKLQALPSYGLSIOIRLIATSSLSKLPSTRETFVNLLEATLTPSHCCAFRL----- 285
Qy 287 ELHPICNKSILRQDIDMTQIGDQVRSLLIDPEISYGR---GSDMMYNEFDYDLGNEVVDV 343
Db 286 ---PTKEQNFHSHISENFSCQESTVRKVSNTLYSSMLAESLSGWDYEGFCLPKTP- 341
Qy 344 TCSKPDPAFNCEDINGNIRLVLIWISILAITGNTVVLVLTTSQYKLTVPRLMCNL 403
Db 342 RCAPEPAFNCEDINGYDFLRVLINILINILAINGNMTVFLVLTTSYKLTVPRLMCNL 401
Qy 404 AFADLCIGYLLIASVDIHTKSOYHNVAIDWQTGAGDAAGFTTFVASELSVYTLTAT 463
Db 402 SFADFCGLYLLIASVDSQTKQYHNVAIDWQTGAGDAAGFTTFVASELSVYTLTAT 461
Qy 464 LERWHTITHAMOLECKVOLRHAASVMVLGWTFAFAAALPPIFGISSYMKVSCICLPMIDIS 523
Db 462 LERWHTITYAHLQKRLRHAILIMLGGWLFSSLIAMLPLVGVSNTKVSICFPMDVET 521
Qy 524 PLSQLYMALVNLVNLVAVVVICGCTHYLYLTVRNPITVSSSDTKIAKRMATLFTDFLC 583
Db 522 TLSQVYITLILINVAFFIICACYIKIYFAVRPELMAKNDKTKIAKMAILFTDFTC 581
Qy 584 MAPISFFAISASLKVPLTISKALILVLFYIPINSCANPFLYATFTKFRDRDFILLSKF 643
Db 582 MAPISFFAISAEKVPPLTIVNSKVLVLFYIPINSCANPFLYATFTKFRDRDFILLSKF 641
Qy 644 GCYEQHAQIYRTETSSATHNFAKSHCS 673
Db 642 GCCRRRAELRYRK-----DPSAVTSNCKN 665

RESULT 10
US-07-741-453A-61
Sequence 61, Application US/07741453A
Patent No. 6228597
GENERAL INFORMATION:
APPLICANT: PARMENTIER, MARC
APPLICANT: LIBERT, FREDERIC
APPLICANT: DUMONT, JACQUES

APPLICANT: VASSART, GILBERT
TITLE OF INVENTION: POLYPEPTIDES HAVING THYROTROPIN-RECEPTOR
TITLE OF INVENTION: ACTIVITY, NUCLEIC ACID SEQUENCES CODING FOR SUCH RECEPTORS
TITLE OF INVENTION: AND POLYPEPTIDES, AND APPLICATIONS OF THESE POLYPEPTIDES
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHMAN DARB & CUSHMAN
STREET: 1615 L STREET, N.W.
CITY: WASHINGTON, D.C.
COUNTRY: U.S.A.
ZIP: 20036
COMPUTER READABLE FORM:
MEDIUM TYPE: Disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0; Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07741.453A
FILING DATE: 19911015
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: KOKULIS, PAUL N.
REGISTRATION NUMBER: 16773
REFERENCE/DOCKET NUMBER: 91913/1107/US/ST
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 861-3000
TELEFAX: (202) 822-0944
TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO: 61:
SEQUENCE CHARACTERISTICS:
LENGTH: 764 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-741-453A-61

Query Match 46.6%; Score 1674; DB 4; Length 764;
Best Local Similarity 49.4%; Pred. No. 9.5e-128;
Matches 34; Conservative 112; Mismatches 188; Indels 56; Gaps 12;

Qy 3 LLLVSLAFLGTGSGCHHMLCHCSN----RVFLQDSKVTEIPTDLPNALFLRVLTKL 58
Db 10 VLLDLDPDLG-GMGSSPPCEHQEEDFRV-TCKD--IQRPS-LPSTOTLKLIEHTL 64
Qy 59 RVIPKGFAGDLEKIEISQNDVLEIADVFESNPKLHEIRKANNLIYINPEAFON 118
Db 65 RTPSHAFSNLPNISRIYVSDLTLOQLESHSFYNLSKVTHEIRNTRNLTYIDPDALKE 124
Qy 119 LPSRLYLLISNTGKIKHLPVHKIOSLO-KVLLDIDODNINIHVARNSEFMGLSFESVILWL 177
Db 125 LPLKLFICFTNGKMPDLPKVTSTDIFFILEITDNPYMTSIPVNAFOGCLNETLTKL 184
Qy 178 SKNGIEITHCAFNQTOLDLNLSDNNLEELPNDVFOGA-SGPVILDISRTKVHSLPNH 236
Db 185 YNNGFTSVQGYAFNGTKLDAYLNKNKYLTVIDDAFGVYSGPSLLDVSTQSYTALPSK 244
Qy 237 GLENLKLARSTYRLKLPNLFVTLMEASLYPSHCCAFANLKRQISELHPI-CNKS 295
Db 245 GLEHLKELIARNTWTLKPLSLFSLHLTRADLSYPHSCCAFKKQKIRGILESIMCNE 304
Qy 296 IL-----RODIDDMT-----QIGDQVSLID-----DEPSY 321
Db 305 SMQSLRQRKSVNALNSPLHQEYENLGDSIVGYKEKSFQDTHNNAHYVFFEEQDEII 364
Qy 322 GKSDM-----MYNEFDYDLGNEVVDVTSKPDPAFNCEDINGNIRLVLIWFI 371
Db 365 GFGQELKNPQEBETLQAFDSDHYDYTCGSDSEDMVCTPKSDENPCEDINGYKFLRVVWF 424
Qy 372 SILAITGNTVVLVLTTSQYKLTVPRLMCNLAFADLCIGYLLIASVDIHTKSOYHN 431
Db 425 SLLALGNVFLVLLILTSHYKLVNVPRLMCNLAFADFCMGWMLLLIASVDLYTHSEYHN 484

432 AIDQGTGACDAGFTTFASELSVYTLTAITLERHHTITHAMOLECKVOLRHAASVWVL 491
485 AIDQGTGACDAGFTTFASELSVYTLTAITLERHHTITHAMOLECKVOLRHAASVWVL 544
492 GWTFAAALPPIPGISYKVSICLPMDSPLSOLYVALLVNLVAVVYVCCGYTHI 551
545 GWCCFLALLPLVGISSYKVSICLPMDSPLSOLYVALLVNLVAVVYVCCGYTHI 604
552 YLTVRNPITVSSSDTKAKRMATLITFDLCHAPISFAISLAKVPLITYSKAKILLY 611
605 YITVRNPOTNGCDTKAKRMATLITFDLCHAPISFAISLAKVPLITYSKAKILLY 664
612 LPTVNSCANPFLITATPKRNPDRDFFILLSKFCGYCMAOQYR 654
665 LPTVNSCANPFLITATPKRNPDRDFFILLSKFCGYCMAOQYR 707

RESULT 11
US-07-741-453A-54
Sequence 54, Application US/07741453A
Patent No. 6228597
GENERAL INFORMATION:
APPLICANT: PARMENTIER, MARC
APPLICANT: LIBERT, FREDERIC
APPLICANT: DUMONT, JACQUES
APPLICANT: VASSART, GILBERT
TITLE OF INVENTION: POLYPEPTIDES HAVING THYROTROPIN-RECEPTOR
TITLE OF INVENTION: ACTIVITY, NUCLEIC ACID SEQUENCES CODING FOR SUCH RECEPTORS
TITLE OF INVENTION: AND POLYPEPTIDES, AND APPLICATIONS OF THESE POLYPEPTIDES
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHMAN DARBY & CUSHMAN
STREET: 1615 L STREET, N.W.
CITY: WASHINGTON, D.C.
COUNTRY: U.S.A.
ZIP: 20036
COMPUTER READABLE FORM:
MEDIUM TYPE: Disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/07/741.453A
FILING DATE: 19911015
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 91913/1107/US/ST
REFERENCE/DOCKET NUMBER: 91913/1107/US/ST
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 861-3000
TELEFAX: (202) 822-0944
TELEX: 6714627 CUSH
INFORMATION FOR SEO ID NO: 54:
SEQUENCE CHARACTERISTICS:
LENGTH: 764 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-07-741-453A-54

Query Match 46.64; Score 1673.5; DB 4; Length 764;
Best Local Similarity 47.44; Procl. No 16-127;
Matches 351; Conservative 116; Mismatches 217; Indels 61; Gaps 11;

4 LVLALAFITGTCGCHHMLKCSN---RVFLCDKSKVTEIPTOLPRNATELRVUTKLR 59
11 LLLALPRSLG-GAGCSPCECHQEDDFV-TCRD--IHRIPT-LPPSTQTLKFIETOLK 65
60 VIPAGSFAFGDKEIETSLQNDVFNPLKLEIRKANNLLINPEAFOML 119
66 TIPSRAFNLNPSRIYLSIDATLQRLSHSFNLSKMTHEIRNLSLSDPDALKEL 125

120 PSRLYLLISMTGKHLPAVKHTOSLOK-VLLDIOONINIHIVARNPMGLSFESVILMS 178
126 PLKFLGIFNTGLGVFDVTKYVSTVDFLEITDNPYTHASIPANAPQGLNETLTKLY 185
179 KNGIEELHKEAFNGTOLDELANSNNLEELPDVFOGA-SGRVILDISRTKXHSPLNG 237
186 NNGFTSIOHAPNSTKLDAYLNNKYLSTADKDAFGGVSGPTLLDVSYSTALPSKG 245
238 LENLKKLARASTYRLKLPNLKDKFVTLMEASLTPSHCCAPANLAKROISELHPI-CNKS1 296
246 LEHLKELIARTWTLKPLSLSLFLHTRADLSYPSHCCAFKNOKKIRGILESIMCNSS 305
297 LRO-----DIDDMTOIGDQRVSLDDDEPSYKGSDDMY----- 329
306 IRLSRQKSVNLTNGPPDQDEYELGDSHAGYKDNQFQDTSNSHYVFFEEDEILG 365
330 -----NEFDYDLGNEVDVTCSPKPAFNPCEDEINGYNILRVLIWFIS 372
366 FQGLKKNPOETLOAFDSHYDTVCGGNEDEWCTPKASDEFNPCEDEINGYKRVIVWVFS 425
373 ILAITGNTVLYVLTSTQKLYTRPRMLKNLADGIGYLLIASVDIHTKSOHYNA 432
426 LLALLGNFVLVLLTSYKLYTRPRMLKNLADGIGYLLIASVDIHTKSOHYNA 485
433 IDMTGACGACGAGFTTFASELSVYTLTAITLERHHTITHAMOLECKVOLRHAASVWVL 492
486 IDMTGPGCNTAGFTTFASELSVYTLTAITLERHHTITHAMOLECKVOLRHAASVWVL 545
493 MTEFAAALPPIPGISYKVSICLPMDSPLSOLYVALLVNLVAVVYVCCGYTHI 552
546 WCCFLALLPLVGISSYKVSICLPMDSPLSOLYVALLVNLVAVVYVCCGYTHI 605
553 LTVRNPITVSSSDTKAKRMATLITFDLCHAPISFAISLAKVPLITYSKAKILLY 612
606 ITVRNPOTNGCDTKAKRMATLITFDLCHAPISFAISLAKVPLITYSKAKILLY 665
613 FYPVNSCANPFLITATPKRNPDRDFFILLSKFCGYCMAOQYR 667
666 FYPVNSCANPFLITATPKRNPDRDFFILLSKFCGYCMAOQYR 725
668 KSHCSAPRPTNSYVLPVPLNRSN 692
726 RDMRQSLPNMDEYELLENLSTPN 750

RESULT 12
US-07-741-453A-56
Sequence 56, Application US/07741453A
Patent No. 6228597
GENERAL INFORMATION:
APPLICANT: PARMENTIER, MARC
APPLICANT: LIBERT, FREDERIC
APPLICANT: DUMONT, JACQUES
APPLICANT: VASSART, GILBERT
TITLE OF INVENTION: POLYPEPTIDES HAVING THYROTROPIN-RECEPTOR
TITLE OF INVENTION: ACTIVITY, NUCLEIC ACID SEQUENCES CODING FOR SUCH RECEPTORS
TITLE OF INVENTION: AND POLYPEPTIDES, AND APPLICATIONS OF THESE POLYPEPTIDES
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHMAN DARBY & CUSHMAN
STREET: 1615 L STREET, N.W.
CITY: WASHINGTON, D.C.
COUNTRY: U.S.A.
ZIP: 20036
COMPUTER READABLE FORM:
MEDIUM TYPE: Disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/07/741.453A
FILING DATE: 19911015


```
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: KOKULIS, PAUL N.
REGISTRATION NUMBER: 16773
REFERENCE/DOCKET NUMBER: 91913/1107/US/ST
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 861-3000
TELEFAX: (202) 822-0944
TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO: 56:
SEQUENCE CHARACTERISTICS:
LENGTH: 792 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-741-453A-56

Query Match 46.5%; Score 1670; DB 4; Length 792;
Best Local Similarity 50.3%; Pred. No. 2.1e-127;
Matches 368; Conservative 100; Mismatches 166; Indels 98; Gaps 21;

Qy 45 PRNRIELRVLTKL--RVIPKGFAGDGLKIEISONDVLE-----VIEADVFSNLPK 96
Db 59 PRAGLS-RLSLTYLPKIPVISOAFRLNVEVVKIEISQDSLEPIGHCCKTEANAFONLLN 117
Qy 97 LHEIRIEKANNLVINPEAFONLPSRLYLISNTGIKH-----LPAVHKIOSLO-KVLL 149
Db 118 LSELIQNTNLVIEGATNLPRLKYLISCTGIRKPIGHCGLPQVTKIFSEFNIL 177
Qy 150 DIQDNIHIVARNFMSGLSFESVILSKNGIBEIHNC-----AFNGTQDLELNLSN 203
Db 178 EICNLHITVPANAFQGMNESITLKYNGFEPICHCIEIQSHAFNGTLLISLEKEN 237
Qy 204 NLEELPNVPOGASGVILDISTKVHS-----LPNHGLENLKKURARSTYRLKLPN 257
Db 238 AHLKMHNDAPRGARGSLDISSTKLOAPIGHGCLPSYGLSITQTLIATSSYSLKPLPS 297
Qy 258 LDKFVTLMEASLTVPSCCAFANL-----KQ-----ISELHPICNKSILRODIDD 303
Db 298 REKTNLNDALTLTPSHCCAFRNPUPPIGHGCTKQNFSEFIFKNFSKQCESTARPNNET 357
Qy 304 MTOIGDQSVLIDDEPSYKGSMDMYNEFDY-DLCNEVVDVTCSPKPDAPNCPEDIMGYN 362
Db 358 LYSALFAESELSDWDPIGHCGYD--YGPIGHGFCSPKT-LQCAPEADAPNCPEDIMGYD 414
Qy 363 ILRVLIWFISLATGNTVLV-----LTTQYKLTVPRLMCLNLAFAADLCIGIYLL 416
Db 415 FLRVLIWLIINLAINGNVTVLFAPIGHGCLLTSHYKLTVPRLMCLNLSFADFCMGLYLL 474
Qy 417 IASVDIHTKSOYHNAIDW-----OTGAGCDRAGFETVFASELVSVYTLTATILRHWTI 470
Db 475 IASVDAQTKGYHNAIDWPIGHGCTGNGCSVAGFTVFASELVSVYTLTATILRHWTI 534
Qy 471 THAMOLECKVOLRHA-----ASVWVLGWTFAFAALFPFIFGISSYMKVSCICLPMDIDSP 524
Db 535 TYAIQDQKRLRHAPIGHGCGIPIMLGWLFSTLIAMLPVGVSSYMKVSCICLPMDVETT 594
Qy 525 LSQLYVMALLV-----LNVAFVVICGYTHIYLVNRPVIVSSSDTKAKRMATLIF 578
Db 595 LSQVYILTILPIGHGCLNVVAFIICACIYKIYFAVQNPMLMATNKDTKIAKKMAVLIF 654
Qy 579 TDFLCMA-----PISFPAISALKVPLITVYSKAILLVLEVPYNSCANPXYAIFTKNF 632
Db 655 TDFTCMAPIGHGCGIPISFAALKVPLITVYNSKAILLVLEVPYNSCANPXYAIFTKAF 714
Qy 633 RRD-----FFILSKFCYEQMQIYRTETSSATHNPHARKSHC-----SSAP-RVTN 679
Db 715 RRDPIGHGCGFFLLLSKSCCKHQALRYRKFDSA-----YCKNGFTCSNPFSTR 765
Qy 680 SYVLVPLNHSQ 691
Db 766 KLTLPLIGHGCG 777
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RESULT 13
US-07-741-453A-59
Sequence 59, Application US/07741453A
Patent No. 6228597
GENERAL INFORMATION:
APPLICANT: PARMENTIER, MARC
APPLICANT: LIBERT, FREDERIC
APPLICANT: DUMONT, JACQUES
APPLICANT: VASSART, GILBERT
TITLE OF INVENTION: POLYPEPTIDES HAVING THYROTROPIN-RECEPTOR
TITLE OF INVENTION: ACTIVITY, NUCLEIC ACID SEQUENCES CODING FOR SUCH RECEPTORS
TITLE OF INVENTION: AND POLYPEPTIDES, AND APPLICATIONS OF THESE POLYPEPTIDES
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHMAN DARBAY & CUSHMAN
STREET: 1615 L STREET, N.W.
CITY: WASHINGTON, D.C.
COUNTRY: U.S.A.
ZIP: 20036
COMPUTER READABLE FORM:
MEDIUM TYPE: Disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA: US/07/741.453A
APPLICATION NUMBER: 91913/1107/US/ST
FILING DATE: 19911015
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: KOKULIS, PAUL N.
REGISTRATION NUMBER: 16773
REFERENCE/DOCKET NUMBER: 91913/1107/US/ST
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 861-3000
TELEFAX: (202) 822-0944
TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO: 59:
SEQUENCE CHARACTERISTICS:
LENGTH: 764 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-741-453A-59

Query Match 46.2%; Score 1659; DB 4; Length 764;
Best Local Similarity 48.9%; Pred. No. 1.6e-126;
Matches 344; Conservative 112; Mismatches 191; Indels 56; Gaps 12;

Qy 3 LLLVSLAFALGTGGGCHHWHCHCSN-----RVFLQDSKVTEIPTDLPRLNATELRFVLTKL 58
Db 10 VLLDLPRDLG-GMGCSSPPCECHQEDFRV-TCKD--IQRIPS-LPESTQTLKLIETHL 64
Qy 59 RVIPKGFAGDGLKIEISONDVLEADVFNLPKLEIRIEKANNLVINPEAFON 118
Db 65 RTIPSHAFSNLPNISRIVTSIDLTQQLSHSFNLSKVTHIEIRNTNLTYYIDPAUKE 124
Qy 119 LPSRLYLISNTGKHLPAVHKIOSLO-KVLLDIQDNIHIVARNFMSGLSFESVILWL 177
Db 125 LPLKFLGIFNTGLKMFDPDLTKVSTDIFFILEITDNPYMTSIPVNAFQGLCNETLTKL 184
Qy 178 SKNGIEIHNCAFNQGLDELNLSDNNLEELPNVFOGA-SGPVILDISRTKVHSLPNH 236
Db 185 YNNGFTSVQGFAGNGLDVAVLNKNKYLTVIDKDAFGVYSGPSLDVSTVTPALPSK 244
Qy 237 GLENLKKLRARSTYRLKLPNLDKFTVLMASLTPSHCCAFANLKRQISELHPI-CNKS 295
Db 245 GLEHLKELIARTNLTLLKPLSLFHLTRADLSYPSHCCAFKNOKKIRGLIESLMCNES 304
Qy 296 IL-----QDIDDMT-----QIGDQVSLID-----DEPSY 321

Db 305 SMOISLRQKSVNALNSPLHOFYEBNLDGSIYGVYKESKFOOTHNNHHYVFFEEQDEII 364
 Qy 322 GKGSOW-----MYNEFDYDLCNEVDVTCSPKPAFNPCEIDIMGINILRLVWFI 371
 Db 365 GFGOELKMPQOETLQAFDSHYDVTICGSEDMVCTPKSDEFNPCEIDIMGYKFLRVVWFV 424
 Qy 372 SILAITGNTVLVLTTSQKLTVPFLKCNLAFADLCIGIYLLIASYVDIHTKSQYHN 431
 Db 425 SLLALGHVFLVLLITLTSYKLVNPRFLKCNLAFADFCMGNVLLIILIASYVDLTHSEYHNH 484
 Qy 432 AIDMOTGAGCDAAGFFTFVASELSVYTLTILERNHTITHAMOLECKVOLRHAASVWL 491
 Db 485 AIDMOTGAGCDAAGFFTFVASELSVYTLTILERNHTITHAMOLECKVOLRHAASVWL 544
 Qy 492 GWTFAPAAALPFIIGISSVMKYSICLPMIDSPLSQVYVALLVNLVAFVYVCCGYTHI 551
 Db 545 GWCCFLLALLPLVIGISSVMKYSICLPMIDSPLSQVYVALLVNLVAFVYVCCGYTHI 604
 Qy 552 YLTVRNPTIVSSSOTKIARMAVLIPTDFLCMAPIFPAISAKVPLITYSKAKILLV 611
 Db 605 YLTVRNPTIVSSSOTKIARMAVLIPTDFLCMAPIFPAISAKVPLITYSKAKILLV 664
 Qy 612 LFTYPLNSCAMPFLYAITFKNRDFPILLSKFCYEQMOAQIYR 654
 Db 665 LFTYPLNSCAMPFLYAITFKNRDFPILLSKFCYEQMOAQIYR 707
 RESULT 14
 US-07-757-342D-5
 : Sequence 5, Application US/07757342D
 : Patent No. 6218509
 : GENERAL INFORMATION:
 : APPLICANT: IGARASHI, Masao
 : INVENTOR: IGARASHI, Masao
 : TITLE OF INVENTION: PROTEIN, DNA AND USE THEREOF
 : NUMBER OF SEQUENCES: 10
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &
 : CUSHMAN
 : STREET: 130 Water Street
 : CITY: Boston
 : STATE: Massachusetts
 : COUNTRY: US
 : ZIP: 02109
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Floppy disk
 : COMPUTER: IBM PC compatible
 : SOFTWARE: PILEUP, A-DOS/MS-DOS
 : SOFTWARE RELEASE: Release 11.0, Version 11.25
 : CURRENT APPLICATION NUMBER: US/07/757,342D
 : FILING DATE: 10-Sep-1991
 : CLASSIFICATION: <Unknown>
 : ATTORNEY/AGENT INFORMATION:
 : NAME: BUCKLEY, Linda M.
 : REGISTRATION NUMBER: 31003
 : REFERENCE/DOCKET NUMBER: 41226
 : TELECOMMUNICATION INFORMATION:
 : TELEPHONE: (617)523-3400
 : TELEFAX: (617)523-6440
 : TELEX: 200951 STRE UR
 : INFORMATION FOR SEQ ID NO: 5:
 : SEQUENCE CHARACTERISTICS:
 : LENGTH: 764 amino acids
 : TOPOLOGY: linear
 : MOLECULE TYPE: protein
 : SEQUENCE DESCRIPTION: SEQ ID NO: 5:
 US-07-757-342D-5

Query Match 46.1%; Score 1658; DB 4; Length 764;
 Best Local Similarity 48.9%; Pred. No. 1.9e-126;

Matches 344; Conservative 112; Mismatches 191; Indels 56; Gaps 12;
 Qy 3 LLLVSLAFILCTGCGCHUHLCHSN-----RVFLCDSKVTETPDLPNRIELRFLVTKL 58
 Db 10 VLLDLPRLDLC-GACSSPPECQOEQDFV-TCAD--IQRIPS-LPPSTOTLLEIHL 64
 Qy 59 RVTPKGSFAGCDLKELEISONDVLEIVADVPKLEIRIEKANNLLYINPEAFON 118
 Db 65 RTIPSHAFSLNPNISRIYVSDVTLQOLESHPYNSKSVTHIEIRNRLTYIDPDALKE 124
 Qy 119 LPSLRYLLISNTGKHLPAVAKIQSLQ-KVLLDIODINIHIVARNSPMGLSPESVILWL 177
 Db 125 LPLAFGLIFNTGLKMPOLTKVYVDFIIFILEITDNPYMTSIPVNAPOGLCNETLTKL 184
 Qy 178 SKNGIEETHNCAFNQTQDELNSDNNLEELPNDFVQGA-SGPVILDISRTKVSHPNH 236
 Db 185 YNGFTSVQGYAFNPTKLDAYLKNKRYLTVYTKOAFGGVYSGPSLLDVSTYALPSK 244
 Qy 237 GLENKURARSTYLLKLPNLDKFTVTLKASUTYPSHCCAPANKKQISELHPI-CNKS 295
 Db 245 GLEHKLILARNMTLAKLPKLSLFLHTRADLSTPSNCCNFKKQIRKIGLESACRES 304
 Qy 296 TL-----RODIDDMT-----QTGORVSLID-----DEPSY 321
 Db 305 SMOISLRQKSVNALNSPLHOFYEBNLDGSIYGVYKESKFOOTHNNHHYVFFEEQDEII 364
 Qy 322 GKGSOW-----MYNEFDYDLCNEVDVTCSPKPAFNPCEIDIMGINILRLVWFI 371
 Db 365 GFGOELKMPQOETLQAFDSHYDVTICGSEDMVCTPKSDEFNPCEIDIMGYKFLRVVWFV 424
 Qy 372 SILAITGNTVLVLTTSQKLTVPFLKCNLAFADLCIGIYLLIASYVDIHTKSQYHN 431
 Db 425 SLLALGHVFLVLLITLTSYKLVNPRFLKCNLAFADFCMGNVLLIILIASYVDLTHSEYHNH 484
 Qy 432 AIDMOTGAGCDAAGFFTFVASELSVYTLTILERNHTITHAMOLECKVOLRHAASVWL 491
 Db 485 AIDMOTGAGCDAAGFFTFVASELSVYTLTILERNHTITHAMOLECKVOLRHAASVWL 544
 Qy 492 GWTFAPAAALPFIIGISSVMKYSICLPMIDSPLSQVYVALLVNLVAFVYVCCGYTHI 551
 Db 545 GWCCFLLALLPLVIGISSVMKYSICLPMIDSPLSQVYVALLVNLVAFVYVCCGYTHI 604
 Qy 552 YLTVRNPTIVSSSOTKIARMAVLIPTDFLCMAPIFPAISAKVPLITYSKAKILLV 611
 Db 605 YLTVRNPTIVSSSOTKIARMAVLIPTDFLCMAPIFPAISAKVPLITYSKAKILLV 664
 Qy 612 LFTYPLNSCAMPFLYAITFKNRDFPILLSKFCYEQMOAQIYR 654
 Db 665 LFTYPLNSCAMPFLYAITFKNRDFPILLSKFCYEQMOAQIYR 707
 RESULT 15
 US-07-741-453A-55
 : Sequence 55, Application US/07741453A
 : Patent No. 6428597
 : GENERAL INFORMATION:
 : APPLICANT: PARMENTIER, MARC
 : APPLICANT: LIBERT, FREDERIC
 : APPLICANT: DUMONT, JACQUES
 : APPLICANT: VASSART, GILBERT
 : TITLE OF INVENTION: POLYPEPTIDES HAVING THYROTROPIN-RECEPTOR
 : TITLE OF INVENTION: ACTIVITY, NUCLEIC ACID SEQUENCES CODING FOR SUCH RECEPTORS
 : TITLE OF INVENTION: AND POLYPEPTIDES, AND APPLICATIONS OF THESE POLYPEPTIDES
 : NUMBER OF SEQUENCES: 62
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: CUSHMAN, ARBY & CUSHMAN
 : STREET: 1615 K STREET, N.W.
 : CITY: WASHINGTON, D.C.
 : COUNTRY: U.S.A.
 : ZIP: 20036
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: disk
 : COMPUTER: IBM PC compatible

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Db          715 KAFQDRATHCGFLLLSRFGCGCKRAELYRRK-----EFSAYTSNCKN 758

Search completed: June 16, 2003, 13:37:56
Job time : 23.7674 secs

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Query Match	46.08;	Score 1652.5;	DB 4;	Length 795;
Best Local Similarity	50.74;	Pred. No. 5.6e-126;		
Matches 360;	Conservative 96;	Mismatches 159;	Indels 95;	Gaps 17;
QY	45	PRAIELRFLVTKL--RVIPKGSFAGDGLKIEISONDVLE-----VIEADVFNSLPK 96		
DB	63	PRAGL-ARLSLTYPVKVVISQAFRGLNEVVVKIEISODSLERATHCGRIEANAFDNLN 121		
QY	97	LHEIRIEKANLLYINPEAFONPLSRYLLISNTGIK-----HLPVAVHKTSLO-QVLL 149		
DB	122	LSELLIQNTKLLYIEPGAFTNLPRLKYLISICNTGIATRHCGLPDVTKISSSENFIL 181		
QY	150	DIOONTNIHIVARNSEGLSFESVILMSKNGIEIHC-----AFNGTOLDNELSDN 203		
DB	182	EICNLHTIPGNAFGOMNESVETKLYNGFERATHCGEVSQSHAFNGTLLSLEKEN 241		
QY	204	NNLEELPNDFQAGSGRVILDISRTKVHS-----LPNHGLENLKLRARSTYRLKKLPN 257		
DB	242	IYLEKMHGAFOGATGFSILDISTKLOARATHCGGLPSHGLESIQTLIALSSYSILKTLPS 301		
QY	258	LDFVTLMEASLYPSHCCEAFANKRQ-----ISELHPICNKSILRQDIDD 303		
DB	302	KERFTSLVATLYPSHCCEAFNLPRAATHCGKKEQNFSEFISFNSKQCESTVRAKADNET 361		
QY	304	MTQIGDQRVSLIDDEPSYKGSDMMYNEFDYDLGNEV---VDYTCSPKPAFNPCEDEM 359		
DB	362	L-----YSAIPEENELSGWRATHCGYDGRATHCGFSPKTLOCAPEPDAFNPCEDEM 414		
QY	360	GYNILRLVIFISILAITGNTTVLV-----LTSQYKLVPRFLMCLAFADLCIGY 413		
DB	415	GYAFLRLVILWILINILAFGNLTVLFVRATHCGLLTSRYKLVTPRFLMCLNLSFADFCMGLY 474		
QY	414	LLLIASVDIHTKSYHNYADW-----QTGAGCDAAGFFTVFASELSSVYILTATLBERW 467		
DB	475	LLLIASVDSQTKGQYYNHAIDWRATHCGQTGSGCGAAGFFTVFASELSSVYILTATLBERW 534		
QY	468	HTITHAMOLECKVQLRHAAS-----VWVLGWTFAFAALPPIFGISSYMKVSIICLPMDI 521		
DB	535	HTIYAVOLOQKLRRLHARATHCGCIPIMLGWLFSTLIATNPLGVISNYMKVSIICLPMDV 594		
QY	522	DSPLSQLYVWALLV-----LNVIAFVVVICCYTHIYLTVRNPTIVSSSDTKIAKMAT 575		
DB	595	ESTLSQVYIILSILRATHCGLVNVAFVYVICACYIRIYFVAVQNPETAPNKDTAKIARMAI 654		
QY	576	LIFTDFLCMA-----PISFPAISASLKVPLITYSKAKILVLVFPINSCANPFLYATFT 629		
DB	655	LIFTDFCMARATHCGPISFPAISAAKFVPLITWTNSKILVLVFPVMSCANPFLYATFT 714		
QY	630	KNFRD-----FFILLSKFGCYEQMAQIYRTETSSATHNPHARKSCSS 673		

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 16, 2003, 13:36:01 : Search time 170.089 Seconds
(without alignments)
434.981 Million cell updates/sec

Title: US-09-877-804-6
Perfect score: 3594
Sequence: 1 MALLVSLAFITGSGCHH.....SAPRTNSTVLYPLNHSN 692

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 408643 seqs, 106915682 residues
Total number of hits satisfying chosen parameters: 408643

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_AA:

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2:	/cgn2_6/ptodata/2/pubpaa/ECT_NEW_PUB pep.*
3:	/cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB pep.*
4:	/cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB pep.*
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10:	/cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB pep.*
11:	/cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3594	100.0	692	9	US-09-965-536A-11
2	3594	100.0	692	10	US-09-877-804-6
3	3560	99.1	688	9	US-09-965-536A-12
4	3516	97.8	675	10	US-09-877-804-7
5	3243.5	89.5	695	10	US-09-804-626-8
6	3076.5	85.6	687	9	US-09-965-536A-13
7	2605.5	72.5	693	9	US-09-965-536A-14
8	2107.5	58.6	458	10	US-09-862-767A-9
9	1992	51.0	348	10	US-09-877-804-3
10	1797	50.0	700	10	US-09-877-804-4
11	1797	50.0	700	10	US-09-877-804-5
12	1783.5	49.6	676	9	US-09-965-536A-15
13	1776	49.4	699	10	US-09-804-626-6
14	1653.5	46.0	764	9	US-10-045-6248-2
15	1505.5	41.9	516	10	US-09-862-767A-4
16	1393	37.6	458	10	US-09-862-767A-5
17	1191	33.1	359	10	US-09-862-767A-7
18	810.5	22.6	861	10	US-09-804-5518-20
19	675	18.8	341	10	US-09-877-804-4

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Sequence 2, Appl1
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Sequence 7, Appl1
Sequence 8, Appl1
Sequence 4, Appl1

518 10 US-09-804-626-2
907 9 US-09-965-536A-16
907 9 US-10-251-385-264
907 9 US-10-251-385-278
631 10 US-09-862-767A-2
1112 9 US-09-965-536A-10
1112 9 US-10-270-336-6
915 9 US-10-270-336-5
1405 9 US-10-176-847-90
1405 9 US-10-270-336-7
823 9 US-10-270-336-6
823 9 US-10-270-336-2
757 10 US-09-928-175-24
718 10 US-09-928-175-21
737 10 US-09-928-175-20
737 9 US-10-229-735-3
713 9 US-09-965-536A-6
713 10 US-09-928-175-3
737 9 US-09-965-536A-2
754 9 US-10-229-735-1
754 10 US-10-222-686-2
754 10 US-09-928-175-2
694 10 US-09-928-175-8
730 10 US-09-928-175-7
431 10 US-09-862-767A-8
431 10 US-09-862-767A-4
422 11.7
422 11.7

ALIGNMENTS

RESULT 1
US-09-965-536A-11
: Sequence 11, Application US/09965536A
: Publication No. US20030027323A1
: GENERAL INFORMATION:
: APPLICANT: FEDER, J. N.
: APPLICANT: MILLER, G.
: APPLICANT: HAWKEN, C. S.
: APPLICANT: HAWKEN, R.
: TITLE OF INVENTION: A NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGPBWMY,
: FILE OF INVENTION: EXPRESSED HIGHLY IN BRAIN AND OVARIAN TISSUES
: FILE REFERENCE: DOOINP
: CURRENT APPLICATION NUMBER: US/09/965.536A
: PRIOR FILING DATE: 2001-09-26
: PRIOR APPLICATION NUMBER: 60/235.713
: PRIOR FILING DATE: 2000-09-27
: PRIOR APPLICATION NUMBER: 60/261.781
: PRIOR FILING DATE: 2001-01-16
: PRIOR APPLICATION NUMBER: 60/306.605
: PRIOR FILING DATE: 2001-07-19
: PRIOR APPLICATION NUMBER: 60/310.436
: PRIOR FILING DATE: 2001-08-03
: NUMBER OF SEQ ID NOS: 6
: SOFTWARE: Patent In Ver. 2.1
: SEQ ID NO 11
: TYPE: PRT
: ORGANISM: RAT
US-09-965-536A-11

Query Match 100.0% ; Score 3594 ; DB 9 ; Length 692;
Best Local Similarity 100.0% ; Pred. No. 3e-287;
Matches 692; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 MALLVSLAFITGSGCHHCHSRRVFLCDSKVTEIPTDLPNRIELRFLVTKLRV 60
Db 1 MALLVSLAFITGSGCHHCHSRRVFLCDSKVTEIPTDLPNRIELRFLVTKLRV 60
OY 61 IPKSGFAGGDEKLEISQNDVLEIVADVSNLPKLTETRIKANNLLYINPEAFONLP 120
Db 61 IPKSGFAGGDEKLEISQNDVLEIVADVSNLPKLTETRIKANNLLYINPEAFONLP 120

QY 121 SLRYLLISNTGIGKHLPAVHKIQSLQKVLDDIQDNNIHIHIVARNSPMGLSFESVILWLSKN 180
DB 121 SLRYLLISNTGIGKHLPAVHKIQSLQKVLDDIQDNNIHIHIVARNSPMGLSFESVILWLSKN 180
QY 181 GIEEIHNCFAFNGTQDLELNDNNLELNDVFOGASGPVILDSRTKVVHSLPNHGLE 240
DB 181 GIEEIHNCFAFNGTQDLELNDNNLELNDVFOGASGPVILDSRTKVVHSLPNHGLE 240
QY 241 LKLLRARSTYRLKLLPNLDKFTVLTMEASLTYPSSHCCAFANLKRQISELHPICNKSILROD 300
DB 241 LKLLRARSTYRLKLLPNLDKFTVLTMEASLTYPSSHCCAFANLKRQISELHPICNKSILROD 300
QY 301 IDDMTQIGDQVSLIDDEPSYKSGSDMMYNEFDYDLCNEVVDVTCSPKPDAPNCPEDIMG 360
DB 301 IDDMTQIGDQVSLIDDEPSYKSGSDMMYNEFDYDLCNEVVDVTCSPKPDAPNCPEDIMG 360
QY 361 YNLRVLWFTSILAITGNTTVLVLTTSQYKLVTPRFLMCLNLAFAADLCIGIYLLIASV 420
DB 361 YNLRVLWFTSILAITGNTTVLVLTTSQYKLVTPRFLMCLNLAFAADLCIGIYLLIASV 420
QY 421 DIHTKSOYHNAIDQMTGAGDAAGFTVFASLSVYTLTITLERWHITITHAMOLECKV 480
DB 421 DIHTKSOYHNAIDQMTGAGDAAGFTVFASLSVYTLTITLERWHITITHAMOLECKV 480
QY 481 QLRHAASVWVLGWTFAFAAALFPPIGSISSYKVSICLPMDDSPSLQYVYVALLVNLVA 540
DB 481 QLRHAASVWVLGWTFAFAAALFPPIGSISSYKVSICLPMDDSPSLQYVYVALLVNLVA 540
QY 541 FWICGCTHYLYTVRNPTIYSSSDTKIAKRMATLIPTDFLCNAPISFFAISLKVPL 600
DB 541 FWICGCTHYLYTVRNPTIYSSSDTKIAKRMATLIPTDFLCNAPISFFAISLKVPL 600
QY 601 ITVSKAKILLVLYFPINSCANPFLYAIPTKFRDRDFILLSKFGCYEMOAIYRTETSSA 660
DB 601 ITVSKAKILLVLYFPINSCANPFLYAIPTKFRDRDFILLSKFGCYEMOAIYRTETSSA 660
QY 661 THNFHARKSHCSSAPRVNTNSYVLPNHSN 692
DB 661 THNFHARKSHCSSAPRVNTNSYVLPNHSN 692

RESULT 2

US-09-877-804-6
; Sequence 6, Application US/09877804
; Patent No. US20020061557A1
; GENERAL INFORMATION:
; APPLICANT: Nikolic, Karoly
; APPLICANT: McFarland, Keith C.
; APPLICANT: Segalo, Deborah L.
; APPLICANT: Seeburg, Peter H.
; TITLE OF INVENTION: Glycoprotein Hormone Receptor Molecules
; FILE REFERENCE: P0576P1C2
; CURRENT APPLICATION NUMBER: US/09-04
; CURRENT FILING DATE: 2001-09-04
; PRIOR APPLICATION NUMBER: US 08/207,814
; PRIOR FILING DATE: 1994-03-07
; PRIOR APPLICATION NUMBER: US 07/781,153
; PRIOR FILING DATE: 1991-10-31
; PRIOR APPLICATION NUMBER: US 07/347,683
; PRIOR FILING DATE: 1989-05-05
; NUMBER OF SEQ ID NOS: 22
; SEQ ID NO 6
; LENGTH: 692
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: deduced sequence
US-09-877-804-6

Query Match 100.0%; Score 3594; DB 10; Length 692;
Best Local Similarity 100.0%; Pred. No. 3e-287;
Matches 692; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MALLVSLAF LGTSGCHHMLCHCSNRVFLCQDSKVTEIPTDLPRNAIELRVLTCLR 60
DB 1 MALLVSLAF LGTSGCHHMLCHCSNRVFLCQDSKVTEIPTDLPRNAIELRVLTCLR 60
QY 61 IPKGSFAGFGLKIEIISONDVLEIADVFSNLPKLHEIRIEKANNLLYINPEAFONLP 120
DB 61 IPKGSFAGFGLKIEIISONDVLEIADVFSNLPKLHEIRIEKANNLLYINPEAFONLP 120
QY 121 SLRYLLISNTGIGKHLPAVHKIQSLQKVLDDIQDNNIHIHIVARNSPMGLSFESVILWLSKN 180
DB 121 SLRYLLISNTGIGKHLPAVHKIQSLQKVLDDIQDNNIHIHIVARNSPMGLSFESVILWLSKN 180
QY 181 GIEEIHNCFAFNGTQDLELNDNNLELNDVFOGASGPVILDSRTKVVHSLPNHGLE 240
DB 181 GIEEIHNCFAFNGTQDLELNDNNLELNDVFOGASGPVILDSRTKVVHSLPNHGLE 240
QY 241 LKLLRARSTYRLKLLPNLDKFTVLTMEASLTYPSSHCCAFANLKRQISELHPICNKSILROD 300
DB 241 LKLLRARSTYRLKLLPNLDKFTVLTMEASLTYPSSHCCAFANLKRQISELHPICNKSILROD 300
QY 301 IDDMTQIGDQVSLIDDEPSYKSGSDMMYNEFDYDLCNEVVDVTCSPKPDAPNCPEDIMG 360
DB 301 IDDMTQIGDQVSLIDDEPSYKSGSDMMYNEFDYDLCNEVVDVTCSPKPDAPNCPEDIMG 360
QY 361 YNLRVLWFTSILAITGNTTVLVLTTSQYKLVTPRFLMCLNLAFAADLCIGIYLLIASV 420
DB 361 YNLRVLWFTSILAITGNTTVLVLTTSQYKLVTPRFLMCLNLAFAADLCIGIYLLIASV 420
QY 421 DIHTKSOYHNAIDQMTGAGDAAGFTVFASLSVYTLTITLERWHITITHAMOLECKV 480
DB 421 DIHTKSOYHNAIDQMTGAGDAAGFTVFASLSVYTLTITLERWHITITHAMOLECKV 480
QY 481 QLRHAASVWVLGWTFAFAAALFPPIGSISSYKVSICLPMDDSPSLQYVYVALLVNLVA 540
DB 481 QLRHAASVWVLGWTFAFAAALFPPIGSISSYKVSICLPMDDSPSLQYVYVALLVNLVA 540
QY 541 FWICGCTHYLYTVRNPTIYSSSDTKIAKRMATLIPTDFLCNAPISFFAISLKVPL 600
DB 541 FWICGCTHYLYTVRNPTIYSSSDTKIAKRMATLIPTDFLCNAPISFFAISLKVPL 600
QY 601 ITVSKAKILLVLYFPINSCANPFLYAIPTKFRDRDFILLSKFGCYEMOAIYRTETSSA 660
DB 601 ITVSKAKILLVLYFPINSCANPFLYAIPTKFRDRDFILLSKFGCYEMOAIYRTETSSA 660
QY 661 THNFHARKSHCSSAPRVNTNSYVLPNHSN 692
DB 661 THNFHARKSHCSSAPRVNTNSYVLPNHSN 692

RESULT 3

US-09-965-536A-12
; Sequence 12, Application US/09965536A
; Publication No. US20030027323A1
; GENERAL INFORMATION:
; APPLICANT: FEDER, J. N.
; APPLICANT: MINTIER, G.
; APPLICANT: RAMANATHAN, C. S.
; APPLICANT: HAWKEN, D. R.
; TITLE OF INVENTION: A NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGPBMY5,
; EXPRESSED HIGHLY IN BRAIN AND OVARIAN TISSUES
; FILE REFERENCE: D0041NP
; CURRENT APPLICATION NUMBER: US/09/965,536A
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 60/235,713
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/261,781
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: 60/306,605
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 60/310,436
; PRIOR FILING DATE: 2001-08-03
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: Patentin Ver. 2.1

Query Match 99.13; Score 3560; DB 9; Length 688;
Best Local Similarity 99.31; Pred. No. 1.9e-284;
Matches 687; Conservative 0; Mismatches 1; Indels 4; Gaps 1;
TYPE: PRT
ORGANISM: Rattus norvegicus
US-09-877-804-12

QY 1 MALLVSLVLAFLGTSGCHHMLCHSRRVFLCODSKVTEIPTDLPNNAIELRFLVTLKRV 60
DB 1 MALLVSLVLAFLGTSGCHHMLCHSRRVFLCODSKVTEIPTDLPNNAIELRFLVTLKRV 60
QY 61 IPKGSFAGGDLKIEISONDVLEIADVSNPLKHEIRIEKANNLLYINPEAFONLP 120
DB 61 IPKGSFAGGDLKIEISONDVLEIADVSNPLKHEIRIEKANNLLYINPEAFONLP 120
QY 121 SLRYLISHTGKIHLPNKHQKQVLDIQDNINHIYVANSFNGLSFESVILWLSKN 180
DB 121 SLRYLISHTGKIHLPNKHQKQVLDIQDNINHIYVANSFNGLSFESVILWLSKN 176
QY 181 GTEIHNCAFNQDDELNLSDNNHLEELPNDVFOGASGPVILDSRTKVSHPNHLGN 240
DB 177 GTEIHNCAFNQDDELNLSDNNHLEELPNDVFOGASGPVILDSRTKVSHPNHLGN 236
QY 241 LKLRARSTYRLKLPNDKFTVLAESLTPSHCCAFANLKRQISELHPICNKSILROD 300
DB 237 LKLRARSTYRLKLPNDKFTVLAESLTPSHCCAFANLKRQISELHPICNKSILROD 296
QY 301 IDMTQIGQDQVSLDDSPSTGKSDMHYNEFDYDLCNEVDYVTCSPKDFNCPEDING 360
DB 297 IDMTQIGQDQVSLDDSPSTGKSDMHYNEFDYDLCNEVDYVTCSPKDFNCPEDING 356
QY 361 THILRVLWLPISLITATGNTVLYLVLTTSQKLYVPRFLMCLNFAFADLCIGIYLLLSY 420
DB 357 THILRVLWLPISLITATGNTVLYLVLTTSQKLYVPRFLMCLNFAFADLCIGIYLLLSY 416
QY 421 DIHTKSYHTAIDMTGAGCDAGCFPTFVASELSVTLTATLERHHTITHAMQLECKV 480
DB 417 DIHTKSYHTAIDMTGAGCDAGCFPTFVASELSVTLTATLERHHTITHAMQLECKV 476
QY 481 QLRHAASVWYLGHTFAAALPFIIGISSYKVSICLPHMDIDPSLSQLYVALLVNLVA 540
DB 477 QLRHAASVWYLGHTFAAALPFIIGISSYKVSICLPHMDIDPSLSQLYVALLVNLVA 536
QY 541 PVVIGCGTHIYLTVRNPTIVSSSDTKIAKRMATLIFTDFLCNAPISFFAISASLKVPL 600
DB 537 PVVIGCGTHIYLTVRNPTIVSSSDTKIAKRMATLIFTDFLCNAPISFFAISASLKVPL 596
QY 601 ITVSKAILLVLPYIPNSCANPLVIAFTKRNFRDFFILLSKFCGYEMQAOIYRTETSSA 660
DB 597 ITVSKAILLVLPYIPNSCANPLVIAFTKRNFRDFFILLSKFCGYEMQAOIYRTETSSA 656
QY 661 THNPHARKSHCSSAPRVNTSVLVPLNHSOON 692
DB 657 THNPHARKSHCSSAPRVNTSVLVPLNHSOON 688

RESULT 4
US-09-877-804-7
; Sequence 7, Application 05/09877804
; Patent No. US20020061557A1
; GENERAL INFORMATION:
; APPLICANT: Nikolic, Karoly
; APPLICANT: Szele, Randolph C.
; APPLICANT: Szele, Randolph L.
; APPLICANT: Szele, Peter H.
; TITLE OF INVENTION: Glycoprotein Hormone Receptor Molecules
; FILE REFERENCE: P0576PIC2
; CURRENT APPLICATION NUMBER: US/09/877,804
; CURRENT FILING DATE: 2001-09-04
; PRIOR APPLICATION NUMBER: US 08/207,814

PRIOR FILING DATE: 1994-03-07
PRIOR APPLICATION NUMBER: US 07/781,153
PRIOR FILING DATE: 1991-10-31
PRIOR APPLICATION NUMBER: US 07/347,683
PRIOR FILING DATE: 1989-05-05
NUMBER OF SEQ ID NOS: 22
SEQUENCE NO. 7675
LENGTH: 675
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: deduced sequence
US-09-877-804-7

Query Match 97.81; Score 3516; DB 10; Length 675;
Best Local Similarity 100.0%; Pred. No. 7.6e-281;
Matches 675; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: deduced sequence
US-09-877-804-7

QY 18 CHHWLCHSRRVFLCODSKVTEIPTDLPNNAIELRFLVTLKRVIPKGSFAGGDLKIEI 77
DB 1 CHHWLCHSRRVFLCODSKVTEIPTDLPNNAIELRFLVTLKRVIPKGSFAGGDLKIEI 60
QY 78 SONDVLEIADVSNPLKHEIRIEKANNLLYINPEAFONLPSRLYLLISHTGKIHLP 137
DB 61 SONDVLEIADVSNPLKHEIRIEKANNLLYINPEAFONLPSRLYLLISHTGKIHLP 120
QY 138 VHKIOSLQKVLDDIQDNINHIYVANSFNGLSFESVILWLSKNGTETIHNCAFNCTOLDE 197
DB 121 VHKIOSLQKVLDDIQDNINHIYVANSFNGLSFESVILWLSKNGTETIHNCAFNCTOLDE 180
QY 198 LNLSDNNHLEELPNDVFOGASGPVILDSRTKVSHPNHLGNLKKLRARSTYRLKLPN 257
DB 181 LNLSDNNHLEELPNDVFOGASGPVILDSRTKVSHPNHLGNLKKLRARSTYRLKLPN 240
QY 258 LKPVTLMEASLTPSHCCAFANLKRQISELHPICNKSILRODDMTQIGQDQVSLDD 317
DB 241 LKPVTLMEASLTPSHCCAFANLKRQISELHPICNKSILRODDMTQIGQDQVSLDD 300
QY 318 EBSYKGSDDMYNEFDYDLCNEVDYVTCSPKDFNCPEDIMGYNLVLIWLPISLITAT 377
DB 301 EBSYKGSDDMYNEFDYDLCNEVDYVTCSPKDFNCPEDIMGYNLVLIWLPISLITAT 360
QY 378 GNTTVLVLTTSQKLYVPRFLMCLNFAFADLCIGIYLLLSYVDIHTKSYHTAIDMTQ 437
DB 361 GNTTVLVLTTSQKLYVPRFLMCLNFAFADLCIGIYLLLSYVDIHTKSYHTAIDMTQ 420
QY 438 GAGDAAGFTVFASELSVTLTATLERHHTITHAMQLECKVQLRHAASVWYLGHTFAF 497
DB 421 GAGDAAGFTVFASELSVTLTATLERHHTITHAMQLECKVQLRHAASVWYLGHTFAF 480
QY 498 AALPFIIGISSYKVSICLPHMDIDPSLSQLYVALLVNLVIAFVVICGCTHIYLTVRN 557
DB 481 AALPFIIGISSYKVSICLPHMDIDPSLSQLYVALLVNLVIAFVVICGCTHIYLTVRN 540
QY 558 PTVSSSDTKIAKRMATLIFTDFLCNAPISFFAISASLKVPLITVSKAILLVLPYIPN 617
DB 541 PTVSSSDTKIAKRMATLIFTDFLCNAPISFFAISASLKVPLITVSKAILLVLPYIPN 600
QY 618 SCANPFLYIAFTKRNFRDFFILLSKFCGYEMQAOIYRTETSSATHNPHARKSHCSSAPRV 677
DB 601 SCANPFLYIAFTKRNFRDFFILLSKFCGYEMQAOIYRTETSSATHNPHARKSHCSSAPRV 660

RESULT 5
US-09-804-626-8
; Sequence 6, Application US/09804626
; Patent No. US20020128190A1
; GENERAL INFORMATION:
; APPLICANT: Lobel, Leslie

; APPLICANT: Lustbader, Joyce
; TITLE OF INVENTION: EXPRESSION OF PROPERLY FOLDED AND SOLUBLE EXTRACELLULAR DOMAIN OF
; FILE OF INVENTION: GONADOTROPIN RECEPTOR
; FILE REFERENCE: 0575/62259/JPW/SHS
; CURRENT APPLICATION NUMBER: US/09/804,626
; CURRENT FILING DATE: 2001-03-09
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8
; LENGTH: 695
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-804-626-8

Query Match 89.5%; Score 3215.5; DB 10; Length 695;
Best Local Similarity 88.9%; Pred. No. 4.2e-256;
Matches 618; Conservative 33; Mismatches 41; Indels 3; Gaps 2;
QY 1 MALLVSLAFALGTGSGCHHLCNSRVFLCQSKVTEIPTDLP RNAIELRFVLT KLV 60
DB 1 MALLVSLAFALGTGSGCHHLCNSRVFLCQSKVTEIPTDLP RNAIELRFVLT KLV 60
QY 61 IPKSGFAGDLEKTEISONDVLEIADVFSNLPKLHEIRIEKANNLLYINPEAFQNL 120
DB 61 IQKGFAGDLEKTEISONDVLEIADVFSNLPKLHEIRIEKANNLLYINPEAFQNL 120
QY 121 SLRYLLISNTGKHLPAVKHQSLOKVLDDIODNINIHIVARNSPMGSLFESVILWLSKN 180
DB 121 NLOYLLISNTGKHLPAVKHQSLOKVLDDIODNINIHIVARNSPMGSLFESVILWLSKN 180
QY 181 GIEETHNCAFNGTQDLDELNSDNNLEELPNDVFOGASGPVILDISRTKVHSLPNHGLN 240
DB 181 GIEETHNCAFNGTQDLDELNSDNNLEELPNDVFOGASGPVILDISRTKVHSLPNHGLN 240
QY 241 LKKLRARSTYRLKKLPNDOKFVTLMEASLTYP SHCCAFANLKRQISELHPICNKSILROD 300
DB 241 LKKLRARSTYRLKKLPNDOKFVTLMEASLTYP SHCCAFANLKRQISELHPICNKSILROE 300
QY 301 IDDMTOIGDQVSLTDDPSYKSGSDMAYNEFDYDLCEVVDVTCSPKPAFNPCEIDM 359
DB 301 VDMTOIGDQVSLTDDPSYKSGSDMAYNEFDYDLCEVVDVTCSPKPAFNPCEIDM 360
QY 360 GYNILRVLIWFISILAITGNTTVLVLTTSQYKLTVPFLMCLNFAFADLCIGIYLLIAS 419
DB 361 GYNILRVLIWFISILAITGNTTVLVLTTSQYKLTVPFLMCLNFAFADLCIGIYLLIAS 420
QY 420 VDIHTKSOYHNAIDWQTGAGCDAAGFTVFASLSVYTLTAITLERWHHTITHAMOLECK 479
DB 421 VDIHTKSOYHNAIDWQTGAGCDAAGFTVFASLSVYTLTAITLERWHHTITHAMOLECK 480
QY 480 VOLRHAASVWLVGTFEFAAALFPFGISYMKVSIKLPMDIDSPLSOLYVWALLVNLV 539
DB 481 VOLRHAASVWLVGTFEFAAALFPFGISYMKVSIKLPMDIDSPLSOLYVWALLVNLV 540
QY 540 AFVWICGCTHYIYLVTRNPTIVSSSDTKIAKRMATLIFTDFLCNAPISFFAISASLKV 599
DB 541 AFVWICGCTHYIYLVTRNPTIVSSSDTKIAKRMATLIFTDFLCNAPISFFAISASLKV 600
QY 600 LITVSKAKILLVLPINSCANPFLYIAITKPNRRDFFILLSKFCGYEQMOAQTRETSS 659
DB 601 LITVSKAKILLVLPINSCANPFLYIAITKPNRRDFFILLSKFCGYEQMOAQTRETSS 660
QY 660 ATHNHARKSHCSSAPRYT--NSYLVLPNLHSSON 692
DB 661 TVNTHPRNGHSSAPRYTSGSTYILVPLSHLAQN 695

RESULT 6

US-09-965-536A-13
; Sequence 13, Application US/09965536A
; Publication No. US2003002732A1
; GENERAL INFORMATION:
; APPLICANT: FEDER, J. N.

; APPLICANT: MINTIER, G.
; APPLICANT: RAMANATHAN, C. S.
; APPLICANT: HAWKEN, D. R.
; TITLE OF INVENTION: A NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGPBWMV5,
; FILE REFERENCE: EXPRESSED HIGHLY IN BRAIN AND OVARIAN TISSUES
; FILE REFERENCE: DCO41NP
; CURRENT APPLICATION NUMBER: US/09/965,536A
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 60/235,713
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/261,781
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: 60/306,605
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 60/310,436
; PRIOR FILING DATE: 2001-08-03
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 687
; TYPE: PRT
; ORGANISM: Equus asinus
US-09-965-536A-13

Query Match 85.6%; Score 3076.5; DB 9; Length 687;
Best Local Similarity 86.0%; Pred. No. 1.1e-244;
Matches 597; Conservative 38; Mismatches 50; Indels 9; Gaps 3;
QY 1 MALLVSLAFALGTGSGCHHLCNSRVFLCQSKVTEIPTDLP RNAIELRFVLT KLV 60
DB 1 MALLVSLAFALGTGSGCHHLCNSRVFLCQSKVTEIPTDLP RNAIELRFVLT KLV 60
QY 61 IPKSGFAGDLEKTEISONDVLEIADVFSNLPKLHEIRIEKANNLLYINPEAFQNL 120
DB 61 IPKGFAGDLEKTEISONDVLEIADVFSNLPKLHEIRIEKANNLLYIOHDAFQNL 120
QY 121 SLRYLLISNTGKHLPAVKHQSLOKVLDDIODNINIHIVARNSPMGSLFESVILWLSKN 180
DB 121 NLOYLLISNTGKHLPAVKHQSLOKVLDDIODNINIHIVARNSPMGSLFESVILWLSKN 180
QY 181 GIEETHNCAFNGTQDLDELNSDNNLEELPNDVFOGASGPVILDISRTKVHSLPNHGLN 240
DB 181 GIEETHNCAFNGTQDLDELNSDNNLEELPNDVFOGASGPVILDISGTRIHSPLNYGLEN 240
QY 241 LKKLRARSTYRLKKLPNDOKFVTLMEASLTYP SHCCAFANLKRQISELHPICNKSILROD 300
DB 241 LKKLRARSTYRLKKLPNDOKFVTLMEASLTYP SHCCAFANLKRQISELHPICNKSILROE 300
QY 301 IDDMTOIGDQVSLTDDPSYKSGSDMAYNEFDYDLCEVVDVTCSPKPAFNPCEIDM 360
DB 301 VDMTOIGDQVSLTDDPSYKSGSDMAYNEFDYDLCEVVDVTCSPKPAFNPCEIDM 353
QY 361 GYNILRVLIWFISILAITGNTTVLVLTTSQYKLTVPFLMCLNFAFADLCIGIYLLIAS 420
DB 361 GYNILRVLIWFISILAITGNTTVLVLTTSQYKLTVPFLMCLNFAFADLCIGIYLLIAS 413
QY 421 VDIHTKSOYHNAIDWQTGAGCDAAGFTVFASLSVYTLTAITLERWHHTITHAMOLECK 480
DB 421 VDIHTKSOYHNAIDWQTGAGCDAAGFTVFASLSVYTLTAITLERWHHTITHAMOLECK 473
QY 481 VOLRHAASVWLVGTFEFAAALFPFGISYMKVSIKLPMDIDSPLSOLYVWALLVNLV 540
DB 481 VOLRHAASVWLVGTFEFAAALFPFGISYMKVSIKLPMDIDSPLSOLYVWALLVNLV 533
QY 541 AFVWICGCTHYIYLVTRNPTIVSSSDTKIAKRMATLIFTDFLCNAPISFFAISASLKV 600
DB 541 AFVWICGCTHYIYLVTRNPTIVSSSDTKIAKRMATLIFTDFLCNAPISFFAISASLKV 593
QY 601 LITVSKAKILLVLPINSCANPFLYIAITKPNRRDFFILLSKFCGYEQMOAQTRETSS 660
DB 601 LITVSKAKILLVLPINSCANPFLYIAITKPNRRDFFILLSKFCGYEQMOAQTRETSS 653
QY 661 TVNTHPRNGHSSAPRYT--NSYLVLPNLHSSON 692

RESULT 9
US-09-877-804-8
; Sequence 8, Application US/09877804
; Patent No. US20020061557A1
; GENERAL INFORMATION:
; APPLICANT: Nikolics, Karoly
; APPLICANT: McFarland, Keith C.
; APPLICANT: Segalo, Deborah L.
; APPLICANT: Seeburg, Peter H.
; TITLE OF INVENTION: Glycoprotein Hormone Receptor Molecules
; FILE REFERENCE: P0576P1C2
; CURRENT APPLICATION NUMBER: US/09/877,804
; CURRENT FILING DATE: 2001-09-04
; PRIOR APPLICATION NUMBER: US 08/207,814
; PRIOR FILING DATE: 1994-03-07
; PRIOR APPLICATION NUMBER: US 07/781,153
; PRIOR FILING DATE: 1991-10-31
; PRIOR APPLICATION NUMBER: US 07/347,683
; PRIOR FILING DATE: 1989-05-05
; NUMBER OF SEQ ID NOS: 22
; SEQ ID NO 8
; LENGTH: 348
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: deduced sequence
US-09-877-804-8

Query Match 51.0%; Score 1832; DB 10; Length 348;
Best Local Similarity 100.0%; Pred. No. 1.1e-142;
Matches 348; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 18 CHWLVCHSNNRVFCQDSKVTETDLP RNAIELRVLT LKRVIPKSGFAGGDLKIEI 77
Db 1 CHWLVCHSNNRVFCQDSKVTETDLP RNAIELRVLT LKRVIPKSGFAGGDLKIEI 60

Qy 78 SONDLVEIADVSNLPKLEIRKANNLLYINPEAFONLPSRLYLLISNTGKHLPA 137
Db 61 SONDLVEIADVSNLPKLEIRKANNLLYINPEAFONLPSRLYLLISNTGKHLPA 120

Qy 138 VHKIQLQKVLDDIODNINIHIARNSPMGLSFESVILWLSKNGIEETHNCAFNGLD 197
Db 121 VHKIQLQKVLDDIODNINIHIARNSPMGLSFESVILWLSKNGIEETHNCAFNGLD 180

Qy 198 LNLSDNNLEELPNDVFGAGSPVLTDSRTKVSLSLPHNGLENLKKLRARSTYRLKLPN 257
Db 181 LNLSDNNLEELPNDVFGAGSPVLTDSRTKVSLSLPHNGLENLKKLRARSTYRLKLPN 240

Qy 258 LDKFVTLMEASLTYP SHCCAFANLKRQISELHPICNKSILRQDIDDMTQIGDQVSLIDD 317
Db 241 LDKFVTLMEASLTYP SHCCAFANLKRQISELHPICNKSILRQDIDDMTQIGDQVSLIDD 300

Qy 318 EPSYKSGSDMYNEFDYDLCNEVDVTCSPKPDAPNCPEDIMGYNILR 365
Db 301 EPSYKSGSDMYNEFDYDLCNEVDVTCSPKPDAPNCPEDIMGYNILR 348

RESULT 10
US-09-877-804-3
; Sequence 3, Application US/09877804
; Patent No. US20020061557A1
; GENERAL INFORMATION:
; APPLICANT: Nikolics, Karoly
; APPLICANT: McFarland, Keith C.
; APPLICANT: Segalo, Deborah L.
; APPLICANT: Seeburg, Peter H.
; TITLE OF INVENTION: Glycoprotein Hormone Receptor Molecules
; FILE REFERENCE: P0576P1C2
; CURRENT APPLICATION NUMBER: US/09/877,804
; CURRENT FILING DATE: 2001-09-04
; PRIOR APPLICATION NUMBER: US 08/207,814
; PRIOR FILING DATE: 1994-03-07
; PRIOR APPLICATION NUMBER: US 07/781,153

; PRIOR FILING DATE: 1991-10-31
; PRIOR APPLICATION NUMBER: US 07/347,683
; PRIOR FILING DATE: 1989-05-05
; NUMBER OF SEQ ID NOS: 22
; SEQ ID NO 3
; LENGTH: 674
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: deduced sequence
US-09-877-804-3

Query Match 50.0%; Score 1797; DB 10; Length 674;
Best Local Similarity 56.5%; Pred. No. 2e-139;
Matches 359; Conservative 105; Mismatches 149; Indels 22; Gaps 7;

Qy 45 PRNAIELRVLT LK--RVIPKSGFAGGDLKIEISQNDVLEIEADVSNLPKLEHTRI 102
Db 25 PRAGL-ARLSITVLPVKVIPSQAFRGLNEVVKIEISQSDSLERIEANAFDNLNLSLLI 83

Qy 103 EKANNLLYINPEAFONLPSRLYLLISNTGKHLPAVHKIOSLO-KVLLDIODNINIHI 161
Db 84 QNTKNLLYIEPGAFTNLPRLKYLISICNTGIRTPDVTKISSSEFNFILEICDNLHITIP 143

Qy 162 RNSFMGLSPFESVILWLSKNGIEETHNCAFNCTQDDELNDNNLEELPNDVFGAGSPV 221
Db 144 GNAFQGMNNEVSVTLKLYGNGFEEVQSHAFNGTTLSLELKENIYLEKMHSGAFGATGPS 203

Qy 222 ILDSRTKVSLSLPHNGLENLKKLRARSTYRLKLPNDKFTVLMASLTYP SHCCAFANL 281
Db 204 ILDISSTKQLNALSHGLESIOTLIALSSYLSLTKLPSEKFTSLVLTITP SHCCAFANL 263

Qy 282 KRQISELHPICNKSILRQDIDDMTQIGDQVSLIDDPSYGV---KSDMYNEFDYDLCN 338
Db 264 PKK-----EQNFSEFSEFENFSKQCESTVRKADNETLYSAIFEENELSGWDYDYGFS 315

Qy 339 EVDVTCSPKPDAPNCPEDIMGYNILRVLIWFIILAITGNTTVLVLTTSQYKLTVPFR 398
Db 316 PKT-LQCAPEPDAPNCPEDIMGYAFRLVLIWFIILAITGNTTVLVLTTSQYKLTVPFR 374

Qy 399 LMCNLAFLADLCIGYLLLIASVDIHTKSOYHNYAIDMTQAGCDAAGFTTVFASLSVYT 458
Db 375 LMCNLSFADFCMGLYLLLIASVDISQTKGQYVNHAIIDMTQSGCGAAGFTTVFASLSVYT 434

Qy 459 LTATLTERWHITITAMOLECKVQLRHASVWVLTGWTAFAAALPFIQGISYMKVSIQCLP 518
Db 435 LTVTLEWRHTITITAVQLDQKRLRHAIPIMLGGMLFSTLIATMPLVGISYMKVSIQCLP 494

Qy 519 MDIDPSQLVYVALLVNLVLAFFVVICGYTHYLTIVRNPTIVSSSDTKTAKRMATLIF 578
Db 495 MDVESTLSQVILSILINLVAVFVICACYIRITFAVONPELTAPNKDTKAKRMATLIF 554

Qy 579 TDFLCMAPISEFAISASLKVPLITVSKAKILLVLFYIPINSCANPFLYAIFTKFNRRDFFI 638
Db 555 TDFTCMAPISEFAISAAFKVPLITVNTSKILLVLFYIPVNSCANPFLYAIFTKAKQDRELL 614

Qy 639 LLSKFGCYEMOQAIYRTETSSATNFHARKSHCSS 673
Db 615 LLSRFGCCRRAEYLRK-----EFSAYTSNCRN 643

RESULT 11
US-09-877-804-2
; Sequence 2, Application US/09877804
; Patent No. US20020061557A1
; GENERAL INFORMATION:
; APPLICANT: Nikolics, Karoly
; APPLICANT: McFarland, Keith C.
; APPLICANT: Segalo, Deborah L.
; APPLICANT: Seeburg, Peter H.
; TITLE OF INVENTION: Glycoprotein Hormone Receptor Molecules
; FILE REFERENCE: P0576P1C2
; CURRENT APPLICATION NUMBER: US/09/877,804

APPLICANT: JANKEN, D. B.
TITLE OF INVENTION: NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGBRMB'S
FILE REFERENCE: DQALNP
CURRENT APPLICATION NUMBER: US/09/965,536A
CURRENT FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: 60/235,713
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: 60/261,781
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: 60/306,605
PRIOR FILING DATE: 2001-07-19
PRIOR APPLICATION NUMBER: 60/310,436
PRIOR FILING DATE: 2001-08-03
NUMBER OF SEQ ID NOS: 61
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 15
LENGTH: 676
ORGANISM: Gallitrix jacchus
US-09-965-536A-15

Query Match 50.0%; Score 1797; DB 10; Length 700;
Best Local Similarity 56.5%; Pred. No. 2, 1e-139;
Matches 359; Conservative 105; Mismatches 149; Indels 22; Gaps 7;

QY 45 PRNAIELRFLVTLK--RVIPKGSFAGDLEKIEISQNDVLEIADVFNSLPLKRIEIRI 102
DB 51 PRAGL-ARLSLTLPVKVPSOAFRGNEVVKIEISQDSLERIANAFDNLNLSLTI 109
QY 103 EKANLLYINPEAFONLPSRLYLLISMTGIGKLPVAVHKIQSLQ-KVLLDQDNIHIVIA 161
DB 110 QMTKLLYIEGAPNLPRLKYLSTICNTGRTLPVTKISSSEFNFILEICDNLHTTIP 169
QY 162 RNSPGLSPESIVIMLSKNGIEIHCNCFNGQDELKNSDNNLEELPNDVFOGAGPV 221
DB 170 GNAQGNMESVPLKLGNGFEVOSHAFNGTIVLSLEKENTYLERKHSAGPAGTGPS 229
QY 222 ILDSRTKVSHPGLENLKLBARSYRLKLPNDKFTYLMWASITYPSSHCAPANL 281
DB 230 ILDSRTKLOALPSHGLSIOTLIATSSYSLKLPSEKFTSLVATLITPSSHCAPANL 289
QY 282 KROISELPHCNKSIILRODDMTQIGDQVSLDDDEPSY---KGSMDMYNEFDYDLCN 338
DB 290 PKK-----EONFSFIPENFSKQCESTVAKADNETLYSAIFEENELSGMDYDYGCS 341
QY 339 EYVDYSCPKDAPNCPEDINGNLRVLNFIISLAIITGNTVVLVLTSTYKLTVPFR 398
DB 342 PRT-LQCAPEPDAPNCPEDINGVAPLRVLNFIILAIIPGLVLTSTYKLTVPFR 400
QY 399 IACNLAPADIGIGILLIASVDIHTKSOYHVAIDMOTGAGCDAGPFTVPASLSVTT 458
DB 401 IACNLSPADCKGLILLIASVDSQIGYTHALDQGTGSGGANGFTVPASLSVTT 460
QY 459 LTATILERWHITTHAMOLECKVOLRHAASVYVGLMTFAPAAALPFIPIGSISSYMKVSLCP 518
DB 461 LTATILERWHITTAVALDOKLRLHAIPIMLGMLFESTLIATMTPLVIGISNTMYSLCP 520
QY 519 MDIDSPLSQLYMALLVLNVLAVFYVIGCYTHIYLVNRPITVSSSDTKIARMAITLIF 578
DB 521 MDVESTLSQVILSLILNVVAVFYVACACIRIYFAVQNPGLTAPNKTOKIARMAITLIF 580
QY 579 TDFLCHAPISFPAISLAKVPLTVSKAKILLVLVLPINSCAMPFLYAIPTKPRDPTI 638
DB 581 TDFCHAPISFPAISLAKVPLTVSKAKILLVLVLPINSCAMPFLYAIPTKPRDPTI 640
QY 639 ILSKPECTEMOAOIYRTETSSATHPHARKSCSS 673
DB 641 ILSRPGCCRRRAELTRK-----EFSNYSNCLN 669

RESULT 12
US-09-965-536A-15
Sequence 15, Application US/09965536A
Publication No. US20030027323A1
GENERAL INFORMATION:
APPLICANT: FEDER, J. N.
APPLICANT: MINAMIAN, C. S.
APPLICANT: RAMANATHAN, C. S.

Query Match 49.6%; Score 1783.5; DB 9; Length 676;
Best Local Similarity 55.8%; Pred. No. 2, 6e-138;
Matches 359; Conservative 99; Mismatches 140; Indels 45; Gaps 6;
QY 55 LTKL-----RVIPKGSFAGDLEKIEISQNDVLEIADVFNSLPLKRIEIRI 107
DB 55 LTRLSLAYLPVKVPSOAFRGNEVVKIEISQDSLERIANAFDNLNLSLTIQMTKN 114
QY 108 LLYINPEAFONLPSRLYLLISMTGIGKLPVAVHKIQSLQ-KVLLDQDNIHIVARNSP 166
DB 115 LHTEPGATMLPRLKYLSTICNTGRTLPVTKISSSEFNFILEICDNLHTTIPGNAFO 174
QY 167 GHSVPLIMLSKNGIEIHCNCFNGQDELKNSDNNLEELPNDVFOGAGPVILDIS 226
DB 175 GANNESITLKLXNGFEVOSHAFNGTIVLSLEKENVHLERHNGAFRGYTPSLDIS 234
QY 227 RYKVSHPGLENLKLBARSYRLKLPNDKFTYLMWASITYPSSHCAPANLROIS 286
DB 235 STKLOALPSHGLSIOTLIATSSYSLKLPSEKFTSLVATLITPSSHCAPANVPTK-- 292
QY 287 ELHPICNKSILRODDMTQIGDQVSLDDDEPSYKGSMDMYNEFDYDLCNEVVDVTC 346
DB 293 -----DTPAIFAESGSCMDYDYG-FLPKTPRCA 321
QY 347 PKDAPNCPEDINGNLRVLNFIISLAIITGNTVVLVLTSTYKLTVPFRFLMCLNAPA 406
DB 322 PEPDAPNCPEDINGDIFLRLNFIILAIIPGLVLTSTYKLTVPFRFLMCLNAPA 381
QY 407 DLCTGYLLIATSVIHTKSOYHVAIDMOTGAGCDAGPFTVPASLSVTTITATLER 466
DB 382 DFCNGVLLLIASVDSQIGYTHIYLVNRPITVSSSDTKIARMAITLITPFR 441
QY 467 WHITTHAMOLECKVOLRHAASVYVGLMTFAPAAALPFIPIGSISSYMKVSLCPMDIDSP 526
DB 442 WHITTAHLDOKLRLHAIPIMLGMLFESTLIATMTPLVIGVSNMYKVSICLPMHETPFS 501
QY 527 QLYVMALLVLNVLAVFYVIGCYTHIYLVNRPITVSSSDTKIARMAITLITDPLCMAP 586
DB 502 QAYVILVLLVAVFYVIGCYTHIYLVNRPITVSSSDTKIARMAITLITDPLCMAP 561
QY 587 ISFPAISLAKVPLTVSKAKILLVLVLPINSCAMPFLYAIPTKPRDPTIILSKPGCY 646
DB 562 ISFPAISLAKVPLTVSKAKILLVLVLPINSCAMPFLYAIPTKPRDPTIILSKPGCY 621
QY 647 EMOAIYRTETSSA-THNFIARKSCSSAPRVNYSVVLVPLNH 688
DB 622 KURAEYLRKDKFSNYSNT---KNGFTGSGKPSOSTLKLPAH 661

RESULT 13
US-09-804-626-6

```
; Sequence 6, Application US/09804626
; Patent No. US20020128190A1
; GENERAL INFORMATION:
; APPLICANT: Lusbader, Joyce
; TITLE OF INVENTION: EXPRESSION OF PROPERLY FOLDED AND SOLUBLE EXTRACELLULAR DOMAIN OF
; TITLE OF INVENTION: CONADOTROPIN RECEPTOR
; FILE REFERENCE: 0575/62259/JPW/SHS
; CURRENT APPLICATION NUMBER: US/09/804,626
; CURRENT FILING DATE: 2001-03-09
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patencin version 3.0
; SEQ ID NO 6
; LENGTH: 699
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-804-626-6

Query Match      49.4%; Score 1776; DB 10; Length 699;
Best Local Similarity 55.4%; Pred. No. 1.le-137;
Matches 349; Conservative 108; Mismatches 147; Indels 26; Gaps 6;

QY 55 LTKL-----RVTPKGSFAGFDLEKIEISONDVLEIADVFSNLPKLHEIRKANN 107
DB 51 LTRLAYLPVKVIPSQAFGLNEVIKIEISQIDSLERIEANAFDNLNLSLILQNTKN 110
QY 108 LLYINPEAFONLPSRLYLISNTGKIKHLPVAKI--QSLQKVLDDODNINIHIARNFSM 166
DB 111 LRYTEGAFINLPRLKUSICNTGIRKFPDVTKFSSNSFILEICDNLHTTIPGNAFQ 170
QY 167 GLSFESVILWLSKNGIEIHNCAFNGTQDELINLSDNNLELNDVPGASGPVILDIS 226
DB 171 GNNESVTLKLYNGFEVQSHAFNGTTLTSLKENVHLEKMHNGARGTGPKYLDIS 230
QY 227 RTKVSHPHNGLENLKLBARSTYRLKLPNDLPVTLMEASLYPSHCCAFANLKROIS 286
DB 231 STKLOALPSYGLSIOQLRTSYSSSLKPLSRETFFVNLLEATLYPSHCCAFRLN----- 285
QY 287 ELHPICNKSILRQDIDDMTOIGDQVRSLIDDEPSYK--GSDMMYNEFDYDLGNEVDV 343
DB 286 ---PTKEQNFHSISENFKOCESYRKVNKNTLYSSMLAESELGWDIEYGFCLPKTP- 341
QY 344 TCSKPDAPNCPEDIMGYNIILRVLIWFISILAITGNTTVLVLTTSOYKLTVPFRLMCLN 403
DB 342 RCAPEPDAPNCPEDIMGYDFLRVLILINILAINGMTVFLVLTSTRYKLTVPFRLMCLN 401
QY 404 AFADLCIGIYLLIASVDIHTKSQYHNAIDWQTCGAGCDAAGFFTVFASLSVYTLTIT 463
DB 402 SFADFCMGLYLLIASVDSDQTKQYHNAIDWQTCGAGCAGTAGFFTVFASLSVYTLTIT 461
QY 464 LERWHTITHAMOLECKVOLRAHSAVMVLGWTAFANAALFPFISGYSYMKVSLCLPMDIDS 523
DB 462 LERWHTIYAHLOKLERAILIMLGNLWLFSSLIAMLPVLGVSNMKVSLCLPMDVET 521
QY 524 PLSQYVLMALLVNLVLAFFVIGCGYTHIYLVARNPTIYSSSDTKIAKRMATLIFTDFLC 583
DB 522 TLSQVYILTLINLVVAFIICACVYKIYFAVRNPELMATKDTKIAKMAILIFTDFTC 581
QY 584 MAPISFFAISLSKPLVLTISKAKILLVLPINSCANPFLYAIPTKFNRRDFFILLSKF 643
DB 582 MAPISFFAISAFKPLVLTIVNSKVLVLPINSCANPFLYAIPTKFNRRDFFILLSKF 641
QY 644 GYEMOAOIYRTETSSATHNFHARKSHCSS 673
DB 642 GCCRRAEYLRK-----DFSAYTSCKN 665
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RESULT 14

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US-10-045-624B-2
; Sequence 2, Application US/10045624B
; Publication No. US20030009778A1
; GENERAL INFORMATION:
; APPLICANT: Allen, Keith D.
```

```
; TITLE OF INVENTION: TRANSGENIC MICE CONTAINING THYROID
; TITLE OF INVENTION: STIMULATING HORMONE RECEPTOR (TSH-R) GENE DISRUPTIONS
; FILE REFERENCE: R-666
; CURRENT APPLICATION NUMBER: US/10/045,624B
; CURRENT FILING DATE: 2002-08-19
; PRIOR APPLICATION NUMBER: US 10/045,624
; FILING DATE: 2001-10-26
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 764
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-045-624B-2
```

```
Query Match      46.0%; Score 1653.5; DB 9; Length 764;
Best Local Similarity 48.9%; Pred. No. 1.5e-127;
Matches 346; Conservative 106; Mismatches 194; Indels 61; Gaps 11;

QY 3 LLLVSLLAFLGT--GSGCHHWLCHCSNRVFLCQDSKVT-----EIPDLPRAIELRVL 55
DB 7 LLLVLLALSRLRKEKACAPCECHQE-----DDFRVTCHELHRIPS-LPFSTOTLKLE 61
QY 56 TKLRVIRKPSGAGFDLEKIEISONDVLEIADVFSNLPKLHEIRIEKANNLLVINPEA 115
DB 62 THLKTIPSLATSSLPNISRIYLSIDATLQRIEPHSFYNLKRWTHIEIRNTRSLTIDPDA 121
QY 116 FQNLPSRLYLISNTGKIKHLPVAKIQLSLO--KVLDDIODNINIHIARNFSMGLSFESI 174
DB 122 LTLPPLKFLGIFNTGRIFFDPLTKIYSTDITDFFILEITDNPYMTSPVENAFQGLCNETLT 181
QY 175 LWSLNGEETEHNCANFGTQDELNLSNNLEELPNDFOGA--SGPVILDSIRTKVHSL 233
DB 182 LKLYNNGFTSQGHAFNGCTKLDVYLNKNKYLTATDNDAFGCVYSGPTLVDSSVSTAL 241
QY 234 PNHGLENLKLRARSTYRLKLPNDLPVTLMEASLYPSHCCAFANLKROISELHPI-C 292
DB 242 PSKGLEHLKELIAKDTWTLKPLSLSLHLTRADLSYPSHCCAFANOKKIRGILESMLC 301
QY 293 NKSILR-----QDIDDMTOIGDQVRSLIDDEPS----- 320
DB 302 NESSIRNLQRKSVNLRGPIYQVEYEDPGD--NSVGKQNSKFSQSPNSHYVFFEQE 360
QY 321 ---YCKGSDM-----MYNEFDYDLGNEVDVTCSPKPDAPNCPEDIMGYNIILRVL 367
DB 361 DEVYFGQELKNPOEETLQAFESHYDYTVCGDNEDMWCTPKSDEFPNCPEDIMGYRFLRV 420
QY 368 IWFISILAITGNTTVLVLTTSOYKLTVPFRLMCLAFADLCIGIYLLIASVDIHTKSO 427
DB 421 VWFVSLALLGNIFVLLILLTSHYKLTVPFRLMCLAFADFCMGVYLLLIASVDIHTISE 480
QY 428 YHNVAIDWQTCGAGCDAAGFFTVFASLSVYTLTITLERWHTITHAMOLECKVOLRAHSA 487
DB 481 YYNHAIDWQTCGAGCDAAGFFTVFASLSVYTLTITLERWHTITHAMOLECKVOLRAHSA 540
QY 488 VMVLGWTAFANAALFPFISGYSYMKVSLCLPMDIDSPLSQYVLMALLVNLVLAFFVIGCG 547
DB 541 IMAGWVSCFLLALLPMVGISSYAKVSLCLPMDITPLALAYLVILVLLVNLVLAFFVIGCG 600
QY 548 YTHIYLVARNPTIYSSSDTKIAKRMATLIFTDFLCMAPIFFAISLSKPLVLTISKAK 607
DB 601 YVKIYITVRNPOYNPRDKDTKIAKRMATLIFTDFLCMAPIFFAISLSKPLVLTISKAK 660
QY 608 ILLVLFYINSCANPFLYAIPTKFNRRDFFILLSKFGCYEMOAOIYRT 654
DB 661 ILLVLFYINSCANPFLYAIPTKFNRRDFFILLSKFGCYEMOAOIYRT 707
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RESULT 15

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US-09-804-626-4
; Sequence 4, Application US/09804626
; Patent No. US20020128190A1
; GENERAL INFORMATION:
```

APPLICANT: Lobel, Leslie
APPLICANT: Lobel, Leslie
TITLE OF INVENTION: EXPRESSION OF PROPERLY FOLDED AND SOLUBLE EXTRACELLULAR DOMAIN OF
FILE REFERENCE: 0575/62259/3PW/SWS
CURRENT APPLICATION NUMBER: US/09/804,626
CURRENT FILING DATE: 2001-03-09
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PatentIn version 3.0
SEQ ID NO 4
LENGTH: 516
TYPE: PRT
ORGANISM: Homo Sapiens
US-09-804-626-4

Query Match 41.9%; Score 1505.5; DB 10; Length 516;
Best Local Similarity 85.5%; Pred. No. 1.3e-115;
Matches 289; Conservative 22; Mismatches 26; Indels 1; Gaps 1;

Qy 28 RVLCOQSKYETPTDLPNAIELEFVLTGLRVIPKSPAGFGDLEKIEISONDVLEIE 87
Db 168 RVLCOQSKYETPTDLPNAIELEFVLTGLRVIPKSPAGFGDLEKIEISONDVLEIE 227

Qy 88 ADVFSLPKLHEIRIEKANNLLYINPEAFONLPSLRVLLISNTGKIKHLPVYHKSQKV 147
Db 228 ADVFSLPKLHEIRIEKANNLLYITPEAFONLPSLRVLLISNTGKIKHLPVYHKSQKV 287

Qy 148 LLDIQDNINIHIVARNFGLSFESVILWLSKNGIEEIHNCAPNGTQDDELNLSONNLE 207
Db 288 LLDIQDNINIHIVARNFGLSFESVILWLSKNGIEEIHNCAPNGTQDDELNLSONNLE 347

Qy 208 ELPNDFGAGSGPVILDISRTKVSPLNHLGLENLKLKARSTYRLKXKLPNLDKFTJMEA 267
Db 348 ELPNDFGAGSGPVILDISRTKVSPLNHLGLENLKLKARSTYRLKXKLPNLDKFTJMEA 407

Qy 268 SLTYSHCAPANKROISELHPYCHKSILRQDIDMTQIGDQVSLTDP-EPSTGKQSD 326
Db 408 SLTYSHCAPANKROISELHPYCHKSILRQDIDMTQIGDQVSLTDP-EPSTGKQSD 467

Qy 327 MWTNEFDYDLCEVVDVTCSPKPDAPNCPEDIMGYNIL 364
Db 468 MWTNEFDYDLCEVVDVTCSPKPDAPNCPEDIMGYNIL 505

Search completed: June 16, 2003, 13:52:47
Job time : 173.089 secs

F:554/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted
F:595/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted

Query Match 100.0% Score 3594; DB 2; Length 692; -
Best Local Similarity 100.0%; Pred. No. 5.6e-242;
Matches 692; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Oy 1 MALLVSLAFLGSGCHWLCNSNRVFLCQDSKVTETPTDPRNAIELRFLVTLKRV 60
Db 1 MALLVSLAFLGSGCHWLCNSNRVFLCQDSKVTETPTDPRNAIELRFLVTLKRV 60

Oy 61 IPKGSFAGFGLERIEISQNDVLEIADVFNSLPKLHEIRIEKANNLLYINPAFONLP 120
Db 61 IPKGSFAGFGLERIEISQNDVLEIADVFNSLPKLHEIRIEKANNLLYINPAFONLP 120

Oy 121 SLRYLLSNTGKHLPAVHKIQSLQKVLDDIQDNNINHIIVARNFSFGLSFEVILWLSKN 180
Db 121 SLRYLLSNTGKHLPAVHKIQSLQKVLDDIQDNNINHIIVARNFSFGLSFEVILWLSKN 180

Oy 181 GIEETHNCAFNCTOLDELNLSDNNLELNDVFGAGSPVILDSRTKVHSLPNHGLEN 240
Db 181 GIEETHNCAFNCTOLDELNLSDNNLELNDVFGAGSPVILDSRTKVHSLPNHGLEN 240

Oy 241 LKLLRASTYRLKLPNDKFTVLTMEASLTYPSCCAFAFLKROISELHPICNKSILROD 300
Db 241 LKLLRASTYRLKLPNDKFTVLTMEASLTYPSCCAFAFLKROISELHPICNKSILROD 300

Oy 301 IDDMTQIGDQVSLIDDEPSYKGSDDMMYNEFDYDLNCEVVDVTCSPKPDFAFNCEIDMG 360
Db 301 IDDMTQIGDQVSLIDDEPSYKGSDDMMYNEFDYDLNCEVVDVTCSPKPDFAFNCEIDMG 360

Oy 361 YNILLRVLWFTSILAITGNTVLLVLTTSQYKLTVPRLMCLNAPADLCIGIYLLLTASV 420
Db 361 YNILLRVLWFTSILAITGNTVLLVLTTSQYKLTVPRLMCLNAPADLCIGIYLLLTASV 420

Oy 421 DIHTKSOYHNTAIDWQTGAGDAAGFFTVFASLSVYLTATILERTWHITTHAMOLECKV 480
Db 421 DIHTKSOYHNTAIDWQTGAGDAAGFFTVFASLSVYLTATILERTWHITTHAMOLECKV 480

Oy 481 QLRHAASVNVLGWTFAPAAALPFIPIGSISSMKVSIICLPMIDSPLSQLYVLLVNLVA 540
Db 481 QLRHAASVNVLGWTFAPAAALPFIPIGSISSMKVSIICLPMIDSPLSQLYVLLVNLVA 540

Oy 541 FVWICGCTHYLTVRNPTIYVSSSDTKIARMTLFTDFLCWAPISFFAISASLKVPL 600
Db 541 FVWICGCTHYLTVRNPTIYVSSSDTKIARMTLFTDFLCWAPISFFAISASLKVPL 600

Oy 601 ITVSKAKILLVLYPINSCLNPFYIAFTKFNRRDFFILLKFGCYENQAOIYRTETSSA 660
Db 601 ITVSKAKILLVLYPINSCLNPFYIAFTKFNRRDFFILLKFGCYENQAOIYRTETSSA 660

Oy 661 THNFHARKSHCSSAPRVNTSVYVLPNLHSSON 692
Db 661 THNFHARKSHCSSAPRVNTSVYVLPNLHSSON 692
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RESULT 2

QHUFU

folliotropin receptor precursor - human
N:Alternate names: follicle stimulating hormone receptor (FSHR)
N:Contains: folliotropin receptor precursor long splice form; folliotropin receptor precursor
C:Species: Homo sapiens (man)
C:Date: 30-Sep-1991 #sequence_revision 06-Sep-1996 #text_change 22-Jun-1999
C:Accession: 157661; 156448; PC1147; S30560; 157672; JN0122
R:Gromoll, J.; Dankbar, B.; Gudermann, T.
Mol. Cell. Endocrinol. 102, 93-102, 1994
A:Title: Characterization of the 5' flanking region of the human follicle-stimulating hormone
A:Reference number: 157661; MUID:95011044; PMID:7926278
A:Accession: 157661
A:Status: translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-51 <GRO>
A:Cross-references: GB:S73199; NID:g685036; PIDN:AAB32071.1; PID:g685037

R:Gromoll, J.; Ried, T.; Holtgreve-Grez, H.; Nieschlag, E.; Gudermann, T.
J. Mol. Endocrinol. 12, 265-271, 1994
A:Title: Localization of the human FSH receptor to chromosome 2 p21 using a genomic p
A:Reference number: 156448; MUID:95000244; PMID:7916967
A:Accession: 156448
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 286-695 <GRO>
A:Cross-references: GB:S73526; NID:g688069; PIDN:AAB32225.1; PID:g688070;
R:Gromoll, J.; Gudermann, T.; Nieschlag, E.
Biochem. Biophys. Res. Commun. 188, 1077-1083, 1992
A:Title: Molecular cloning of a truncated isoform of the human follicle stimulating h
A:Reference number: PC1147; MUID:93075197; PMID:1359889
A:Accession: PC1147
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-223,286-294,'P',296-342 <GR3>
A:Cross-references: EMBL:X68044; NID:g31473; PIDN:CAA48179.1; PID:g31474
A:Experimental source: testis

R:Gromoll, J.
submitted to the EMBL Data Library, August 1992
A:Reference number: S30560
A:Accession: S30560
A:Molecule type: mRNA
A:Residues: 1-12,'R',14-223,286-294,'P',296-342 <GR4>
A:Cross-references: EMBL:X68044; NID:g31473; PIDN:CAA48179.1; PID:g31474
R:Kelton, C.A.; Cheng, S.V.; Nugent, N.P.; Schweickhardt, R.L.; Rosenthal, J.L.; Over
Mol. Cell. Endocrinol. 89, 141-151, 1992
A:Title: The cloning of the human follicle stimulating hormone receptor and its expe
A:Reference number: 157672; MUID:93246012; PMID:1301382
A:Accession: 157672
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: mRNA
A:Residues: 1-679,'N',681-695 <REL>
A:Cross-references: GB:S59900; NID:g300072; PIDN:AAB26480.1; PID:g300073
R:Minagishi, T.; Nakamura, K.; Takakura, Y.; Ibukki, Y.; Igarashi, M.
Biochem. Biophys. Res. Commun. 175, 1125-1130, 1991
A:Title: Cloning and sequencing of human FSH receptor cDNA.
A:Reference number: JN0122; MUID:91222171; PMID:1709010
A:Accession: JN0122
A:Molecule type: mRNA
A:Residues: 1-111,'T',113-196,'AV',199-306,'A',308-695 <MIN>
A:Cross-references: EMBL:M65085; NID:g182770; PIDN:AAAS2477.1; PID:g182771
C:Genetics:
A:Gene: GDB:FSHR
A:Cross-references: GDB:127510; OMIM:136435
A:Map position: 2p21-2p16
A:Introns: 223/3
A:Note: the exact position of the intron cannot be determined from the experimental d
C:Function:

A:Description: receptor that mediates the biochemical effects of follitropin
C:Superfamily: glycoprotein hormone receptor; leucine-rich alpha-2-glycoprotein repea
C:Keywords: alternative splicing; G protein-coupled receptor; glycoprotein; hormone r
F:1-695/Product: follitropin receptor precursor, long splice form #status predicted <
F:1-223,286-695/Product: follitropin receptor precursor, short splice form #status pr
F:1-15/Domain: signal sequence #status predicted <SIG>
F:16-695/Product: follitropin receptor #status predicted <MAT>
F:16-366/Domain: extracellular hormone binding #status predicted <EHB>
F:56-70/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR1>
F:71-95/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR2>
F:96-120/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>
F:121-145/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR4>
F:146-169/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR5>
F:172-193/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR6>
F:194-218/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR7>
F:367-387/Domain: transmembrane #status predicted <TM1>
F:398-421/Domain: transmembrane #status predicted <TM2>
F:444-465/Domain: transmembrane #status predicted <TM3>
F:486-508/Domain: transmembrane #status predicted <TM4>
F:529-550/Domain: transmembrane #status predicted <TM5>
F:574-597/Domain: transmembrane #status predicted <TM6>
F:609-630/Domain: transmembrane #status predicted <TM7>
F:191,199,293,318/Binding site: carbohydrate (Asn) (covalent) #status predicted

F:555/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted
F:596/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted
Query Match 89.9%; Score 3230.5; DB 1; Length 695;
Best Local Similarity 89.4%; Pred. No. 16-216;
Matches 621; Conservative 30; Mismatches 39; Indels 3; Gaps 2;

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QY 1 MALLVSLAPFATGSGCHHCHCHSRVFLCQDSKVTETPTDLPNATIELRFLVTKLRV 60
DB 1 MALLVSLAPFATGSGCHHCHCHSRVFLCQDSKVTETPTDLPNATIELRFLVTKLRV 60
QY 61 IPKSGFAGPQLEKIEISQNDVLEIADVSNLPLKHEIRIKANMLLYINPEAFONLP 120
DB 61 IQKSGFAGPQLEKIEISQNDVLEIADVSNLPLKHEIRIKANMLLYINPEAFONLP 120
QY 121 SURYLLISWTGKHLPVAVKIOSQVLOKVLQDQNNIHIIVARNSPGLSPFESVILMLSKN 180
DB 121 SURYLLISWTGKHLPVAVKIOSQVLOKVLQDQNNIHIIVARNSPGLSPFESVILMLSKN 180
QY 181 GTEIHNCAFNGTQDLNLSNNNLLELPNDVFGAGSPVILDTSRKTVHSLPHNGLEN 240
DB 181 GTEIHNCAFNGTQDLNLSNNNLLELPNDVFGAGSPVILDTSRKTVHSLPHNGLEN 240
QY 241 LKKLRARSTYRLKLPNDKFTVTLMEASLUTYPSHCCAFANLKRQISELHPICNKSILROD 300
DB 241 LKKLRARSTYRLKLPNDKFTVTLMEASLUTYPSHCCAFANLKRQISELHPICNKSILROE 300
QY 301 IDMTQIGQORVSLDD-EPSTGKSGDMTNEFDYDLCNEVDVTCSPKDPANPCEDIM 359
DB 301 IDMTQIGQORVSLDD-EPSTGKSGDMTNEFDYDLCNEVDVTCSPKDPANPCEDIM 359
QY 360 GYNILRVLWFIISLTAITGNTVYLVLTTSQYKLTVPRLMKNLAFADLCIGIYLLLIAS 419
DB 360 GYNILRVLWFIISLTAITGNTVYLVLTTSQYKLTVPRLMKNLAFADLCIGIYLLLIAS 419
QY 420 VOIHTKSOYHNYALDMQTAGCDAAGPFTVFASLSVYTLTATLTERHHTITHAMOLECK 479
DB 420 VOIHTKSOYHNYALDMQTAGCDAAGPFTVFASLSVYTLTATLTERHHTITHAMOLECK 479
QY 480 VOLRHAASVYVLGTFATAALFPFISSTYKYSICLPMIDISPLSOLYVALLVNLV 539
DB 480 VOLRHAASVYVLGTFATAALFPFISSTYKYSICLPMIDISPLSOLYVALLVNLV 539
QY 540 APVVICGCTTHIYLVNPTIVSSSDTKIAKRMATLIPTDFLCHAPISFFAISASUKVP 599
DB 540 APVVICGCTTHIYLVNPTIVSSSDTKIAKRMATLIPTDFLCHAPISFFAISASUKVP 599
QY 600 LITVSKAKILLVLPINSCANFLYALPTKFRDRDFILLSKFCGCEYMOAQIYRTTSS 659
DB 600 LITVSKAKILLVLPINSCANFLYALPTKFRDRDFILLSKFCGCEYMOAQIYRTTSS 659
QY 660 ATNHPHARKSCSSAPRYTN--NSYVLVPLNHSQN 692
DB 661 TAINSHPRNGHCSSAURVTNGSSYILVPLSLAQN 695
```

RESULT 3

JN0898

foliitropin receptor precursor - crab-eating macaque
N:Alternate names: follicle-stimulating hormone receptor (FSHR)
C:Species: Macaca fascicularis (crab-eating macaque)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: JN0898; S36452
R:Gronow, J.; Dankbar, B.; Sharma, R.S.; Nieschlag, E.
Biochem. Biophys. Res. Commun. 136:1068-1072(1995)
A:Gene name: FSHR; Chromosome: 17p11.31
A:Reference: JN0898; PubMed: 75041854; PMID:75041854
A:Accession: JN0898
A:Molecule type: mRNA
A:Residues: 1-695 <GRO>
A:Cross-references: ENBL:X74454; NID:q396801; PIDN:CAA52463.1; PID:q396802
A:Note: the authors translated the codon AGT for residue 488 as Arg
C:Function:

A:Description: receptor that mediates the biochemical effects of follitropin
C:Suprafamily: glycoprotein hormone receptor; leucine-rich alpha-2-glycoprotein repoa
C:Keywords: G protein-coupled receptor; glycoprotein; hormone receptor; phosphoprotein
F:1-17/Domain: signal sequence #status predicted <SIG>
F:18-695/Product: follitropin receptor #status predicted <PPH>
F:71-95/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR2>
F:96-120/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>
F:121-145/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR4>
F:146-169/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR5>
F:172-193/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR6>
F:194-218/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR7>
F:367-387/Domain: transmembrane #status predicted <TM1>
F:399-421/Domain: transmembrane #status predicted <TM2>
F:444-465/Domain: transmembrane #status predicted <TM3>
F:486-508/Domain: transmembrane #status predicted <TM4>
F:529-550/Domain: transmembrane #status predicted <TM5>
F:569-630/Domain: transmembrane #status predicted <TM6>
F:131-199-293-318/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:555/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted
F:596/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted

Query Match 89.4%; Score 3226.5; DB 1; Length 695;
Best Local Similarity 89.4%; Pred. No. 26-216;
Matches 621; Conservative 30; Mismatches 41; Indels 3; Gaps 2;

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QY 1 MALLVSLAPFATGSGCHHCHCHSRVFLCQDSKVTETPTDLPNATIELRFLVTKLRV 60
DB 1 MALLVSLAPFATGSGCHHCHCHSRVFLCQDSKVTETPTDLPNATIELRFLVTKLRV 60
QY 61 IPKSGFAGPQLEKIEISQNDVLEIADVSNLPLKHEIRIKANMLLYINPEAFONLP 120
DB 61 IQKSGFAGPQLEKIEISQNDVLEIADVSNLPLKHEIRIKANMLLYINPEAFONLP 120
QY 121 SURYLLISWTGKHLPVAVKIOSQVLOKVLQDQNNIHIIVARNSPGLSPFESVILMLSKN 180
DB 121 SURYLLISWTGKHLPVAVKIOSQVLOKVLQDQNNIHIIVARNSPGLSPFESVILMLSKN 180
QY 181 GTEIHNCAFNGTQDLNLSNNNLLELPNDVFGAGSPVILDTSRKTVHSLPHNGLEN 240
DB 181 GTEIHNCAFNGTQDLNLSNNNLLELPNDVFGAGSPVILDTSRKTVHSLPHNGLEN 240
QY 241 LKKLRARSTYRLKLPNDKFTVTLMEASLUTYPSHCCAFANLKRQISELHPICNKSILROD 300
DB 241 LKKLRARSTYRLKLPNDKFTVTLMEASLUTYPSHCCAFANLKRQISELHPICNKSILROE 300
QY 301 IDMTQIGQORVSLDD-EPSTGKSGDMTNEFDYDLCNEVDVTCSPKDPANPCEDIM 359
DB 301 IDMTQIGQORVSLDD-EPSTGKSGDMTNEFDYDLCNEVDVTCSPKDPANPCEDIM 359
QY 360 GYNILRVLWFIISLTAITGNTVYLVLTTSQYKLTVPRLMKNLAFADLCIGIYLLLIAS 419
DB 360 GYNILRVLWFIISLTAITGNTVYLVLTTSQYKLTVPRLMKNLAFADLCIGIYLLLIAS 419
QY 420 VOIHTKSOYHNYALDMQTAGCDAAGPFTVFASLSVYTLTATLTERHHTITHAMOLECK 479
DB 420 VOIHTKSOYHNYALDMQTAGCDAAGPFTVFASLSVYTLTATLTERHHTITHAMOLECK 479
QY 480 VOLRHAASVYVLGTFATAALFPFISSTYKYSICLPMIDISPLSOLYVALLVNLV 539
DB 480 VOLRHAASVYVLGTFATAALFPFISSTYKYSICLPMIDISPLSOLYVALLVNLV 539
QY 540 APVVICGCTTHIYLVNPTIVSSSDTKIAKRMATLIPTDFLCHAPISFFAISASUKVP 599
DB 540 APVVICGCTTHIYLVNPTIVSSSDTKIAKRMATLIPTDFLCHAPISFFAISASUKVP 599
QY 600 LITVSKAKILLVLPINSCANFLYALPTKFRDRDFILLSKFCGCEYMOAQIYRTTSS 659
DB 600 LITVSKAKILLVLPINSCANFLYALPTKFRDRDFILLSKFCGCEYMOAQIYRTTSS 659
QY 660 ATNHPHARKSCSSAPRYTN--SYVLVPLNHSQN 692
DB 661 TAINSHPRNGHCSSAURVTNGSSYILVPLSLAQN 695
```

RESULT 4

145896
follicle stimulating hormone receptor - bovine
C:Species: Bos primigenius taurus (cattle)
C:Date: 15-Oct-1996 #sequence_revision 15-Oct-1996 #text_change 21-Jan-2000
C:Accession: J45896
R:Houde, A.; Lambert, A.; Saumande, J.; Silversides, D.W.; Lussier, J.G.
Mol. Reprod. Dev. 39, 127-135, 1994
A:Title: Structure of the bovine follicle-stimulating hormone receptor complementary DNA
A:Reference number: 145896; MUID:95127199; PMID:7826612
A:Accession: J45896
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-695 <HOU>
A:Cross-references: GB:L22319; NID:g404671; PIDN:AC37324.1; PID:g404672
C:Genetics:
A:Gene: FSHR
C:Superfamily: glycoprotein hormone receptor; leucine-rich alpha-2-glycoprotein repeat
F:71-95/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR>

Query Match 89.3%; Score 3208.5; DB 2; Length 695;
Best Local Similarity 87.8%; Pred. No. 3.5e-215;
Matches 610; Conservative 46; Mismatches 36; Indels 3; Gaps 2;

QY 1 MALLVSLAFLGTGSGCHHCHCSNRVFLCQSKVTEIPTDLPRNAIELRFLVTKLRV 60
DB 1 MALLVALLAFLSGGCHHCHCSNGVFLCQSKVTEIPSDLPDRAVELRFLVTKLRV 60
QY 61 IPKGSFAGFGDLEKIEISQNDVLEIADVFSNPKLHEIRIEKANNLLYINPEAFQNL 120
DB 61 IPKGSFAGFGDLEKIEISQNDVLEIADVFSNPKLHEIRIEKANNLLYIDPAFQNL 120
QY 121 SLRYLLISNTGKHLPAVHKIQSLQKVLDDQDNINIHIVARNSPMGSLFESVILWLSKN 180
DB 121 NLRYLLISNTGKHLPAVHKIQSLQKVLDDQDNINIHIVARNSPMGSLFESVILWLSKN 180
QY 181 GIEETHNCAFNGTQDLDELNDNNLELPNDVFOGAGSPVLLDLSRTKVVHSLPNHGLN 240
DB 181 GIEETHNCAFNGTQDLDELNDNNLELPNDVFOGAGSPVLLDLSRTKVVHSLPNHGLN 240
QY 241 LKKLRARSTYRLKLPNDKFTVMEASLTYPSCCAFANLKRQISELHPICNKSILRQD 300
DB 241 LKKLRARSTYRLKLPNDKFTVMEASLTYPSCCAFANLKRQISELHPICNKSILRQ 300
QY 301 IDDMTQIGDQVSLI - DDEPSYSGSDMYNEFDYDLNVEVDVTCSPKPAFNPCEDEM 359
DB 301 VDDMTQARGQRVSLAEDDEPSYAKGFDYMYSEFDYDLNVEVDVTCSPKPAFNPCEDEM 360
QY 360 GYNILRLVIFTSILAITGNTVLTVOYKLTVPFLMCLNLAFAADLCIGIYLLITAS 419
DB 361 GDDILRLVIFTSILAITGNTVLTVOYKLTVPFLMCLNLAFAADLCIGIYLLITAS 420
QY 420 VDIHTKSOYHNYADWOTGACDAAGFFTVFASLSVYTLTAITLERWHTITHAMOLECK 479
DB 421 VDVHTKSOYHNYADWOTGACDAAGFFTVFASLSVYTLTAITLERWHTITHAMOLECK 480
QY 480 VOLRHAASVWLGWTFATAAALPFIPTGSSYMKVSIKLPMDIDPSQLYVALLVNLV 539
DB 481 VOLRHAASIMLVGWFATAAALPFIPTGSSYMKVSIKLPMDIDPSQLYVALLVNLV 540
QY 540 APVVICGCTHYLTVRNPTIVSSSDTKIAKRMATLFTDFLCNAPISFAISASLKP 599
DB 541 APVVICGCTHYLTVRNPTIVSSSDTKIAKRMATLFTDFLCNAPISFAISASLKP 600
QY 600 LITVSKAILLVLPINSCANPFLYIAFTKNFRDFFILLSKFCGYEQAQYRTSS 659
DB 601 LITVSKAILLVLPINSCANPFLYIAFTKNFRDFFILLSKFCGYEQAQYRTSS 660
QY 660 ATHNPHARKSHCSAPRVN -- SYVLVPLNISSON 692
DB 661 TANNPHRNGHCPAPRVNNGSNYTLIPLRLAKN 695

RESULT 5

JC1493
follicotropin receptor - sheep
N:Alternate names: follicle stimulating hormone receptor
C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 21-Jan-2000
C:Accession: JC1493; J47080
R:Khan, H.; Yarney, T.A.; Sairam, M.R.
Biochem. Biophys. Res. Commun. 190, 888-894, 1993
A:Title: Cloning of alternatively spliced mRNA transcripts coding for variants of ovine
A:Reference number: JC1493; MUID:93176195; PMID:8439338
A:Accession: JC1493
A:Molecule type: mRNA
A:Residues: 1-695 <KHA>
A:Experimental source: testis
R:Yarney, T.A.; Sairam, M.R.; Khan, H.; Ravindranath, N.; Payne, S.; Seidah, N.G.
Mol. Cell. Endocrinol. 93, 219-226, 1993
A:Title: Molecular cloning and expression of the ovine testicular follicle stimulating
A:Reference number: J47080; MUID:93351750; PMID:8394255
A:Accession: J47080
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-695 <YAR>
A:Cross-references: GB:L07302; NID:g165884; PIDN:AAA31525.1; PID:g165885
C:Genetics:
A:Gene: FSH-R
C:Superfamily: glycoprotein hormone receptor; leucine-rich alpha-2-glycoprotein repeat
F:71-95/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR>
F:191,199/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 89.0%; Score 3199.5; DB 2; Length 695;
Best Local Similarity 87.2%; Pred. No. 1.5e-214;
Matches 606; Conservative 48; Mismatches 38; Indels 3; Gaps 2;

QY 1 MALLVSLAFLGTGSGCHHCHCSNRVFLCQSKVTEIPTDLPRNAIELRFLVTKLRV 60
DB 1 MALFLVALLAFLSGGCHHCHCSNGVFLCQSKVTEIPSDLPDRAVELRFLVTKLRV 60
QY 61 IPKGSFAGFGDLEKIEISQNDVLEIADVFSNPKLHEIRIEKANNLLYINPEAFQNL 120
DB 61 IPEGAFSGFGDLEKIEISQNDVLEIADVFSNPKLHEIRIEKANNLLYIDPAFQNL 120
QY 121 SLRYLLISNTGKHLPAVHKIQSLQKVLDDQDNINIHIVARNSPMGSLFESVILWLSKN 180
DB 121 NLRYLLISNTGKHLPAVHKIQSLQKVLDDQDNINIHIVARNSPMGSLFESVILWLSKN 180
QY 181 GIEETHNCAFNGTQDLDELNDNNLELPNDVFOGAGSPVLLDLSRTKVVHSLPNHGLN 240
DB 181 GIEETHNCAFNGTQDLDELNDNNLELPNDVFOGAGSPVLLDLSRTKVVHSLPNHGLN 240
QY 241 LKKLRARSTYRLKLPNDKFTVMEASLTYPSCCAFANLKRQISELHPICNKSILRQD 300
DB 241 LKKLRARSTYRLKLPNDKFTVMEASLTYPSCCAFANLKRQISELHPICNKSILRQ 300
QY 301 IDDMTQIGDQVSLI - DDEPSYSGSDMYNEFDYDLNVEVDVTCSPKPAFNPCEDEM 359
DB 301 VDDMTQARGQRVSLAEDDEPSYAKGFDYMYSEFDYDLNVEVDVTCSPKPAFNPCEDEM 360
QY 360 GYNILRLVIFTSILAITGNTVLTVOYKLTVPFLMCLNLAFAADLCIGIYLLITAS 419
DB 361 GYDILRLVIFTSILAITGNTVLTVOYKLTVPFLMCLNLAFAADLCIGIYLLITAS 420
QY 420 VDIHTKSOYHNYADWOTGACDAAGFFTVFASLSVYTLTAITLERWHTITHAMOLECK 479
DB 421 VDVHTKSOYHNYADWOTGACDAAGFFTVFASLSVYTLTAITLERWHTITHAMOLECK 480
QY 480 VOLRHAASVWLGWTFATAAALPFIPTGSSYMKVSIKLPMDIDPSQLYVALLVNLV 539
DB 481 VVHRHAASIMLVGWFATAAALPFIPTGSSYMKVSIKLPMDIDPSQLYVALLVNLV 540

OY 540 AFVVICGTHYIYLVNPTIVSSSDTKAKMATLIFTDFELCMAPISFAISASLAVP 599
Db 541 AFVVICGTHYIYLVNPTIVSSSDTKAKMATLIFTDFELCMAPISFAISASLAVP 600
OY 600 LITVSKAILLVLPINSCANPLVAIFTKNRPDPFILLSKFCYEMOQIYRTETSS 659
Db 601 LITVSKAILLVLPINSCANPLVAIFTKNRPDPFILLSKFCYEMOQIYRTETSS 660
OY 660 ATNHFAHKSCHSAPRVN--SYVLVPLNHSSON 692
Db 661 TANHPRNGHCPAPRVNCSNTYLPLRLAKN 695

RESULT 6
JC2237
follicitropin receptor, testis - horse
N:Alternate names: eFSHR
C:Species: Equus caballus (domestic horse)
C>Date: 28-Aug-1985 #sequence_revision 07-Oct-1994 #text_change 13-Aug-1999
C:Accession: JC2237; JC2370
R:Robert, P.; Ansell, S.; Christophe, S.; Benifla, J.L.; Bellet, D.; Roman, A.; Bideret
Biochem. Biophys. Res. Commun. 201, 201-207, 1994
A:Title: Cloning and sequencing of the equine testicular follicitropin receptor.
A:Reference number: JC2237; MUID:94256980; PMID:8198575
A:Accession: JC2237
A:Molecule type: mRNA
A:Residues: 1-694 <R0>
A:Cross-references: GB:S70150; MUI:9546896; PIDN:AAB30854.1; PID:9546897
A:Experimental source: testis
C:Superfamily: glycoprotein hormone receptor; leucine-rich alpha-2-glycoprotein repeat
F:56-70/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR1>
F:71-95/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR2>
F:96-120/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR3>
F:121-145/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR4>
F:146-169/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR5>
F:172-193/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR6>
F:194-218/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR7>
F:366-386/Domain: transmembrane #status predicted <TM1>
F:398-420/Domain: transmembrane #status predicted <TM2>
F:443-464/Domain: transmembrane #status predicted <TM3>
F:485-507/Domain: transmembrane #status predicted <TM4>
F:528-549/Domain: transmembrane #status predicted <TM5>
F:573-596/Domain: transmembrane #status predicted <TM6>
F:608-629/Domain: transmembrane #status predicted <TM7>

Query Match 87.4%; Score 3140; DB 2; Length 694;
Best Local Similarity 87.6%; Pred. No. 26-210;
Matches 609; Conservative 35; Mismatches 47; Indels 4; Gaps 3;

OY 1 MALLVSLAPLGTGSGCHHCHCSNRVFLCDSKVTETPDLPRNATLRFVTLKRV 60
Db 1 MALLVSLAPLGTGSGCHHCHCSNRVFLCDSKVTETPDLPRNATLRFVTLKRV 60
OY 61 IPKSGFAGFGLKLEISQNDVLEADVFNLPKLEIRIEKANNLLYINPEAFONLP 120
Db 61 IPKSGFAGFGLKLEISQNDVLEADVFNLPKLEIRIEKANNLLYINPEAFONLP 120
OY 121 SLRTLLISPTGKILPAVHKIQSLQKVLDDIQDNIINITHIVARNSPMGLSFESVILWLSKN 180
Db 121 SLRTLLISPTGKILPAVHKIQSLQKVLDDIQDNIINITHIVARNSPMGLSFESVILWLSKN 180
OY 181 GIEETHNCAPNQTDLDELNLNNLDELNDVDFGASGPVILDSITKVSILNUGLEN 240
Db 181 GIEETHNCAPNQTDLDELNLNNLDELNDVDFGASGPVILDSITKVSILNUGLEN 240
OY 241 LKRLARSTYKALPNLDRFTYLMKASITYPSCCAPANLKRQISELIPTCNKSLROD 300
Db 241 LKRLARSTYKALPNLDRFTYLMKASITYPSCCAPANLKRQISELIPTCNKSLROD 300
OY 301 IDMTQIGDQSVLT--DDEFTSGKSDMTREFDYDLGNEVDVTCSPKDPANPCEDIM 359
Db 301 IDMTQIGDQSVLT--DDEFTSGKSDMTREFDYDLGNEVDVTCSPKDPANPCEDIM 359

Db 301 V-DNTQARGERYSLAEDDESSYPKGFDMHSEFEDYDLGNEVDVTCSPKDPANPCEDIM 359
OY 360 GYILRLVLIWFISLITATCTVTYLVLTYSOKLTVPRFLKCNLAFADLCIGIYLIIAS 419
Db 360 GYILRLVLIWFISLITATCTVTYLVLTYSOKLTVPRFLKCNLAFADLCIGIYLIIAS 419
OY 420 VDIHTKSYHNTAIDMGTGACDAGFTTFVASELSVYTLTATLERNHITTHAMOLECK 479
Db 420 VDIHTKSYHNTAIDMGTGACDAGFTTFVASELSVYTLTATLERNHITTHAMOLECK 479
OY 480 VOLRHAASVYVLGTMFAAALPFIPIGSISSVMKVSICLPHDIDSPISOLYVALLVNLV 539
Db 480 VOLRHAASVYVLGTMFAAALPFIPIGSISSVMKVSICLPHDIDSPISOLYVALLVNLV 539
OY 540 AFVVICGTHYIYLVNPTIVSSSDTKAKMATLIFTDFELCMAPISFAISASLAVP 599
Db 540 AFVVICGTHYIYLVNPTIVSSSDTKAKMATLIFTDFELCMAPISFAISASLAVP 599
OY 600 LITVSKAILLVLPINSCANPLVAIFTKNRPDPFILLSKFCYEMOQIYRTETSS 659
Db 600 LITVSKAILLVLPINSCANPLVAIFTKNRPDPFILLSKFCYEMOQIYRTETSS 659
OY 660 ATNHFAHKSCHSAPRVN--SYVLVPLNHSSON 692
Db 660 TANHPRNGHCPAPRVNCSNTYLPLRLAKN 695

RESULT 7
JC4301
follicitropin receptor - pig
N:Alternate names: follicle-stimulating hormone receptor
C:Species: Sus scrofa domestica (domestic pig)
C>Date: 16-Nov-1995 #sequence_revision 08-Feb-1996 #text_change 21-Jan-2000
C:Accession: JC4301
R:Remy, J.; 257-263, 1995
A:Title: The porcine follicitropin receptor: cDNA cloning, functional expression and characterization.
A:Reference number: JC4301; MUID:96011644; PMID:7590277
A:Accession: JC4301
A:Molecule type: mRNA
A:Residues: 1-694 <R0>
A:Cross-references: GB:L31966
A:Experimental source: ovarian granulosa cells
C:Comment: This receptor belongs to the family of the G-protein coupled receptors. It
ermatogenesis in male and oogenesis in female.
C:Genetics:
A:Gene: fshr
A:Map position: 3 q2.2-q2.3
C:Superfamily: glycoprotein hormone receptor; leucine-rich alpha-2-glycoprotein repeat
F:56-70/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR1>
F:71-95/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR2>
F:96-120/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR3>
F:121-145/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR4>
F:146-169/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR5>
F:172-193/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR6>
F:194-218/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR7>
F:366-386/Domain: transmembrane #status predicted <TM1>
F:398-420/Domain: transmembrane #status predicted <TM2>
F:443-464/Domain: transmembrane #status predicted <TM3>
F:485-507/Domain: transmembrane #status predicted <TM4>
F:528-549/Domain: transmembrane #status predicted <TM5>
F:573-596/Domain: transmembrane #status predicted <TM6>
F:608-629/Domain: transmembrane #status predicted <TM7>

Query Match 86.8%; Score 3118; DB 2; Length 694;
Best Local Similarity 86.0%; Pred. No. 6.9e-209;
Matches 598; Conservative 40; Mismatches 53; Indels 4; Gaps 3;

OY 1 MALLVSLAPLGTGSGCHHCHCSNRVFLCDSKVTETPDLPRNATLRFVTLKRV 60
Db 1 MALLVSLAPLGTGSGCHHCHCSNRVFLCDSKVTETPDLPRNATLRFVTLKRV 60
OY 61 IPKSGFAGFGLKLEISQNDVLEADVFNLPKLEIRIEKANNLLYINPEAFONLP 120
Db 61 IPKSGFAGFGLKLEISQNDVLEADVFNLPKLEIRIEKANNLLYINPEAFONLP 120
OY 121 SLRTLLISPTGKILPAVHKIQSLQKVLDDIQDNIINITHIVARNSPMGLSFESVILWLSKN 180
Db 121 SLRTLLISPTGKILPAVHKIQSLQKVLDDIQDNIINITHIVARNSPMGLSFESVILWLSKN 180

Db 120 NLRVLLISNTGCVKHLPAVKHQLQKVLDDIQDNIHTVERNSFMGLSFESMILWLSKN 179
Qy 181 GIEIHNCAFNQTDLDELNDNLELNDVDFGAGSPVILIDISRTKVKHSLNPHGLE 240
Db 180 GIREIHNCAFNQTDLDELNDNLELNDVDFGAGSPVILIDISRTKVKHSLNPHGLE 239
Qy 241 LKKLRARSTYRLKLPNDLKFTVMEASLTVPSCCAAFANLKRQISELHPTCNKSLRQD 300
Db 240 LKKLRARSTYRLKLPNDLKFTVMEASLTVPSCCAAFANLKRQISELHPTCNKSLRQD 299
Qy 301 IDDMTQIGDQSVLIDD-EPYSGKSDMMYNEFDYDLCNEVVDVTCSPKPAFNPCE 359
Db 300 VDMTQARGQSVLAEDGESSLAKFEEDMYSEFNYDLCNEVVDVTCSPKPAFNPCE 359
Qy 360 GYNILRVLIWISILAITGNTVTLVLTTSQYKLTVPFRLMCNLAFAADLCIGIYLL 419
Db 360 GHDILRVLIWISILAITGNTVTLVLTTSQYKLTVPFRLMCNLAFAADLCIGIYLL 419
Qy 420 VDIHTKSOYHNYAIDMOTGAGDAAGFTVFASLSVYTLTAITLERHHTITHAMOLECK 479
Db 420 IDIHTKSOYHNYAIDMOTGAGDAAGFTVFASLSVYTLTAITLERHHTITHAMOLECK 479
Qy 480 VOLRHAASVMVLGWTFAFAALFFPIFGISSYMKVSIKLPMDIDSPLSQLYVVLVNL 539
Db 480 QVVRHAASIMLYGWIFAFVTFALFFPIFGISSYMKVSIKLPMDIDSPLSQLYVVLVNL 539
Qy 540 APVWICGCTHYIYLVNPTIVSSSSDYKIAKRMATLIFTDFLCNAPISFFAISASL 599
Db 540 AFWVWICGCTHYIYLVNPTIVSSSSDYKIAKRMATLIFTDFLCNAPISFFAISASL 599
Qy 600 LITVSKAKTLVLYFPINSCANPFLYAIPTKFRDRDFFILLKFCGYEQAQIYRTSS 659
Db 600 LITVSKAKTLVLYFPINSCANPFLYAIPTKFRDRDFFILLKFCGYEQAQIYRTSS 659
Qy 660 ATHNPHARKSHCSSAPRVN--SYVLVPLNHSQN 692
Db 660 TAHHNPHRGCHPCPPAPRITNSSSYTLPLSLHAQN 694

RESULT 8
JC7361
follicitropin receptor precursor - newt
N:Alternate names: follicle-stimulating hormone receptor
C:Species: Cynops pyrrhogaster (newt)
C:Date: 17-Nov-2000 #sequence_revision 17-Nov-2000 #text_change 31-Dec-2000
R:Nakayama, Y.; Yamamoto, T.; Oba, Y.; Nagahama, Y.; Abe, S.
Biochem. Biophys. Res. Commun. 275, 121-128, 2000
A:Title: Molecular cloning, functional characterization, and gene expression of a follicle-stimulating hormone receptor from the newt, *Cynops pyrrhogaster*
A:Reference number: JC7361
A:Contents: Testis
A:Accession: JC7361
A:Molecule type: mRNA
A:Residues: 1-696 <NAK>
A:Cross-references: DBJ:AB005587
C:Comment: This protein, containing seven transmembrane domains and a large glycosylated in and thyroid stimulating hormone. This receptor has a common signal transduction pathway in and thyroid stimulating hormone.
A:Gene: fsh-r
C:Superfamily: glycoprotein hormone receptor; leucine-rich alpha-2-glycoprotein repeat H
C:Keywords: disulfide bond; glycolysis; glycoprotein; hormone receptor; testis; transmembrane
F:1-17/Domain: signal sequence #status predicted <SIG>
F:18-696/Product: follicle-stimulating hormone receptor #status predicted <MAT>
F:18-359/Domain: extracellular #status predicted <EXT>
F:370-389/Domain: transmembrane #status predicted <TM1>
F:402-424/Domain: transmembrane #status predicted <TM2>
F:447-468/Domain: transmembrane #status predicted <TM3>
F:489-511/Domain: transmembrane #status predicted <TM4>
F:532-553/Domain: transmembrane #status predicted <TM5>
F:577-600/Domain: transmembrane #status predicted <TM6>
F:612-633/Domain: transmembrane #status predicted <TM7>
F:46,190,198,267,292/Binding site: carbohydrate (Asn) (covalent) #status predicted

F:445-520/Disulfide bonds: #status predicted

Query Match 69.6%; Score 2503; DB 2; Length 696;
Best Local Similarity 70.2%; Pred. No. 3.9e-166;
Matches 488; Conservative 86; Mismatches 113; Indels 8; Gaps 5;
Qy 1 MALLVSLAFGLTSGCHHLCNHNKRVFLCQDSKVTEITDPLPRNRIELRVLTUKRV 60
Db 1 MSLAILCLLLAVGSSFGCHP--VCLNRVFTQESHVVOIPRDIIPRNSITELRVLTUV 59
Qy 61 IPKSGFAGFGLDLEKIEISQNDVLEIADVPSNLPKLEHRIEKANLLYINPEAFONLP 120
Db 60 IPKAFSGFEDVENIEISQNDVLTIEANVSHLPKLEHRIEKANLLYIDPDAFQNP 119
Qy 121 SLRVLLISNTGKHLPAVKHQLQKVLDDIQDNIHTVERNSFMGLSFESVILWLSKN 180
Db 120 SLKYLISNTGKHLPAVKHQLQKVLDDIQDNIHTVERNSFMGLSFESVILWLSKN 179
Qy 181 GIEIHNCAFNQTDLDELNDNLELNDVDFGAGSPVILIDISRTKVKHSLNPHGLE 240
Db 180 GIEIHNCAFNQTDLDELNDNLELNDVDFGAGSPVILIDISRTKVKHSLNPHGLE 239
Qy 241 LKKLRARSTYRLKLPNDLKFTVMEASLTVPSCCAAFANLKRQISELHPTCNKSLRQD 300
Db 240 LKKLRARSTYRLKLPNDLKFTVMEASLTVPSCCAAFANLKRQISELHPTCNKSLRQD 299
Qy 301 IDDMTQIGDQSVLIDD-EPYSGKSDMMYNEFDYDLCNEVVDVTCSPKPAFNPCE 355
Db 300 VDMTQARGQSVLAEDGESSLAKFEEDMYSEFNYDLCNEVVDVTCSPKPAFNPCE 359
Qy 360 GYNILRVLIWISILAITGNTVTLVLTTSQYKLTVPFRLMCNLAFAADLCIGIYLL 415
Db 360 GHDILRVLIWISILAITGNTVTLVLTTSQYKLTVPFRLMCNLAFAADLCIGIYLL 419
Qy 416 LITVSKAKTLVLYFPINSCANPFLYAIPTKFRDRDFFILLKFCGYEQAQIYRTSS 475
Db 420 LITVSKAKTLVLYFPINSCANPFLYAIPTKFRDRDFFILLKFCGYEQAQIYRTSS 479
Qy 476 LKCVQLRHAASVMVLGWTFAFAALFFPIFGISSYMKVSIKLPMDIDSPLSQLYV 535
Db 480 LKCVQLRHAASVMVLGWTFAFAALFFPIFGISSYMKVSIKLPMDIDSPLSQLYV 539
Qy 536 LNVLPVWICGCTHYIYLVNPTIVSSSSDYKIAKRMATLIFTDFLCNAPISFFAIS 595
Db 540 LNVLPVWICGCTHYIYLVNPTIVSSSSDYKIAKRMATLIFTDFLCNAPISFFAIS 599
Qy 596 LKVPVLTVSKAKTLVLYFPINSCANPFLYAIPTKFRDRDFFILLKFCGYEQAQIYRT 655
Db 600 LKVPVLTVSKAKTLVLYFPINSCANPFLYAIPTKFRDRDFFILLKFCGYEQAQIYRT 659
Qy 656 ETSSATHNPHARKSHCSSAPRVN--SYVLVPLNHSQN 688
Db 660 ETSSATHNPHARKSHCSSAPRVN--SYVLVPLNHSQN 694

RESULT 9

A41344
lutropin-choriogonadotropin receptor precursor (splice form A) - pig
N:Alternate names: luteinizing hormone-choriogonadotropin receptor
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 21-Jan-2000
C:Accession: A41344
R:Loosfelt, H.; Mistrati, M.; Atger, M.; Salesse, R.; Vu Hai-Luu Thi, M.T.; Jolivet, Science 245, 525-528, 1989
A:Title: Cloning and sequencing of porcine LH-hCG receptor cDNA: variants lacking the extracellular domain
A:Reference number: A41344; MUID:89332517; PMID:2502844
A:Accession: A41344
A:Molecule type: mRNA
A:Residues: 1-696 <LOO>
A:Cross-references: NID:g164528; PIDN:AAA31062.1; PID:g164529
C:Superfamily: glycoprotein hormone receptor; leucine-rich alpha-2-glycoprotein repeat
C:Keywords: alternative splicing; G-protein-coupled receptor; glycoprotein; membrane
F:1-27/Domain: signal sequence #status predicted <SIG>

A:Residues: 1-700 <RES>
A:Cross-references: GB:S40803; MID:g252163; PIDN:AAB22680.1; PID:g252164
C:Genetics:
A:Introns: 58/2; 82/2; 107/2; 132/2; 157/2; 183/2; 206/2; 231/2; 293/2; 320/2
C:Superfamily: glycoprotein hormone receptor; leucine-rich alpha-2-glycoprotein repeat
F:153-177/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR>

Query Match 50.0%; Score 1797; DB 2; Length 700;
Best Local Similarity 56.5%; Pred. No. 4.8e-117;
Matches 359; Conservative 105; Mismatches 149; Indels 22; Gaps 7;

QY 45 PRNATLRLPVTLK--RVIPKSPAGFGDLEKIEISQNDVLEIADVPFNLPKLHEIRI 102
DB 51 PRAGL-ARLSLTYLPVKVIPSQAFRLNEVVKIEISQSDSLERIEANFDNLNLSLLI 109
QY 103 EKANNLLYNPAFONFLPSRLYLLISNTGKHLPAVKHIOISLQ-KVLLDIDONINHIYA 161
DB 110 QNTKLLIYEPGAFNLPRLKYLSTCNTGIRLPDVTKISSSEFPNLEICDNLHITTP 169
QY 162 RNSFMGLSPESVILWSKNGIEIEHNCAPNGTQDELNLSNNLEELPNDFVFGASGPV 221
DB 170 GNAFGMNNESVTLKLYGNPREVQSHAFNGTTLISLEKENIYLEKMHSGAFQATGFS 229
QY 222 ILDISRTKVHSLPNHGLENLKRLARSTYRLKKNLDPNLFVTLMEASLTYPSSHCCAFANL 281
DB 230 ILDISRTKVHSLPNHGLENLKRLARSTYRLKKNLDPNLFVTLMEASLTYPSSHCCAFANL 289
QY 282 KROISELHPICKNSILRODIDDMTOIGDQVSLIDDEPSYG---KGSMDMYNEFDYDLGN 338
DB 290 PKK-----EQNFSFIFENFSKQCESTVTKKADNETLYSAIFTEENELSGWDYDYGFS 341
QY 339 EYVDVTCSPKDPFNPCEIDMGYNILRLWIFISILAITGNTVLVLTTSYKLTVPFR 398
DB 342 PRT-LQCAEPDAPNCPEDIMCYAFRLVLINILAFNLTLVLLTSYKLTVPFR 400
QY 399 LMCNLAPADLCIGYLLIASVDIHTKSOYHNAIDMOTGACDAGFTFVASELSVYT 458
DB 401 LMCNLSFADFCMGLYLLIASVDSOTKQGYHNAIDMOTGSCGAGFTFVASELSVYT 460
QY 459 LTAITLERWHTTHAMOLECKVOLRAASVMVLGTFEFAAALFPLFGISSYMKVSIICLP 518
DB 461 LVITLERWHTTYAVQLDQKRLRHAPIMLGGMLFSTLIATMPLVGLSNTMKVSIICLP 520
QY 519 MDIDSPSLQYVALLVNLVAFVVCIGCYTHIYLTVRNPTIVSSSDTKIAKRMATLIF 578
DB 521 MDVESTLSQVYILSILLNVAVFVICACYIRYFAVQNPETAPOKTKIAKMAILIF 580
QY 579 TDFLCNAPISFAISASLKVPLITVSKAILLVLPYIPNSCANPFLYIFTNFRDPEFI 638
DB 581 TDFTCNAPISFAISAAFKVPLITVTSKILLVLPYIPNSCANPFLYIAIFTRAFQDFLL 640
QY 639 LLSKFCYEQMAQIYRTTSSATHNPHARKSHCSS 673
DB 641 LLSRFCCCKRAELRYRK-----EFSATYSNCKN 669

RESULT 12
A49744
lutropin-choriogonadotropin receptor precursor - rat
N:Alternate names: lutalinizing hormone-choriogonadotropin receptor
C:Species: Rattus norvegicus (Norway rat)
C:Date: 03-May-1994 #sequence_revision 13-Sep-1998 #text_change 13-Aug-1999
C:Accession: A49744; A40545; A41343; A61453; A32460
R:Koo, Y.B.; Ji, I.; Slaughter, R.G.; Ji, T.H.
Endocrinology 128, 2297-2308, 1991
A:Title: Structure of the lutalinizing hormone receptor gene and multiple exons of the co
A:Reference number: A49744; MID:91209270; PMID:2019252
A:Accession: A49744
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-700 <KOO>
A:Cross-references: GB:M68917
A:Note: authors translated the codon CAA for residue 307 as Glu, AAC for residue 355 as

R:Tsal-Morris, C.H.; Bucsko, E.; Wang, W.; Xie, X.Z.; Dufau, M.L.
J. Biol. Chem. 266, 11355-11359, 1991
A:Title: Structural organization of the rat lutalinizing hormone (LH) receptor gene.
A:Reference number: A40545; MID:91250455; PMID:2040640
A:Accession: A40545
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-320 <TSA>
A:Cross-references: GB:M63918; GB:M63919; GB:M63920; GB:M63921; GB:M63922; GB:M63923
R:McFarland, K.C.; Sprengel, R.; Phillips, H.S.; Koehler, M.; Rosemblyt, N.; Nikolic
Science 245, 494-499, 1989
A:Title: Lutropin-choriogonadotropin receptor: an unusual member of the G protein-co
A:Reference number: A41343; MID:89332512; PMID:2502842
A:Accession: A41343
A:Molecule type: mRNA
A:Residues: 1-700 <MCF>
A:Cross-references: GB:M26199; MID:g205178; PIDN:AAA41528.1; PID:g205179
R:Dufau, M.L.; Minegishi, T.; Bucsko, E.S.; Delgado, C.J.; Zhang, R.
J. Steroid Biochem. 33, 715-720, 1989
A:Title: Characterization and structure of ovarian and testicular LH/hCG receptors.
A:Reference number: A61453; MID:90097014; PMID:2601325
A:Accession: A61453
A:Status: preliminary
A:Molecule type: protein
A:Residues: 27-33, 'X', 35-37, 'X', 39, 'X', 41-44 <DUF>
R:Roche, P.C.; Ryan, R.J.
J. Biol. Chem. 264, 4636-4641, 1989
A:Title: Purification, characterization, and amino-terminal sequence of rat ovarian
A:Reference number: A32460; MID:89174723; PMID:2925659
A:Accession: A32460
A:Molecule type: protein
A:Residues: 27-32, 'LX', 35-37 <ROC>
C:Genetics:
A:Introns: 58/2; 82/2; 107/2; 132/2; 157/2; 183/2; 206/2; 231/2; 293/2; 320/2
C:Superfamily: glycoprotein hormone receptor; leucine-rich alpha-2-glycoprotein repe
C:Keywords: alternative splicing; G protein-coupled receptor; glycoprotein; hormone
F:54-77/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR1>
F:78-102/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR2>
F:103-121/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>
F:128-152/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR4>
F:153-177/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR5>
F:180-201/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR6>
F:202-226/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR7>
F:368-389/Domain: transmembrane #status predicted <TM1>
F:400-422/Domain: transmembrane #status predicted <TM2>
F:444-466/Domain: transmembrane #status predicted <TM3>
F:489-511/Domain: transmembrane #status predicted <TM4>
F:530-551/Domain: transmembrane #status predicted <TM5>
F:575-598/Domain: transmembrane #status predicted <TM6>
F:610-631/Domain: transmembrane #status predicted <TM7>
F:103, 178, 199, 295, 303, 317/Binding site: carbohydrate (Asn) (covalent) #status predic
F:647, 648/Binding site: palmitate (Cys) (covalent) #status predicted
F:681/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predict

Query Match 50.0%; Score 1797; DB 2; Length 700;
Best Local Similarity 56.5%; Pred. No. 4.8e-117;
Matches 359; Conservative 105; Mismatches 149; Indels 22; Gaps 7;

QY 45 PRNATLRLPVTLK--RVIPKSPAGFGDLEKIEISQNDVLEIADVPFNLPKLHEIRI 102
DB 51 PRAGL-ARLSLTYLPVKVIPSQAFRLNEVVKIEISQSDSLERIEANFDNLNLSLLI 109
QY 103 EKANNLLYNPAFONFLPSRLYLLISNTGKHLPAVKHIOISLQ-KVLLDIDONINHIYA 161
DB 110 QNTKLLIYEPGAFNLPRLKYLSTCNTGIRLPDVTKISSSEFPNLEICDNLHITTP 169
QY 162 RNSFMGLSPESVILWSKNGIEIEHNCAPNGTQDELNLSNNLEELPNDFVFGASGPV 221
DB 170 GNAFGMNNESVTLKLYGNPREVQSHAFNGTTLISLEKENIYLEKMHSGAFQATGFS 229
QY 222 ILDISRTKVHSLPNHGLENLKRLARSTYRLKKNLDPNLFVTLMEASLTYPSSHCCAFANL 281
DB 230 ILDISRTKVHSLPNHGLENLKRLARSTYRLKKNLDPNLFVTLMEASLTYPSSHCCAFANL 289

Db 522 TLSQVYLTLLINLVAFACIYKIKYFAVNPENLMAKTKAKKMAILFTDTC 581
 QY 584 MAPISFAISAKVPLITVSKAKILLVLYFPINSCANPFLYAIFTKNFRDRFILLSKF 643
 Db 582 MAPISFAISAAKVPPLITVSKVLLVLYFPINSCANPFLYAIFTKNFRDRFILLSKF 641
 QY 644 GCYEQAOIYRTTSSATHNFAHKSCHSS 673
 Db 642 GCCKRAELRYR-----DFSAYTSCKN 665

RESULT 14

A40077
 thyrotropin receptor precursor - dog
 N:Alternate names: thyroid-stimulating hormone receptor; TSH receptor
 C:Species: Canis lupus familiaris (dog)
 C>Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 13-Aug-1999
 C:Accession: A40077; S06933
 R:Parmentier, M.; Libert, F.; Maenhaut, C.; Lefort, A.; Gerard, C.; Perret, J.; Van Sand
 Science 246, 1620-1622, 1989
 A:Title: Molecular cloning of the thyrotropin receptor.
 A:Reference number: A40077; MUID:90084524; PMID:2556796
 A:Accession: A40077
 A:Status: nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 1-764 <PA2>
 A:CROSS-references: GB:M29957; NID:g164098; PIDN:AAA30901.1; PID:g164099
 R:Parmentier, M.; Libert, F.; Maenhaut, C.; Lefort, A.; Gerard, C.; Perret, J.; van Sand
 Nucleic Acids Res. 17, 10493, 1989
 A:Title: Nucleotide sequence of the dog thyrotropin receptor cDNA.
 A:Reference number: S06933; MUID:9009886; PMID:2602159
 A:Accession: S06933
 A:Status: translation not shown
 A:Molecule type: mRNA
 A:Residues: 1-764 <PA2>

A:CROSS-references: EMBL:X17146; NID:g849; PIDN:CAA35026.1; PID:g850
 C:Superfamily: glycoprotein hormone receptor; leucine-rich alpha-2-glycoprotein repeat
 F:1-20/Domain: G protein-coupled receptor; glycoprotein; transmembrane protein
 F:21-764/Product: thyrotropin receptor #status predicted <SIG>
 F:53-76/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR1>
 F:77-101/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR2>
 F:102-126/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>
 F:127-151/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR4>
 F:152-176/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR5>
 F:179-200/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR6>
 F:201-225/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR7>

Query Match 46.6%; Score 1673.5; DB 2; Length 764;
 Best Local Similarity 47.1%; Pred. No. 2.le-108;
 Matches 351; Conservative 116; Mismatches 217; Indels 61; Gaps 11;

QY 4 LNVSLAFLGTGGCHHWLCHCSN----RVFLCDSKVTEIPDLPRNAIEFLVTLKLR 59
 Db 11 LLLALPSLGL-GRGCPSPPCHEQEDFRV-TCKD--IHRIP-LPSTOTLKFETOLK 65
 QY 60 VIPKSGPAGFDLEKTEISONDVLEADVFNPLKHLIRKANNLLYINPEAFQNL 119
 Db 66 TIPSRAFNPUNRIYLSIDATLQRLSHSFNLSKMTHEIRNTRSLTSIDPDALKEL 125
 QY 120 PSRLYLISNTGKIKHLPVAVHKIOSLQK-VLLDIQDINIHIVARNFMSFSESVILWLS 178
 Db 126 PLLKFLGIFTGLGVDPVTKYVSTOVFFLEITDNPYMASIPANAFGLCNETLLKLY 185
 QY 179 KNGIEETHNCAFNGTQDLNLDNNLEELPNDFVQGA-SGPVILDISRTKVHSLPNHG 237
 Db 186 NNGFTSQGHAFNGTKLDVYLNKNKYLSAIDKDAFGVYSGPTLLDVSYSVTALPSKG 245
 QY 238 LENLKLRASTYLLKLPNLDNFVTLMEASLYPPSHCCAFANLKRQISELHPI-CNKSI 296
 Db 246 LEHLKELIARTWTLLKKLPLSLSLFLHLTRADLSYPHCCAFKNQKIRGILELMCNES 305

QY 297 LRQ-----DIDDMTQIGDQORVSLTIDBPSYCKGSDMMY----- 329
 Db 306 IRSLRORSVNTLNGPFDQYEEYLGDSHAGYKDNSQFQDTSNHYVFEFQDEILG 365
 QY 330 -----NEFDYLCNEVVVDVTSPKPDAPNCPEDMGYILRVLIWFIS 372
 Db 366 FGQELKNPQETLQAFDSHYDYTVCGNEDMVCVTPKSDPEFPCEDMGYKFLRVWFVS 425
 QY 373 ILAITNTTVLVLTTSQYKLTVPRLMCMNLAFADICIGIYLLLIASVDTHTKSQYHNYA 432
 Db 426 LLALLGNVFLVLLTSHYKLTVPRLMCMNLAFADFCMGMYLLLIASVDLYTHSEYNYHA 485
 QY 433 IDMQTGAGCDAAGFFTVFSELSVYTLTALTLEHMTITHAMOLECKVOLRHAASVNLG 492
 Db 486 IDMQTGPCCNTAGFTTVFSELSVYTLTALTLEHMTITHAMOLECKVOLRHAASVNLG 545
 QY 493 WTPFAAAAFPIFGISSYMKVSIICLPMIDISPLSOLYVALLVNLVAFVVICGCTHYIY 552
 Db 546 WVCCELLALLPLVGISSYAKVSIICLPMIDETPLALAYIILVLLINIVAFIIVCSYKVIY 605
 QY 553 LTVRNPTIVSSSDTKIARMAITLFTDFLCMAPISEFFAISLSKVLPLITVSKAKILLVL 612
 Db 606 ITVRNPOYNPGDKDKTKIARMAVLIETDFCMAPISFYALSALMKNKPLITVTSKILLVL 665
 QY 613 FYDINSCANPFLYAIFTKNFRDRFILLSKFCGYEQAOIYRTTSSATHNF-----HAR 667
 Db 666 FYDINSCANPFLYAIFTKNFRDRFILLSKFCGYEQAOIYRTTSSATHNF-----HAR 725
 QY 668 KSHCSAPRVNTSVYVLPVPLNHSN 692
 Db 726 RDMQSLPNMQDEYELLENLHSLTPN 750

RESULT 15

QRHURH

thyrotropin receptor precursor - human
 N:Alternate names: thyroid stimulatory hormone receptor (TSHR)
 C:Species: Homo sapiens (man)
 C>Date: 22-Jan-1993 #sequence_revision 01-Mar-1996 #text_change 22-Jun-1999
 C:Accession: A33789; A33786; A34052; A36120; S38280
 R:Libert, F.; Lefort, A.; Gerard, C.; Parmentier, M.; Perret, J.; Ludgate, M.; Dumor
 Biochem. Biophys. Res. Commun. 165, 1250-1255, 1989
 A:Title: Cloning, sequencing and expression of the human thyrotropin (TSH) receptor:
 A:Reference number: A33789; MUID:90121232; PMID:2610690
 A:Accession: A33789
 A:Status: nucleic acid sequence not shown; not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 1-86; 'L', 88-764 <LIB>
 R:Nagayama, Y.; Kaufman, K.D.; Seto, P.; Rapoport, B.
 Biochem. Biophys. Res. Commun. 165, 1184-1190, 1989
 A:Title: Molecular cloning, sequence and functional expression of the cDNA for the h
 A:Reference number: A33786; MUID:90121223; PMID:2558651
 A:Accession: A33786
 A:Molecule type: mRNA
 A:Residues: 1-600; 'H', 602-764 <NAG>
 A:CROSS-references: GB:M31774; NID:g340003; PIDN:AAA36783.1; PID:g340004
 R:Misrahi, M.; Loosfelt, H.; Atger, M.; Sar, S.; Guiochon-Mantel, A.; Milgrom, E.
 Biochem. Biophys. Res. Commun. 166, 394-403, 1990
 A:Title: Cloning, sequencing and expression of human TSH receptor.
 A:Reference number: A34052; MUID:90147730; PMID:23021212
 A:Accession: A34052
 A:Molecule type: mRNA
 A:Residues: 1-726; 'E', 728-743; 'K', 745-764 <MIS>
 A:CROSS-references: GB:M32215; NID:g307524; PIDN:AAA61236.1; PID:g307525
 A:Note: 13-Pro, 260-Pro, 414-His, 500-Leu, 634-Leu, 727-Asp, and 744-Asn were also f
 R:Frazier, A.L.; Robbins, L.S.; Stork, P.J.; Sprengel, R.; Segaloff, D.L.; Cone, R.D
 Mol. Endocrinol. 4, 1264-1276, 1990
 A:Title: Isolation of TSH and LH/CG receptor cDNAs from human thyroid: regulation by
 A:Reference number: A36120; MUID:91155962; PMID:2293030
 A:Accession: A36120
 A:Status: not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 1-129; 'S', 131; 'AFS', 135-195; 'D', 197; 'F', 199-256; 'S', 258-263; 'A', 265-305,

A: Cross-references: GB:W73747; NID:9903759; PIDN:AA70232.1; PID:9903760
 R:Parra J.; Duprez, L.; van Sande, J.; Cochaux, P.; Garvy, C.; Mockel, J.; Dumont, J.;
 Nature 365, 645-651, 1993
 A: Note: mutations to Cys-619 or to Ile-623 in hyperfunctioning thyroid adenomas cause co-
 A: Reference number: S38280; MUID:94019814; PHID:8413627
 A: Accession: S38280
 A: Molecule type: DNA
 A: Residues: 615-642 <P&R>
 A: Experimental source: thyroid adenomas
 C: Comment: mutations to Cys-619 or to Ile-623 in hyperfunctioning thyroid adenomas cause co-
 C: Comment: See PIR:JC1319 for a splice form of thyrotropin receptor which lacks the seven
 C: Genetics:
 A: Gene: GDB:TSRR
 A: Cross-references: GDB:125313; OMIM:275200
 A: Map position: 14q31-14q31
 A: Introns: 231/2
 A: Note: the list of introns is incomplete; the eighth of eight introns is shown
 C: Function:
 C: Description: receptor that mediates the biochemical effects of thyrotropin
 C: Summary: glycoprotein tyrosine kinase receptor; leucine-rich alpha-2-glycoprotein repeat h
 C: Synonyms: alternative splicing; thyrotropin receptor; thyrotropin receptor; hormone rece
 C: Keywords: signal sequence; status predicted <SFS>
 P: 1-21/Domain: signal sequence status predicted <SFS>
 P: 22-76/Product: thyrotropin receptor status predicted <MAT>
 P: 53-76/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR1>
 P: 77-101/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR2>
 P: 102-126/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>
 P: 127-151/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR4>
 P: 152-176/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR5>
 P: 179-200/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR6>
 P: 201-226/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR7>
 P: 419-440/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR8>
 P: 451-473/Domain: transmembrane status predicted <TM1>
 P: 496-517/Domain: transmembrane status predicted <TM2>
 P: 530-550/Domain: transmembrane status predicted <TM3>
 P: 580-602/Domain: transmembrane status predicted <TM4>
 P: 626-649/Domain: transmembrane status predicted <TM5>
 P: 661-682/Domain: transmembrane status predicted <TM6>
 P: 77,99,113,177,198,302/Binding site: Carbohydrate (Aan) (covalent) #status predicted

Query Match 46.2%; Score 1660; DB 1; Length 764;
 Best Local Similarity 48.9%; Pred. No. 1.8e-107;
 Matches 344; Conservative 112; Mismatches 191; Indels 56; Caps 12;

Oy	3	LLVSLAFLGTCGCHRMHCN---- <td>58</td>	58
Db	10	VLLDLPRLDG-CMGCSPPCEHQEDFRV-TCKD--IORIPS-LPPSTOTLKLIETHL	64
Oy	59	RVIPKSGAGPDLEKTEISQNDVLEADVFSNLPKLHETRIEKANNLLYINPEAFQN	118
Db	65	KTIYPSANSLPISRIYSIDVTIQQLESHPNLSKVYHETRNRLTYIDPAUKR	124
Oy	119	LPSLYVLLISNCTGILPVAHVKTOSLO-KVLLIDQDNINTHVARNSPGLSPESVILWL	177
Db	125	LPALKFLGIPNGLKMPDILTAVYSTDIFILEITDNTYMTSIPVNAFOGLCNETLTKL	184
Oy	178	SKNGIEEIHNCAPNGTOLDLMLSDNNLELNDVFOGA-SGPVILDISRTKVHSLPNH	236
Db	185	YNGFTSVQGVAFNGTKLDVAVLNKKNYLTVDKDAFGVYSGPSLLDVSTVTLPSK	244
Oy	237	GLENLKLRARSTYRLKLPFLNPKFYTLMEASLYPSHCCAFANLKRQISELHPI-CNKS	295
Db	245	GLEHLKELIANMTYTKLPLSLSLFLTRADLSYPSHCCAFNOKKIRGILESIMNES	304
Oy	296	IL-----KQIDDMT-----QIGQORVSLD-----DEPSY	321
Db	305	SNQSLQRKSNLSPLHQEYENKALGDSIVGTEKSKSFQTHNNHYVTFEEQDEII	364
Oy	322	KGKSDN-----WNEFDYDLCHEVDVTCSPKDPANPCEDINGVNLRLVIRFI	371
Db	365	GPCGELANPQBEETLOAFDSHYDTICGSDMDVCTPSDEPNCEDINGVFLVYVWFV	424
Oy	372	SLTAITGTYVTVLVLTYSOKYLVTPRELCHAFADLCIGIYLLLIASVDIHTKSOYHY	431

Db	425	SLALGNGNVEVLLILLTSHYKLVNPRFLMKNLAFADFCMGMYLLLIASVDLYTHSEYNNH	484
Oy	432	AIDMOTGAGCDAAGFFTFASELSVYTLTAITLERHHTITHAMQJCKVOLRHAASVAVL	491
Db	485	AIDMOTGCGCTAGFFTFASELSVYTLTILERMATTFAMRLDKIRLIRHACAMWG	544
Oy	492	GMTPFAAALFTDIEGISSYMYKSGICLMDISDLSOLYVALLVILVLAQVYLCGYTHI	551
Db	545	GMWCFFLLALLPLVGISSYANVSGICLMDIETPLALAYIVFVLTAIVAFVYVCCYVKI	604
Oy	552	YLVTRNPTIVSSSDTKIAKRMATLITDFLCMAPISFPAISASLKVPLITVSKAKILLY	611
Db	605	YIVTRNPOYNPGDKTKIAKRMATLITDFLCMAPISFPAISASLKVPLITVSKAKILLY	664
Oy	612	LYTPNSCANPELAIPTKFNRRDRDFILLSKFCGYEMOAGIYR	654
Db	665	LYTPNSCANPELAIPTKAFORDVDFILLSKFCGICKRQAGYR	707

Search completed: June 16, 2003, 13:16:59

Job time : 28.8296 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 16, 2003, 11:39:51 : Search time 20.2487 Seconds
(without alignments)
1417.454 Million cell updates/sec

Title: US-09-877-804-6
Perfect score: 3594
Sequence: 1 MALLVSLAFVLTGSCCHH.....SAPRTVNTSVLVLNHSN 692

Scoring table: BLOSUM62
Gapop 10.0 , Capext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution.

SUMMARIES				Description	
Result No.	Score	Match	Length DB ID		
1	3594	100.0	692	1	P20395 rattus norv
2	3420	95.2	692	1	FSHR_RAT
3	3335.5	90.0	695	1	FSHR_MOUSE
4	3226.5	89.8	695	1	FSHR_HUMAN
5	3208.5	89.3	695	1	FSHR_MACFA
6	3199.5	89.0	695	1	FSHR_BOVIN
7	3153.5	87.7	695	1	FSHR_SHEEP
8	3074.0	87.4	694	1	FSHR_PIG
9	3016.0	85.5	697	1	FSHR_HORSE
10	2907.5	79.5	697	1	FSHR_DUCK
11	2807.5	70.3	696	1	FSHR_PIG
12	1807.5	50.3	701	1	FSHR_BOVIN
13	1799	50.1	700	1	FSHR_MOUSE
14	1797	50.0	700	1	FSHR_RAT
15	1776	49.4	699	1	FSHR_HUMAN
16	1766.5	49.2	676	1	FSHR_CALJA
17	1673.5	46.6	764	1	FSHR_CANFA
18	1655	46.0	764	1	FSHR_HUMAN
19	1653.5	46.0	764	1	FSHR_MOUSE
20	1642.5	45.7	763	1	FSHR_BOVIN
21	1636.5	45.5	764	1	FSHR_SHEEP
22	1632.5	45.4	764	1	FSHR_RAT
23	1589.5	44.2	538	1	FSHR_SHEEP
24	1536.5	34.6	566	1	FSHR_CHICK
25	1476.5	31.0	566	1	FSHR_MOUSE
26	1444	27.9	907	1	FSHR_MOUSE
27	636	17.7	907	1	FSHR_HUMAN
28	586.5	16.3	951	1	FSHR_MOUSE
29	571	15.9	951	1	FSHR_RAT
30	522.5	14.5	1115	1	FSHR_MOUSE
31	517.5	14.4	828	1	FSHR_HUMAN
32	483.5	13.5	757	1	FSHR_MOUSE
33	472.5	13.1	737	1	FSHR_MOUSE

Q8vxd0 homo sapien
P77395 mus musculus
Q92855 gallus gallus
P49146 homo sapien
P32303 xenopus lae
O02836 sus scrofa
Q9gk74 macaca mule
P35373 xenopus lae
P30874 homo sapien
Q98982 rana catesb
Q28886 macaca fasc

ALIGNMENTS

RESULT 1	FSHR_RAT	STANDARD	PRT: 692 AA
AC	P20395		
DT	01-FEB-1991 (Rel. 17, Created)		
DT	01-FEB-1991 (Rel. 17, Last sequence update)		
DT	16-OCT-2001 (Rel. 40, Last annotation update)		
DE	Follicle stimulating hormone receptor precursor (FSH-R) (POLLITROPIN DE RECEPTOR).		
GN	FSHR		
OS	Rattus norvegicus (Rat).		
OC	Eumariota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.		
OX	NCBI_TaxID=10116;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE-Sercol cells;		
RX	MEDLINE=91125358; PubMed=2126341;		
RA	Sprengel R., Braun T., Nikolics K., Segaloff D.L., Seeburg P.H.:		
RT	The testicular receptor for follicle stimulating hormone: structure and functional expression of the human cDNA.		
RL	Mol. Endocrinol. 4:535-550(1990).		
RN	[2]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=92149579; PubMed=1738373;		
RA	Heckert L.L., Daley I.J., Griswold M.D.:		
RT	"Structural organization of the follicle-stimulating hormone receptor gene."		
RL	Mol. Endocrinol. 6:70-80(1992).		
CC	-I- FUNCTION: RECEPTOR FOR FOLLICLE STIMULATING HORMONE. THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE ADENYLATE CYCLASE.		
CC	-II- SUBCELLULAR LOCATION: Integral membrane protein.		
CC	-III- TISSUE SPECIFICITY: TESTICULAR CELLS AND OVARIAN GRANULOSA CELLS.		
CC	-I- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.		
CC	FSH/LSH/FSH SUBFAMILY.		
CC	-I- SIMILARITY: CONTAINS 6 LEUCINE-RICH REPEATS (LRR).		
CC	THIS SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).		
DR	EMBL: L02842; AAA1175.1;		
DR	PIR: A34546; A34546.		
DR	SWISSPROT: A34546.		
DR	HESP: P21395; 11029.		
DR	InterPro: IPR000276; GPCR_Rhodopn.		
DR	InterPro: IPR001611; LRR.		
DR	InterPro: IPR000372; LRR_Nterm.		
DR	Pfam: PF00001; 7tm.1.1.		
DR	Pfam: PF00360; LRR: 3.		
DR	Pfam: PF01462; LRRNT: 1.		

SMART: SM00013; LRRNT: 1.
 DR PROSITE: PS00237; G-PROTEIN_RECP_F1_1; 1.
 DR PROSITE: PS0262; G-PROTEIN_RECP_F2_2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein; Signal;
 KW Phosphorylation; Repeat; Leucine-rich repeat.
 FT SIGNAL 1 17 POTENTIAL.
 FT CHAIN 18 692 FOLLICLE STIMULATING HORMONE RECEPTOR.
 FT DOMAIN 18 365 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 366 386 1 (POTENTIAL).
 FT DOMAIN 387 397 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 398 420 2 (POTENTIAL).
 FT DOMAIN 421 442 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 443 464 3 (POTENTIAL).
 FT DOMAIN 465 484 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 485 507 4 (POTENTIAL).
 FT DOMAIN 508 527 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 528 549 5 (POTENTIAL).
 FT DOMAIN 550 572 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 573 596 6 (POTENTIAL).
 FT DOMAIN 597 607 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 608 629 7 (POTENTIAL).
 FT DOMAIN 630 692 CYTOPLASMIC (POTENTIAL).
 FT REPEAT 44 68 LRR 1.
 FT REPEAT 69 93 LRR 2.
 FT REPEAT 119 143 LRR 3.
 FT REPEAT 170 192 LRR 4.
 FT REPEAT 193 216 LRR 5.
 FT REPEAT 218 240 LRR 6.
 FT DISULFID 441 516 BY SIMILARITY.
 FT CARBOHYD 191 191 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 199 199 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 293 293 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 692 AA; 77681 MW; 267EA78C7CFD8EC6 CRC64;
 Query Match 100.0%; Score 3594; DB 1; Length 692;
 Best Local Similarity 100.0%; Pred. No. 2e-222;
 Matches 692; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MALLVSLAFLGTGSGCHHLCNSRVFLCQSKVTEIPTDLPRNAIELRFLVTKURV 60
 DB 1 MALLVSLAFLGTGSGCHHLCNSRVFLCQSKVTEIPTDLPRNAIELRFLVTKURV 60
 QY 61 IPKGSFAGFGLKEIETSONDVLEIADVSNLPKLHEIRKANNLLYINPEAFQNP 120
 DB 61 IPKGSFAGFGLKEIETSONDVLEIADVSNLPKLHEIRKANNLLYINPEAFQNP 120
 QY 121 SLRYLLISNTGKHLPAVHKIOSLQKVLDDIQDNIHIVARNFPMGLSFESVILWLSKN 180
 DB 121 SLRYLLISNTGKHLPAVHKIOSLQKVLDDIQDNIHIVARNFPMGLSFESVILWLSKN 180
 QY 181 GIEETHNCAFNGTQDLNLSNDNNLELNDVFGAGSPVILDSRTKVSHPNHLN 240
 DB 181 GIEETHNCAFNGTQDLNLSNDNNLELNDVFGAGSPVILDSRTKVSHPNHLN 240
 QY 241 LKLRARSTYRLKLPNDKFTVLMASLTYPSCCAFANLKRQISELHPICNKSILRQD 300
 DB 241 LKLRARSTYRLKLPNDKFTVLMASLTYPSCCAFANLKRQISELHPICNKSILRQD 300
 QY 301 IDMTQIGDQVSLDDPSYKSGSDMMYNEFDYDLCEVVDVTSKPRDPAFNPCEIDMG 360
 DB 301 IDMTQIGDQVSLDDPSYKSGSDMMYNEFDYDLCEVVDVTSKPRDPAFNPCEIDMG 360
 QY 361 YNLRVLWTFISILAITGNTVVLVTSQYKLTVPFRLMCLNAPADLCIGIYLLIASV 420
 DB 361 YNLRVLWTFISILAITGNTVVLVTSQYKLTVPFRLMCLNAPADLCIGIYLLIASV 420
 QY 421 DHTKSQYHNVAIDQTCAGDCAAGFFTVFSELSVYTLTATLERWHTITHAMOLECKV 480
 DB 421 DHTKSQYHNVAIDQTCAGDCAAGFFTVFSELSVYTLTATLERWHTITHAMOLECKV 480
 QY 481 QLRHAASVYVLGWTFAFAAALFPFGISSYKVSICLPMDIDSPLSQLYVALLVNLVA 540
 DB 481 QLRHAASVYVLGWTFAFAAALFPFGISSYKVSICLPMDIDSPLSQLYVALLVNLVA 540

541 FVVICGCTHYIYLVNPTIVSSSDTKIAKRMATLIPTDFLCMAPISFPAISLKVPL 600
 DB 541 FVVICGCTHYIYLVNPTIVSSSDTKIAKRMATLIPTDFLCMAPISFPAISLKVPL 600
 QY 601 ITVSKAKILLVLEVPINSCANPELYAIFTKNFRDFFILLSKFGCYENAOIYRTETSSA 660
 DB 601 ITVSKAKILLVLEVPINSCANPELYAIFTKNFRDFFILLSKFGCYENAOIYRTETSSA 660
 QY 661 TNHFARKSHCSSAPRVNTSYVLPLNHSQN 692
 DB 661 TNHFARKSHCSSAPRVNTSYVLPLNHSQN 692

RESULT 2
 FSHR_MOUSE
 ID FSHR_MOUSE STANDARD: PRT: 692 AA.
 AC P35378; O9QW8; O9D4C2;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Follicle stimulating hormone receptor precursor (FSH-R) (Follicotropin receptor).
 DE FSHR.
 GN FSHR.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RC SEQUENCE FROM N.A.
 RC STRAIN=129/Sv; TISSUE=Testis;
 RA Tena-Sempere M., Manna P.R., Huhtaniemi I.T.;
 RT "Molecular cloning of the mouse follicle stimulating hormone receptor complementary deoxyribonucleic acid: functional expression of alternatively spliced variants and receptor inactivation by a C56GT transition in exon 7 of the coding sequence."
 RT Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
 RL [2]
 RN SEQUENCE FROM N.A.
 RP STRAIN=C57BL/6J; TISSUE=Testis;
 RC MEDLINE=21085660; PubMed=11217851;
 RX Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamakura I., Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H., Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T., Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Gustincich S., Hall D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L., Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection."
 RL Nature 409:685-690(2001).
 RN [3]
 RP SEQUENCE OF 1-51 FROM N.A.
 RX MEDLINE=93093308; PubMed=1459341;
 RX Huhtaniemi I.T., Eskola V., Pakarinen P., Matikainen T., Sprengel R.;
 RT "The murine luteinizing hormone and follicle-stimulating hormone receptor genes: transcription initiation sites, putative promoter sequences and promoter activity."
 RT Mol. Cell. Endocrinol. 88:55-66(1992).
 CC -!- FUNCTION: RECEPTOR FOR FOLLICLE STIMULATING HORMONE. THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE ADENYLATE CYCLASE.

CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 CC PSH/ASH/7SH SUBFAMILY
 CC -1- SIMILARITY: CONTAINS 6 LEUCINE-RICH REPEATS (LRR).
 CC
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 CC
 CC EMBL: AF095542; AAC67559.1; -
 CC EMBL: AF016635; BAB30351.1; -
 CC EMBL: S49532; AAB24401.1; -
 CC EMBL: M87570; AAK37641.1; -
 CC GDB: 461; 9350002; chr: GPCR_Rhodopsin.
 CC InterPro: IPR001611; LRR_Nterm.
 CC InterPro: IPR000372; LRR_Nterm.
 CC Pfam: PF00001; 7tm.1.1;
 CC Pfam: PF0560; LRR_3;
 CC Pfam: PF01462; LRRNT_1;
 CC PRINTS: PR00237; GPCR_Rhodopsin.
 CC SMART: SM0013; LRRNT_1;
 CC PROSITE: PS00237; G-PROTEIN_RECEP_F1_1;
 CC PROSITE: PS00262; G-PROTEIN_RECEP_F1_2;
 CC G-protein coupled receptor; Transmembrane; Glycoprotein; Signal;
 CC Phosphorylation; Repeat; Leucine-rich repeat.
 CC SIGNAL 1 17 POTENTIAL.
 CC CHAIN 18 692
 CC TRANSMEM 365 382
 CC CYTOPLASMIC 387 397
 CC TRANSMEM 398 420
 CC DOMAIN 421 442
 CC TRANSMEM 443 464
 CC DOMAIN 465 484
 CC TRANSMEM 485 507
 CC DOMAIN 508 527
 CC TRANSMEM 528 549
 CC DOMAIN 550 572
 CC TRANSMEM 573 596
 CC DOMAIN 597 607
 CC TRANSMEM 608 629
 CC DOMAIN 630 692
 CC TRANSMEM 631 692
 CC REPEAT 119 143
 CC REPEAT 170 192
 CC REPEAT 193 216
 CC REPEAT 218 240
 CC DISULFID 441 516
 CC CARBOHYD. 191 191 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC CARBOHYD. 199 199 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC CARBOHYD. 293 293 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC CONFLICT 436 436 O -> K (IN REF. 2).
 CC SEQUENCE 692 AA: 77769 MW: 485729180563A44 CRC64;
 Query Match 95.28; Score 3420; DB 1; Length 692;
 Best Local Similarity 94.28; Pred. No. 2.6e-211;
 Matches 632; Conservative 21; Mismatches 19; Indels 0; Gaps 0;
 Db 1 MALLVSLAFLGTCGCHWVLCNCHSVFLVLCDSKVTETPTDLPRLNATLRLPVVTKLVY 60
 1 MALLVSLAFLGTCGCHWVLCNCHSVFLVLCDSKVTETPTDLPRLNATLRLPVVTKLVY 60
 Oy 61 IPKGSFGCDLKEIISNDVLEADVPSNLPKLEIRIEKANNLLINPEAFONLP 120
 61 IPKGSFGCDLKEIISNDVLEADVPSNLPKLEIRIEKANNLLINPEAFONLP 120
 Db 61 IPKGSFGCDLKEIISNDVLEADVPSNLPKLEIRIEKANNLLINPEAFONLP 120
 61 IPKGSFGCDLKEIISNDVLEADVPSNLPKLEIRIEKANNLLINPEAFONLP 120
 Oy 121 SLRYLLISNTGKHLPAVKIQSLQVLLDQDINIHIVARNSPMGLSFESVILMKN 180

Db 121 SLRYLLISNTGKHLPAVKIQSLQVLLDQDINIHIVARNSPMGLSFESVILMKN 180
 Oy 181 GIEEIHNCANCTQDELAMSDNNNLRELNDVFOGASGPNVLDISRTKVSILPNGLN 240
 181 GIEEIHNCANCTQDELAMSDNNNLRELNDVFOGASGPNVLDISRTKVSILPNGLN 240
 Db 181 GIOEIHNCANCTQDELAMSDNNNLRELNDVFOGASGPNVLDISRTKVSILPNGLN 240
 181 GIOEIHNCANCTQDELAMSDNNNLRELNDVFOGASGPNVLDISRTKVSILPNGLN 240
 Oy 241 LKLRARSTYRLKLPDLKFTVLPFASLTYPHSHCCAFANLKRQISELHPICNKSILROD 300
 241 LKLRARSTYRLKLPDLKFTVLPFASLTYPHSHCCAFANLKRQISELHPICNKSILROD 300
 Db 241 LKLRARSTYRLKLPDLKFTVLPFASLTYPHSHCCAFANLKRQISELHPICNKSILROD 300
 241 LKLRARSTYRLKLPDLKFTVLPFASLTYPHSHCCAFANLKRQISELHPICNKSILROD 300
 Oy 301 IDDMTOIGDQSVLIDDEPSYSGKSGDMYNEFDYDLCNEVDYVTCSPKPDANPCEDIMG 360
 301 IDDMTOIGDQSVLIDDEPSYSGKSGDMYNEFDYDLCNEVDYVTCSPKPDANPCEDIMG 360
 Db 301 IDDMTOIGDQSVLIDDEPSYSGKSGDMYNEFDYDLCNEVDYVTCSPKPDANPCEDIMG 360
 301 IDDMTOIGDQSVLIDDEPSYSGKSGDMYNEFDYDLCNEVDYVTCSPKPDANPCEDIMG 360
 Oy 361 YNLRVLNFIISILAITGNTTVLVLTTSQYKLTVPFLMCLNLAFAADLCIGIYLLLIJASV 420
 361 YNLRVLNFIISILAITGNTTVLVLTTSQYKLTVPFLMCLNLAFAADLCIGIYLLLIJASV 420
 Db 361 YNLRVLNFIISILAITGNTTVLVLTTSQYKLTVPFLMCLNLAFAADLCIGIYLLLIJASV 420
 361 YNLRVLNFIISILAITGNTTVLVLTTSQYKLTVPFLMCLNLAFAADLCIGIYLLLIJASV 420
 Oy 421 DIHTSOHYNAIDMOTGAGCDAGFFTFVASELSVYTLTATLERHWHITTHAMQLECKV 480
 421 DIHTSOHYNAIDMOTGAGCDAGFFTFVASELSVYTLTATLERHWHITTHAMQLECKV 480
 Db 421 DIHTSOHYNAIDMOTGAGCDAGFFTFVASELSVYTLTATLERHWHITTHAMQLECKV 480
 421 DIHTSOHYNAIDMOTGAGCDAGFFTFVASELSVYTLTATLERHWHITTHAMQLECKV 480
 Oy 481 QLRHAASVVLGCMTPFAAALPPIFGISYMKVSYCLPMDIDSPISLYVALLVNLVLA 540
 481 QLRHAASVVLGCMTPFAAALPPIFGISYMKVSYCLPMDIDSPISLYVALLVNLVLA 540
 Db 481 QLRHAASVVLGCMTPFAAALPPIFGISYMKVSYCLPMDIDSPISLYVALLVNLVLA 540
 481 QLRHAASVVLGCMTPFAAALPPIFGISYMKVSYCLPMDIDSPISLYVALLVNLVLA 540
 Oy 541 FVYICGCVTHIYLVTRNPTVYSSSDTKIARMMATLIFTDFLCMAPISFFAISASLKVPL 600
 541 FVYICGCVTHIYLVTRNPTVYSSSDTKIARMMATLIFTDFLCMAPISFFAISASLKVPL 600
 Db 541 FVYICGCVTHIYLVTRNPTVYSSSDTKIARMMATLIFTDFLCMAPISFFAISASLKVPL 600
 541 FVYICGCVTHIYLVTRNPTVYSSSDTKIARMMATLIFTDFLCMAPISFFAISASLKVPL 600
 Oy 601 ITYSKAKILLVLFYPIINSCANPFIYAIPTKFNFRDFPILLSKPCYEQMAQIYRTETSSA 660
 601 ITYSKAKILLVLFYPIINSCANPFIYAIPTKFNFRDFPILLSKPCYEQMAQIYRTETSSA 660
 Db 601 ITYSKAKILLVLFYPIINSCANPFIYAIPTKFNFRDFPILLSKPCYEQMAQIYRTETSSA 660
 601 ITYSKAKILLVLFYPIINSCANPFIYAIPTKFNFRDFPILLSKPCYEQMAQIYRTETSSA 660
 Oy 661 TNHFSRKNPCSSAPRVTVSYVLPNLSQVN 692
 661 TNHFSRKNPCSSAPRVTVSYVLPNLSQVN 692
 Db 661 TNHFSRKNPCSSAPRVTVSYVLPNLSQVN 692
 661 TNHFSRKNPCSSAPRVTVSYVLPNLSQVN 692
 RESULT 3
 FSHR_HUMAN
 ID FSHR_HUMAN STANDARD: PRT: 695 AA.
 AC P23945;
 DT 01-MAR-1992 (Rel. 21, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Follicle stimulating hormone receptor precursor (FSH-R) (Poultropin
 DE receptor).
 GN FSHR.
 OS Homo sapiens (Human).
 OC Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutaria; Primates; Catarrhini; Hominoidea; Homo.
 OC NCBI_TaxID=9606;
 OX 11
 RN SEQUENCE FROM N.A.
 RP TISSUE-Ovary;
 RC MEDLINE=9122171; PubMed=1709010;
 RA Minegishi T., Nakamura K., Takakura Y., Ibuki Y., Igarashi M.;
 RT "Cloning and sequencing of human FSH receptor cDNA";
 RL Biochem. Biophys. Res. Commun. 175:1125-1130(1991).
 RP SEQUENCE FROM N.A.
 RC TISSUE=Testis;
 RA MEDLINE=93246012; PubMed=1301382;
 RA Melton C.A., Cheng S.Y., Nugent N.P., Schweichhardt R.L.,
 RA Chappel S.C., Overton S.A., Wands G.D., Kuzaja J.B., Luchette C.A.,
 RA "The cloning of the human follicle stimulating hormone receptor and
 RT its expression in COS-7, CHO, and Y-1 cells";
 RL Mol. Cell. Endocrinol. 89:141-151(1992).
 RP SEQUENCE FROM N.A.
 RP

RA Tilly L.T., Alhara T., Nishimori K., Jai X.-C., Billig H.,
 RA Kowalski K.I., Perlas E.A., Hsueh A.J.;
 RL Submitted (xxx-1992) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE OF 1-342 FROM N.A.
 RC TISSUE-Testis;
 RX MEDLINE-93075197; PubMed-1359889;
 RA Gromoll J., Gudermann T., Nieschlag E.;
 RT "Molecular cloning of a truncated isoform of the human follicle
 stimulating hormone receptor.";
 RL Biochem. Biophys. Res. Commun. 188:1077-1083(1992).
 RN [5]
 RP SEQUENCE OF 1-51 FROM N.A.
 RX MEDLINE-95011044; PubMed-7926278;
 RA Gromoll J., Dankbar B., Gudermann T.;
 RT "Characterization of the 5' flanking region of the human follicle-
 stimulating hormone receptor gene.";
 RL Mol. Cell. Endocrinol. 102:93-102(1994).
 RN [6]
 RP 3D-STRUCTURE MODELING OF 49-228.
 RX MEDLINE-96363672; PubMed-8747461;
 RA Jiang X., Dreano M., Buckler D.R., Cheng S., Ythier A., Wu H.,
 RA Hendrickson W.A., el Tayar N.;
 RT "Structural predictions for the ligand-binding region of glycoprotein
 hormone receptors and the nature of hormone-receptor interactions.";
 RL Structure 3:1341-1353(1995).
 CC -1- FUNCTION: RECEPTOR FOR FOLLICLE STIMULATING HORMONE. THE ACTIVITY
 OF THIS RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE
 ADENYLATE CYCLASE.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM (SHOWN HERE) AND A
 SHORT FORM; ARE PRODUCED BY ALTERNATIVE SPLICING.
 CC -1- TISSUE SPECIFICITY: SERTOLI CELLS AND OVARIAN GRANULOSA CELLS.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 CC FSH/LSH/TSH SUBFAMILY.
 CC -1- SIMILARITY: CONTAINS 5 LEUCINE-RICH REPEATS (LRR).
 CC -----
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 or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; M65085; AAA52477.1; -;
 DR EMBL; S59900; AAB26480.1; -;
 DR EMBL; M95489; AAA52478.1; -;
 DR EMBL; X68044; CAA48179.1; -;
 DR EMBL; S73199; AAB32071.1; -;
 DR PIR; JN0122; JN0122.
 DR PDB; 1XUN; 15-MAY-97.
 DR Genew; HGNC:3969; FSHR.
 DR MIM; 136435; -;
 DR InterPro; IPR000276; GPCR_Rhodopsn.
 DR InterPro; IPR001611; LRR.
 DR InterPro; IPR000372; LRR_Nterm.
 DR Pfam; PF00001; 7tm_1; 1.
 DR Pfam; PF00560; LRR; 3.
 DR Pfam; PF01462; LRRNT; 1.
 DR SMART; SM00013; LRRNT; 1.
 DR PROSITE; PS00237; G-PROTEIN_RECP_F1_1; 1.
 DR PROSITE; PS00262; G-PROTEIN_RECP_F1_2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein; Signal;
 KW phosphorylation; Repeat; Leucine-rich repeat; Alternative splicing;
 KW 3D-structure.
 FT SIGNAL 1 17 POTENTIAL.
 FT CHAIN 18 695 FOLLICLE STIMULATING HORMONE RECEPTOR.
 FT DOMAIN 18 366 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 367 387 1 (POTENTIAL).
 FT DOMAIN 388 398 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 399 421 2 (POTENTIAL).
 FT DOMAIN 422 443 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 444 465 3 (POTENTIAL).
 FT DOMAIN 466 485 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 486 508 4 (POTENTIAL).
 FT DOMAIN 509 528 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 529 550 5 (POTENTIAL).
 FT DOMAIN 551 573 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 574 597 6 (POTENTIAL).
 FT DOMAIN 598 608 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 609 630 7 (POTENTIAL).
 FT DOMAIN 631 695 CYTOPLASMIC (POTENTIAL).
 FT REPEAT 69 93 LRR 1.
 FT REPEAT 119 143 LRR 2.
 FT REPEAT 170 192 LRR 3.
 FT REPEAT 193 216 LRR 4.
 FT REPEAT 218 240 LRR 5.
 FT DISULFID 442 517 BY SIMILARITY.
 FT CARBOHYD 191 191 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 199 199 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 293 293 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 318 318 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT VARSPLIC 224 285 MISSING (IN SHORT ISOFORM).
 FT VARSPLIC 342 695 MISSING (IN SHORT ISOFORM).
 FT CONFLICT 13 13 S -> R (IN REF. 4).
 FT CONFLICT 112 112 N -> T (IN REF. 1).
 FT CONFLICT 197 198 EL -> AV (IN REF. 1).
 FT CONFLICT 295 295 S -> P (IN REF. 4).
 FT CONFLICT 307 307 T -> A (IN REF. 1).
 FT CONFLICT 680 680 N -> S (IN REF. 1).
 SQ SEQUENCE 695 AA; 78294 MM; 723B8E71F76D2CD5 CRC64;
 Query Match 90.0%; Score 3235.5; DB 1; Length 695;
 Best Local Similarity 89.5%; Pred. No. 1.6e-199;
 Matches 622; Conservative 31; Mismatches 39; Indels 3; Caps 2;
 QY 1 MALLVSLLAFLGTGSGCHHMLCHCSNRVFLCQDSKVTETPTDLPNAIELREVLKRV 60
 DB 1 MALLVSLLAFLSLGSGCHHMLCHCSNRVFLCQESKVTETPTDLPNAIELREVLKRV 60
 QY 61 IPKGFAGDGLKLEKIEISQNDVLEADVFSNLPKLHEIRIEKANNLLYINPEAFONLP 120
 DB 61 IQKGFAGDGLKLEKIEISQNDVLEADVFSNLPKLHEIRIEKANNLLYINPEAFONLP 120
 QY 121 SLRYLLISNTGKHLPAVHKIOSLOKVLIDIODNINIHIVARNISFVGLSFESVILWLN 180
 DB 121 NQYLLISNTGKHLPAVHKIOSLOKVLIDIODNINIHIVARNISFVGLSFESVILWLN 180
 QY 181 GIEETHNCAFNGTQDDELNLSDNNLEELPNDVFOGASGPVILDSRTKVHSLPHNGLEN 240
 DB 181 GIQETHNCAFNGTQDDELNLSDNNLEELPNDVFOGASGPVILDSRTKVHSLPHNGLEN 240
 QY 241 LKKLRARSTYRLKLPNLDKFTVLMASLTYSHCACAFANLKRQISELHPICKNSILROD 300
 DB 241 LKKLRARSTYRLKLPNLDKFTVLMASLTYSHCACAFANLKRQISELHPICKNSILROE 300
 QY 301 IDDMTOIGDQVSLIDD-EPYSGKSGDMVNEFDYDLCNEVDVTCSPKPDAPNCPEDIM 359
 DB 301 VDYMTQTRGORSLSAEDNESSYRGDMYTFEDYDLCNEVDVTCSPKPDAPNCPEDIM 360
 QY 360 GYNILRLVWFISILAITGNTTVLVVLTTSQYKLTVPFLMCLNLAFCICIGIYLLIAS 419
 DB 361 GYNILRLVWFISILAITGNTTVLVVLTTSQYKLTVPFLMCLNLAFCICIGIYLLIAS 420
 QY 420 VDIHTKSOYHNVAIDMQTAGCDAAGFTTFVASELSVYVLTALTLEWHWTHITAMOLECK 479
 DB 421 VDIHTKSOYHNVAIDMQTAGCDAAGFTTFVASELSVYVLTALTLEWHWTHITAMOLECK 480
 QY 480 VOLRHAASVYVLTGTFEFAAALFFIFGSISSYKNSVSLCPLMDIDSPISQVYVALLVNL 539
 DB 481 VOLRHAASVYVLTGTFEFAAALFFIFGSISSYKNSVSLCPLMDIDSPISQVYVALLVNL 540
 QY 540 AFVVICGCTHYIYLVTRNPTIVSSSDTKIARMTATLITDFLCMAPISFFAISASIKVP 599
 DB 541 AFVVICGCTHYIYLVTRNPTIVSSSDTKIARMTATLITDFLCMAPISFFAISASIKVP 600

FT	DOMAIN	466	485	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	486	508	4 (POTENTIAL).
FT	DOMAIN	509	528	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	529	550	5 (POTENTIAL).
FT	DOMAIN	551	573	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	574	597	6 (POTENTIAL).
FT	DOMAIN	598	608	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	609	630	7 (POTENTIAL).
FT	DOMAIN	631	695	CYTOPLASMIC (POTENTIAL).
FT	REPEAT	44	68	LRR 1.
FT	REPEAT	69	93	LRR 2.
FT	REPEAT	170	193	LRR 3.
FT	REPEAT	194	216	LRR 4.
FT	REPEAT	219	236	LRR 5.
FT	REPEAT	242	264	LRR 6.
FT	REPEAT	268	290	LRR 7.
FT	DISULFID	442	517	BY SIMILARITY
FT	CARBOHYD	191	191	N-LINKED (GLCNAC. -) (POTENTIAL).
FT	CARBOHYD	199	199	N-LINKED (GLCNAC. -) (POTENTIAL).
FT	CARBOHYD	293	293	N-LINKED (GLCNAC. -) (POTENTIAL).
FT	CARBOHYD	318	318	N-LINKED (GLCNAC. -) (POTENTIAL).
FT	SEQUENCE	695 AA:	78343 MW:	0D60A233729B520 CRC64;
FT	SEQ			
Query Match				
Best Local Similarity 89.8%; Score 3226.5; DB 1; Length 695;				
Matches 621; Conservative 30; Mismatches 41; Indels 3; Gaps 2;				
QY	1	NALLVLSLLALFGTSCCHWIKCHCSNRYFLODSCSKYETFPDLPNAILERYVTKLRY	60	
DB	1	NALLVLSLLALFSGSCHIRCHCSNRYFLOQSKYETFPDLPNAILERYVTKLRY	60	
QY	61	IPKSGPAGFGDEKLEIISONDVLEVTEADVPSNLKPLHRIETKANNLLYINPEAFONLP	120	
DB	61	IOKAPSGFGDEKLEIISONDVLEVTEADVPSNLKPLHRIETKANNLLYINPEAFONLP	120	
QY	121	SLRYLLISNTGKIHPAVHKIOSQKVLVDIDIONINIHIVARNSPFGLSFESVILMSKN	180	
DB	121	NURYLLISNTGKIHPOVHKIHSQKVLVDIDIONINIHRIETSPFGLSFESVILMSKN	180	
QY	181	GTEIHNCAFNQTQDELMLSDNNLEELPNDFVPGASGVVTLIDISRTKVSHPNUGLEN	240	
DB	181	GIQIHNCAFNQTQDELMLSDNNLEELPNDFVPGASGVVTLIDISRTKVSHPNUGLEN	240	
QY	241	LKILBARSTYKLPNLDKPVYLMASVYPSHCSCAPANKKROISLPIHYNCSILROD	300	
DB	241	LKILBARSTYKLPNLDKPVYLMASVYPSHCSCAPANKKROISLPIHYNCSILROD	300	
QY	301	IDDMTOIGDQRVSLDD- PPSYGGSDMMYNPEFDYDLCEVVDVYTCSPKPAFNPCEIM	359	
DB	301	VDDMTQGRSSLAEDNESSYSGFDMTYAEFDYDLCEVVDVYTCSPKPAFNPCEIM	360	
QY	360	GYNLRVLRNFIISALITGNTVYLVLTISQYKLVPRFLNCIAFADICIGYLLIAS	419	
DB	361	GYNLRVLRNFIISALITGNTVYLVLTISQYKLVPRFLNCIAFADICIGYLLIAS	420	
QY	420	VLIHTSQYHNAYIDMTQAGCDAGFTVPSLSVYTLTATLERHHTTHANQLECK	479	
DB	421	VLIHTSQYHNAYIDMTQAGCDAGFTVPSLSVYTLTATLERHHTTHANQLECK	480	
QY	480	VOLKHAASVWYVLCMTFAFAALPFGTISSTYKVSICLPMDIDPSOLYVMALLVNLV	539	
DB	481	VHVRHAASVWYVCMGTFAFAALPFGTISSTYKVSICLPMDIDPSOLYVNSLVNLV	540	
QY	540	APVYICGCTHYILVTRNPTVTVSSSDTKIAKRMATLFTDFLCNAPISFFAISLAKVP	599	
DB	541	APVYICGCTHYILVTRNPTVTVSSSDTKIAKRMATLFTDFLCNAPISFFAISLAKVP	600	
QY	600	LTVYSKAKILLVLPFTPINSANPPLAYPTNTRPDRPFTLLLSKGCYEMQOYIRFTSS	659	
DB	601	LTVYSKAKILLVLPFTPINSANPPLAYPTNTRPDRPFTLLLSKGCYEMQOYIRFTSS	660	
QY	660	ATHNFAKSCSSCAPRVTH--SYVLVPLNHSOON	692	
DB	661	TANHSNPRNGSCSAHRYTVNGSIIYVLPVLSHAON	695	

RESULT 5
FSHR_BOVIN STANDARD; PRT; 695 AA.

AC P35376; 695 AA.

DT 01-JUN-1994 (Rel. 29, Created)

DT 01-JUN-1994 (Rel. 29, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Follicle stimulating hormone receptor precursor (FSH-R) (Follitropin receptor).

DE FSHR.

GN Bos taurus (Bovine).

OS Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.

OC NCBI_TaxID=9913;

OX [1]

RN SEQUENCE FROM N.A.

RP STRAIN-Holstein; TISSUE-Ovary, and Testis;

RC MEDLINE=95127199; PubMed=7826612;

RX Houde A., Lambert A., Saumande J., Silversides D.W., Lussier J.G.;

RA "Structure of the bovine follicle-stimulating hormone receptor complementary DNA and expression in bovine tissues";

RT Mol. Reprod. Dev. 39:127-135(1994).

RL -1- FUNCTION: RECEPTOR FOR FOLLICLE STIMULATING HORMONE. THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE ADENYLATE CYCLASE.

CC -1- SUBCELLULAR LOCATION: Integral membrane protein.

CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS. FSH/LSH/TSH SUBFAMILY.

CC -1- SIMILARITY: CONTAINS 6 LEUCINE-RICH REPEATS (LRR).

CC -----

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CC -----

CC EMBL: L23219; AAC37324.1; --

DR HSP; P33945; 1XUN.

DR InterPro: IPR000276; GPCR_Rhodopsin.

DR InterPro: IPR001611; LRR.

DR InterPro: IPR003372; LRR_Nterm.

DR Pfam: PF00001; 7tm_1; 1.

DR Pfam: PF00560; LRR; 4.

DR Pfam: PF01462; LRRNT; 1.

DR SMART: SM00013; LRRNT; 1.

DR PROSITE; PS00237; G-PROTEIN_RECPT_F1_1; 1.

DR PROSITE; PS0262; G-PROTEIN_RECPT_F1_2; 1.

DR G-protein coupled receptor; Transmembrane; Glycoprotein; Signal; Phosphorylation; Repeat; Leucine-rich repeat.

KW SIGNAL

FT CHAIN 1

FT 18 695 FOLLICLE STIMULATING HORMONE RECEPTOR.

FT DOMAIN 18 366 EXTRACELLULAR (POTENTIAL).

FT TRANSSEM 367 387 1 (POTENTIAL).

FT DOMAIN 388 398 CYTOPLASMIC (POTENTIAL).

FT TRANSSEM 399 421 2 (POTENTIAL).

FT DOMAIN 422 443 EXTRACELLULAR (POTENTIAL).

FT TRANSSEM 444 465 3 (POTENTIAL).

FT DOMAIN 466 485 CYTOPLASMIC (POTENTIAL).

FT TRANSSEM 486 508 4 (POTENTIAL).

FT DOMAIN 509 528 EXTRACELLULAR (POTENTIAL).

FT TRANSSEM 529 550 5 (POTENTIAL).

FT DOMAIN 551 573 CYTOPLASMIC (POTENTIAL).

FT TRANSSEM 574 597 6 (POTENTIAL).

FT DOMAIN 598 608 EXTRACELLULAR (POTENTIAL).

FT TRANSSEM 609 630 7 (POTENTIAL).

FT DOMAIN 631 695 CYTOPLASMIC (POTENTIAL).

FT REPEAT 44 68 LRR 1.

FT REPEAT 69 LRR 2.

FT REPEAT 119 143 LRR 3.

FT REPEAT 170 192 LRR 4.

FT REPEAT 193 216 LRR 5.

FT REPEAT 218 240 LRR 6.

FT DISULFID 442 517 BY SIMILARITY.

FT CARBOHYD 191 191 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 199 199 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 293 293 N-LINKED (GLCNAC. . .) (POTENTIAL).

SO SEQUENCE 695 AA; 78084 MW; 18F9DFEFC046380D CRC64;

Query Match 89.3%; Score 3208.5; DB 1; Length 695;

Best Local Similarity 87.8%; Pred. No. 8.5e-198;

Matches 610; Conservative 46; Mismatches 36; Indels 3; Gaps 2;

QY 1 MALLVSLAFLGTGSGCHHMLCHCSNRVFLCDSKVTEIPTDLPRNAIELRVLTCLR 60

DB 1 MALLVALLAFLSLGSGCHHRLCHCSNGVFLCQESKVTETPSDLPDAVELRFLVTLR 60

QY 61 IPKSGFAGGDLKIEIISONDVLEIVADVFSNLPKLHEIRIEKANNLLINPEAFONLP 120

DB 61 IPKAGFSGGDLKIEIISONDVLEIVADVFSNLPKLHEIRIEKANNLLIDPDAFONLP 120

QY 121 SLRYLLISNTGIKHLPVAVHKIQSLQKVLIDQININIHIVARNFMSGLSPESVTWLSKN 180

DB 121 NLRYLLISNTGIKHLPVAVHKIQSLQKVLIDQININIHIVARNFMSGLSPESVTWLSKN 180

QY 181 GIEEINCAFNQGLDELNLSDNNLEELPNDVFOGASGPVILDISRTKVSHPNHLGN 240

DB 181 GIOEIHNCAPNGTQDLDELNLSDNLEELPNDVFOGASGPVILDISRTKVSHPNHLGN 240

QY 241 LKLRARSYRKLPNLDKFTVLMASLTYPSCAFANLKRQISLHPICNKSILRQD 300

DB 241 LKLRARSYRKLPNLDKFTVLMASLTYPSCAFANLKRQISLHPICNKSILRQD 300

QY 301 IDDMTQIGQORVSLI--DDEPSYKGDMMYNEFDYDLNEVDVTCSPKDAFNPCEDIM 359

DB 301 VDDMTQARGORVSLAEDEDEPSYKGDMMYNEFDYDLNEVDVTCSPKDAFNPCEDIM 359

QY 360 GYNILRVLWFTSILAITGNTTVLVLTTSQYKLVTPRFLMCLNLAFLADLCIGYLLIAS 419

DB 361 GDDILRVLWFTSILAITGNTTVLVLTTSQYKLVTPRFLMCLNLAFLADLCIGYLLIAS 420

QY 420 VDIHTKSOYHNVAIDMQTGACDAAGFTVFASLSVYTLTALTLEWHITTHAMOLECK 479

DB 421 VDVHTKTEYHNVAIDMQTGACDAAGFTVFASLSVYTLTALTLEWHITTHAMOLECK 480

QY 480 VQLRHAASVYVLGWTFAFAAALFPFIFGSISSYMKVSIKLPMDIDSPISQLYVMSLLVNL 539

DB 481 VQLRHAASVYVLGWTFAFAAALFPFIFGSISSYMKVSIKLPMDIDSPISQLYVMSLLVNL 540

QY 540 AFVVICGCTHYLTVRNPTIVSSSDTKIAKRMATLIETDFLCMAPISFALSKVP 599

DB 541 AFVVICGCTHYLTVRNPTIVSSSDTKIAKRMATLIETDFLCMAPISFALSKVP 600

QY 600 LITVSKAKILLVLYFPINSCANPFLVAIETKPRRDFILLSKFCGYEQAOIYRSTSS 659

DB 601 LITVSKAKILLVLYFPINSCANPFLVAIETKPRRDFILLSKFCGYEQAOIYRSTSS 660

QY 660 ATHNPHARKSHCSSAPRVTN--SYVLVPLNHSQSN 692

DB 661 TAHPNPHRNGCHPPAPRVTVNGSNYTLIPLRLAKN 695

RESULT 6

FSHR_SHEEP

ID FSHR_SHEEP STANDARD; PRT; 695 AA.

AC P35379; Q28573; Q28574; Q9TSI9;

DT 01-JUN-1994 (Rel. 29, Created)

DT 01-JUN-1994 (Rel. 29, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Follicle stimulating hormone receptor precursor (FSH-R) (Follitropin receptor).

GN FSHR.

OS Ovis aries (Sheep).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 CC Bovidae; Caprinae; Ovis.
 CC NCBI_TaxID=9940;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM FSH-R1).
 RP TISSUE=Testis;
 RC MEDLINE=93351750; PubMed=9394255;
 RA Farney T.A., Sairam M.R., Khan H., Ravindranath N., Payne S.,
 RA Seiden N.G.;
 RT Molecular cloning and expression of the ovine testicular follicle
 RT stimulating hormone receptor.;
 RL [1]. Cell. Endocrinol. 9:219-226(1993).
 RP SEQUENCE FROM N.A. (ISOFORMS FSH-R4 AND FSH-R3).
 RC STRAIN=Dorset-Leicester-Suffolk 1; TISSUE=Testis;
 RA MEDLINE=93176195; PubMed=8439338;
 RA Khan H., Farney T.A., Sairam M.R.;
 RT "Cloning of alternatively spliced mRNA transcripts coding for variants
 RT of ovine testicular follicleotropin receptor lacking the G protein
 RT coupling domains.";
 RL Biochem. Biophys. Res. Commun. 190:888-894(1993).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORM FSH-R2), AND CHARACTERIZATION.
 RC STRAIN=Dorset-Leicester-Suffolk 1; TISSUE=Testis;
 RA MEDLINE=98031015; PubMed=9364440;
 RA Farney T.A., Jiang L., Khan H., MacDonald E.A., Laird D.W.,
 RA Sairam M.R.;
 RT Molecular cloning, structure, and expression of a testicular
 RT follicleotropin receptor with selective alteration in the carboxy terminus
 RT that affects signaling.;
 RL Mol. Reprod. Dev. 48:458-470(1997).
 RN [4]
 RP SEQUENCE FROM N.A. (ISOFORM FSH-R3), AND CHARACTERIZATION.
 RC STRAIN=Dorset-Leicester-Suffolk 1; TISSUE=Ovary;
 RA MEDLINE=20391225; PubMed=10527886;
 RA Babu P.S., Jiang L., Sairam M.R., Touyz R.M., Sairam M.R.;
 RT "Structural features and expression of an alternatively spliced growth
 RT factor type I receptor for follicleotropin signaling in the developing
 RT ovary.";
 RL Mol. Cell Biol. Res. Commun. 2:21-27(1999).
 RN [5]
 RP SEQUENCE OF 1-51 FROM N.A.
 RA MEDLINE=98031017; PubMed=9364442;
 RA Sairam M.R., Subbarayan V.S.R.;
 RT Characterization of the ovine follicleotropin receptor gene.;
 RL Mol. Reprod. Dev. 48:480-487(1997).
 CC -1- FUNCTION: Receptor for follicle stimulating hormone. The activity
 CC of Isoform FSH-R1 is mediated by G proteins which activate
 CC adenylyl cyclase. Isoforms FSH-R2 and FSH-R3 also bind FSH, but
 CC this does not result in activation of adenylyl cyclase. Isoform
 CC FSH-R3 may be involved in calcium signaling.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Plasma membrane
 CC (isoforms FSH-R1 and FSH-R2); Cell surface (isoform FSH-R3).
 CC -1- TISSUE SPECIFICITY: 4 isoforms; FSH-R1 (shown here), FSH-R2,
 CC FSH-R3 and FSH-R4; are produced by alternative splicing.
 CC -1- FSH-R1 is expressed in ovary and
 CC FSH-R2 but not in kidney.
 CC -1- SIMILARITY: ISOFORM FSH-R3 IS EXPRESSED IN OVARY AND
 CC FSH-R4/FSH-R3 SUPERFAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 CC -1- SIMILARITY: CONTAINS 6 LEUCINE-RICH REPEATS (LRR).
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 CC or send an email to license@isb-sib.ch).
 CC EMBL; L07302; AAA31523.1;

DR EMBL; L12766; AAA31523.1; -
 DR EMBL; L12766; AAA31523.1; -
 DR EMBL; L36115; AAA31523.1; -
 DR EMBL; A3131735; CAA10495.1; -
 DR EMBL; AF050438; AAC61749.1; -
 DR PIR; JCI493; JCI493;
 DR HSSP; P23945; 1XUN;
 DR InterPro: IPR000276; GPCR_Rhodopsin.
 DR InterPro: IPR001611; LRR.
 DR InterPro: IPR003172; LRR_Nterm.
 DR Pfam; PF00001; 7tm_1; 1.
 DR Pfam; PF00560; LRR; 4.
 DR Pfam; PF01462; LRRNT; 1.
 DR SMART; SMO0013; LRRNT; 1.
 DR PROSITE; PS00237; G-PROTEIN_RECEP_FL_1; 1.
 DR PROSITE; PS02622; G-PROTEIN_RECEP_FL_2; 1.
 DR G-protein coupled receptor; Transmembrane; Glycoprotein; Signal;
 DR 9-protein family; Receptor; Leucine-rich repeat; Alternative splicing.
 DR SIGNAL 1 695
 FT CHAIN 18 695
 FT DOMAIN 18 366
 FT TRANSMEM 367 387
 FT DOMAIN 388 398
 FT TRANSMEM 399 421
 FT DOMAIN 422 443
 FT TRANSMEM 444 465
 FT DOMAIN 466 485
 FT TRANSMEM 486 508
 FT DOMAIN 509 528
 FT TRANSMEM 529 550
 FT DOMAIN 551 573
 FT TRANSMEM 574 597
 FT DOMAIN 598 608
 FT TRANSMEM 609 630
 FT DOMAIN 631 658
 FT REPEAT 659 68
 FT REPEAT 69 93
 FT REPEAT 119 143
 FT REPEAT 170 192
 FT REPEAT 193 216
 FT REPEAT 218 240
 FT REPEAT 242 517
 FT DISULFID 442 517
 FT CARBOHYD 191 191
 FT CARBOHYD 199 199
 FT CARBOHYD 293 293
 FT VARSPLIC 126 133
 FT VARSPLIC 135 695
 FT VARSPLIC 224 239
 FT VARSPLIC 260 695
 FT VARSPLIC 643 670
 FT VARSPLIC 671 695
 SQ SEQUENCE 695 AA; 78237 MW; 75089D8C0D4B CRC64;
 Query Match 89.04; Score 3199.5; DB 1; Length 695;
 Best Local Similarity 87.24; Pred. No. 3.2e-197;
 Matches 606; Conservative 48; Mismatches 38; Indels 3; Gaps 2;
 Oy 1 MALLVSLAPLGTGSCCHMCHCSNRVLCDSKVTEIPDLPNATELRFVLKRV 60
 Db 1 WALFLVALLFSLGSCCHHCHCSNGVFLCDSKVTEIPDLPNATELRFVLKRV 60
 Oy 61 TPKGSPAGDLEKLEISONDVLEVDVPSNPKLHEIRKANNLLYNPEATQNP 120
 Db 61 IPGAFSGCDLEKLEISONDVLEVDVPSNPKLHEIRKANNLLYDPAQNP 120
 Oy 121 SURVLLISMTGKHLPAVHKIQSLQKVLDDQDNINHIYVARNFQSLFVILWSKN 180
 Db 121 NLRVLLISMTGKHLPAVHKIQSLQKVLDDQDNINHIYVARNFQSLFVILWSKN 180

181 GIEETHNCAFNCTQDELNLSDNNLEELPNDVFGASGPVILDISRTKRVSHPNHGLE 240
181 GIOEIHNCANFGTQDELNLSDNNLEELPNDVFGASGPVILDISRTKRVSHPNHGLE 240
241 LKKLRARSYRLKLPNDKFTVLMASITPSYSHCCAFANLKRQISELHPICNKSILROD 300
241 LKKLRARSYRLKLPNDKFTVLMASITPSYSHCCAFANLKRQISELHPICNKSILROD 300
301 IDDMTOIGQORVSLI--DDPSYSGKSGDMYNEFDYDLNCEWVDVTCSPKPDAPNCCEDIM 359
301 VDMTOGQORISLAEDDEPSYAKGDMYSEFDYDLNCEWVDVTCSPKPDAPNCCEDIM 360
360 GYNILRVLIWFISILAITGNTVVLVLTTSQYKLVTPRELMCNLAFADLCIGIYLLLIAS 419
361 GVDILRVLIWFISILAITGNTVVLVLTTSQYKLVTPRELMCNLAFADLCIGIYLLLIAS 420
420 VDIHTKSOYHNAIDQWOTGAGDAAGFFVTFASELSVYVLTALTLEWHITTHAMOLECK 479
421 VDVHTKSOYHNAIDQWOTGAGDAAGFFVTFASELSVYVLTALTLEWHITTHAMOLECK 480
480 VOLRHAASVWLVGWTFAFAALFFPIGSISSKVSICLPMIDSPLSQVLYVWALLVNLV 539
481 VVHRHAASVWLVGWTFAFAALFFPIGSISSKVSICLPMIDSPLSQVLYVWALLVNLV 540
540 AFVWIGCGYTHIYLVNRPNTIVSSSDTKIAKRMATLIETDFLCMAPISEFFAISASLKVP 599
541 AFVWIGCGYTHIYLVNRPNTIVSSSDTKIAKRMATLIETDFLCMAPISEFFAISASLKVP 600
600 LITVSKAKILLVLYPINSANPFLYAIETKFRDRFFILLSKFGCYEHOAQIYRSETSS 659
601 LITVSKAKILLVLYPINSANPFLYAIETKFRDRFFILLSKFGCYEHOAQIYRSETSS 660
660 ATHNPARKSHCSSAPRVN--SYVLVPLNHSSON 692
661 TAHPNPRNGHCHPPAPRVNNGSYVLVPLNHSSON 695

RESULT 7

FSHR_PIG STANDARD; PRT; 695 AA.
AC P49059; 077514;
DT 01-FEB-1996 (Rel. 33, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Follicle stimulating hormone receptor precursor (FSH-R) (Follitropin receptor).
GN FSHR.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Ovary;
RX MEDLINE=96011644; PubMed=7590277;
RA Remy J.J., Lahbib-Mansais Y., Verle M., Bozon V., Couture L., Pajot E., Grebert D., Salesse R.;
RT "The porcine follitropin receptor: cDNA cloning, functional expression and chromosomal localization of the gene.";
RL Gene 163:257-261(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Ovary;
RA Wang Y.F., Meyer K.B., Schmidt K., Wan S.J., Degen S.J.F., la Barbera A.R.;
RT "Porcine follicle-stimulating hormone receptor.";
RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
CC -I- FUNCTION: RECEPTOR FOR FOLLICLE STIMULATING HORMONE. THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE ADENYLATE CYCLASE.
CC -I- SUBCELLULAR LOCATION: Integral membrane protein.
CC -I- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS. FSH/LSH/TSH SUBFAMILY.

-I- SIMILARITY: CONTAINS 6 LEUCINE-RICH REPEATS (LRR).
CC
CC
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CC
CC
CC EMBL: L31966; AAC86933.1;
DR EMBL: AF025377; AAC24981.1;
DR HSSP: P23945; 1XUN.
DR InterPro: IPR000276; GPCR_Rhodpsn.
DR InterPro: IPR001611; LRR.
DR InterPro: IPR000372; LRR_Nterm.
DR Pfam: PF00001; 7tm_1; 1.
DR Pfam: PF00560; LRR; 2.
DR Pfam: PF01462; LRRNT; 1.
DR SMART: SM00013; LRRNT; 1.
DR PROSITE: PS00237; G_PROTEIN_RECP_FL_1; 1.
DR PROSITE: PS00262; G_PROTEIN_RECP_FL_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Signal; Phosphorylation; Repeat; Leucine-rich repeat.
FT SIGNAL 1 17 POTENTIAL.
FT CHAIN 18 695 FOLLICLE STIMULATING HORMONE RECEPTOR.
FT DOMAIN 18 366 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 367 387 1 (POTENTIAL).
FT DOMAIN 388 398 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 399 421 2 (POTENTIAL).
FT DOMAIN 422 443 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 444 465 3 (POTENTIAL).
FT DOMAIN 466 485 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 486 508 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 509 528 4 (POTENTIAL).
FT TRANSMEM 529 550 5 (POTENTIAL).
FT DOMAIN 551 573 6 (POTENTIAL).
FT TRANSMEM 574 597 7 (POTENTIAL).
FT DOMAIN 598 608 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 609 630 7 (POTENTIAL).
FT DOMAIN 631 695 CYTOPLASMIC (POTENTIAL).
FT REPEAT 44 68 LRR 1.
FT REPEAT 69 93 LRR 2.
FT REPEAT 119 143 LRR 3.
FT REPEAT 170 192 LRR 4.
FT REPEAT 193 216 LRR 5.
FT REPEAT 218 240 LRR 6.
FT DISULFID 442 517 BY SIMILARITY.
FT CARBOHYD 191 191 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 199 199 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 293 293 N-LINKED (GLCNAC...) (POTENTIAL).
FT CONFLICT 2 2 S -> A (IN REF. 1).
FT CONFLICT 13 13 T -> S (IN REF. 1).
FT CONFLICT 60 60 V -> A (IN REF. 1).
FT CONFLICT 166 166 V -> M (IN REF. 1).
FT CONFLICT 215 215 Q -> H (IN REF. 1).
FT CONFLICT 247 247 K -> R (IN REF. 1).
FT CONFLICT 257 257 S -> T (IN REF. 1).
FT CONFLICT 334 334 D -> N (IN REF. 1).
FT CONFLICT 349 349 E -> K (IN REF. 1).
FT CONFLICT 352 352 T -> A (IN REF. 1).
FT CONFLICT 383 383 V -> E (IN REF. 1).
FT CONFLICT 407 407 A -> T (IN REF. 1).
FT CONFLICT 421 421 V -> I (IN REF. 1).
FT CONFLICT 427 427 T -> S (IN REF. 1).
FT CONFLICT 435 435 D -> N (IN REF. 1).
FT CONFLICT 483 483 L -> V (IN REF. 1).
FT CONFLICT 550 550 T -> I (IN REF. 1).
FT CONFLICT 586 586 A -> V (IN REF. 1).
FT CONFLICT 607 607 S -> L (IN REF. 1).
FT CONFLICT 691 691 R -> H (IN REF. 1).
SQ SEQUENCE 695 AA; 78172 MW; E9EBED929C79C450 CRC64;

Db 61 IPKAFSGDLEKIEISQNDVLEVEANFVSNLPKLEIRIEKANNLLYIDHDAFQNL 120
Qy 121 SLRYLLISNTGKIKHLPVAVHKIQSLQKVLIDQINITHIVARNSEFMSVILMSKN 180
Db 121 NLYVLLISNTGKIKHLPVAVHKIQSLQKVLIDQINITHIVARNSEFMSVILMSKN 180
Qy 181 GIEIHNCAFNGTQDLNLSNDNNLELNDVFOGASGPVILDISRTKVHSLPNHGLE 240
Db 181 GIEIHNCAFNGTQDLNLSNDNNLELNDVFOGASGPVILDISRTKVHSLPNHGLE 240
Qy 241 LKLRARSTYRLKPLNLDREFTVLMESALTPSHCCAFANLKRQISLHPICHNKSILROD 300
Db 241 LKLRARSTYRLKPLNLDREFTVLMESALTPSHCCAFANLKRQISLHPICHNKSILROD 300
Qy 301 IDMTQIGDQVSLI--DDESYKSGSDMYNEFDYDLCEVNEVDVTCSPKPDAPNCPEDIM 359
Db 301 V-DMTQARGERSVLAEDDESSYPKGFOMYSEFEYDLCEVNEVDVTCSPKPDAPNCPEDIM 359
Qy 360 GYNILRLVIFISILAITGNTVLTWLTTSOYKLTVPFELMCNLFADLCIGIYLLIAS 419
Db 360 GYNILRLVIFISILAITGNTVLTWLTTSOYKLTVPFELMCNLFADLCIGIYLLIAS 419
Qy 420 VDIHTKSOYHNYAIDWOTGACDAAGFTVFASLSVYTLTALRWHITTHAMOLECK 479
Db 420 VDIHTKSOYHNYAIDWOTGACDAAGFTVFASLSVYTLTALRWHITTHAMOLECK 479
Qy 480 VOLRHAASVMVLTGTFAPAAALPFIIGISSYMKVSYICLPMIDSPLSQLYMALLVNLV 539
Db 480 VOLRHAASVMVLTGTFAPAAALPFIIGISSYMKVSYICLPMIDSPLSQLYMALLVNLV 539
Qy 540 AFVVICGTHYILTVRNPTVSSSDTKAKRMATLIFTDLCMAPISEFAISASLKVP 599
Db 540 AFVVICGTHYILTVRNPTVSSSDTKAKRMATLIFTDLCMAPISEFAISASLKVP 599
Qy 600 LITVSKAKILLVFPINSCANPELYAIFTKNFRDRFILLSKFCGYEMQAQYRTTSS 659
Db 600 LITVSKAKILLVFPINSCANPELYAIFTKNFRDRFILLSKFCGYEMQAQYRTTSS 659
Qy 660 ATHNFHARKSCSAPRVN--SYVLVPLNHSOON 692
Db 660 TAHISHPRNGHCPTPTPRVINGANCTVPLSLAQN 694

RESULT 9

FSHR_EQUAS STANDARD; PRT; 687 AA.
AC Q95179;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Follicle stimulating hormone receptor precursor (FSH-R) (Follitropin receptor).
GN FSHR.
OS Equus asinus (Donkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9793;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RX MEDLINE=97338913; PubMed=9195473;
RA Richard F., Martinat N., Remy J.-J., Salesse R., Combarnous Y.;
RT "Cloning, sequencing and in vitro functional expression of recombinant donkey follicle-stimulating hormone receptor: a new insight into the binding specificity of gonadotrophin receptors.";
RL J. Mol. Endocrinol. 18:193-202(1997).
CC -1- FUNCTION: RECEPTOR FOR FOLLICLE STIMULATING HORMONE. THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE ADENYLATE CYCLASE.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS. FSH/LSH/TSH SUBFAMILY.

CC -1- SIMILARITY: CONTAINS 6 LEUCINE-RICH REPEATS (LRR).
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CC
CC EMBL; U73659; RAB18245.1;
DR HSP; P23945; IXUN.
DR InterPro: IPR000276; GPCR_Rhodpsn.
DR InterPro: IPR001611; LRR.
DR InterPro: IPR000372; LRR_Nterm.
DR Pfam: PF00001; 7tm_1; 1.
DR Pfam: PF00560; LRR; 3.
DR Pfam: PF01462; LRRNT; 1.
DR PRINTS: PR00237; GPCRHHODPSN.
DR SMART: SM00013; LRRNT; 1.
DR PROSITE: PS00237; G-PROTEIN_RECEP_FL_1; 1.
DR PROSITE: PS00262; G-PROTEIN_RECEP_FL_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Signal; Phosphorylation; Repeat; Leucine-rich repeat.
FT SIGNAL 1 17
FT CHAIN 18 687
FT DOMAIN 18 358
FT TRANSMEM 359 379
FT DOMAIN 380 390
FT TRANSMEM 391 413
FT DOMAIN 414 435
FT TRANSMEM 436 457
FT DOMAIN 458 477
FT TRANSMEM 478 500
FT DOMAIN 501 520
FT TRANSMEM 521 542
FT DOMAIN 543 565
FT TRANSMEM 566 589
FT DOMAIN 590 600
FT TRANSMEM 601 622
FT DOMAIN 623 687
FT REPEAT 44 68
FT REPEAT 69 93
FT REPEAT 119 143
FT REPEAT 170 192
FT REPEAT 193 216
FT REPEAT 218 240
FT DISULFID 434 509
FT CARBOHYD 191 191
FT CARBOHYD 199 199
FT CARBOHYD 293 293
SQ SEQUENCE 687 AA; 76937 MW; FC3AF0B5531DA9A CRC64;
Query Match 85.6%; Score 3076.5; DB 1; Length 687;
Best Local Similarity 86.0%; Pred. No. 2.3e-189;
Matches 597; Conservative 38; Mismatches 50; Indels 9; Gaps 3;
Qy 1 MALLVSLLAFLGTGSGCHHWHCHSCNRVFCQDSKVTEIPTDLPRNAIELRVLTCLR 60
Db 1 MALLVSLLAFLSLGSGCHHWHCHSCNRVFCQDSKVTEIPTDLPRNAIELRVLTCLR 60
Qy 61 IPKSGAFSGDLEKIEISQNDVLEVEANFVSNLPKLEIRIEKANNLLYINPEAFQNL 120
Db 61 IPKSGAFSGDLEKIEISQNDVLEVEANFVSNLPKLEIRIEKANNLLYIDHDAFQNL 120
Qy 121 SLRYLLISNTGKIKHLPVAVHKIQSLQKVLIDQINITHIVARNSEFMSVILMSKN 180
Db 121 NLYVLLISNTGKIKHLPVAVHKIQSLQKVLIDQINITHIVARNSEFMSVILMSKN 180
Qy 181 GIEIHNCAFNGTQDLNLSNDNNLELNDVFOGASGPVILDISRTKVHSLPNHGLE 240
Db 181 GIEIHNCAFNGTQDLNLSNDNNLELNDVFOGASGPVILDISRTKVHSLPNHGLE 240

241 LKTLRSTYRLKLNLDKPTLTHASLYSUCFANFKRQISELUPYCNKSLRQD 300
 241 LKTLRSTYRLKLNLDKPTLTHASLYSUCFANFKRQISELUPYCNKSLRQD 300
 301 IDMTQDQVSLIDPESFGKSGDMYNEFDYDLCNEVDVTCSPKPAFNPCEDEMG 360
 301 V-DMTQDQVSLIDPESFGKSGDMYNEFDYDLCNEVDVTCSPKPAFNPCEDEMG 360
 361 YNLRVLFNFIISLAITGTTVLVLTTSYKLTVPFRFLNCFADLCIGIYLLLTASV 420
 361 YNLRVLFNFIISLAITGTTVLVLTTSYKLTVPFRFLNCFADLCIGIYLLLTASV 420
 354 YDLRVLNFIISLAITGTTVLVLTTSYKLTVPFRFLNCFADLCIGIYLLLTASV 413
 421 DHTSQTHTAIDMTQDQVSLIDPESFGKSGDMYNEFDYDLCNEVDVTCSPKPAFNPCEDEMG 480
 414 DHTSQTHTAIDMTQDQVSLIDPESFGKSGDMYNEFDYDLCNEVDVTCSPKPAFNPCEDEMG 473
 481 QLRHAASVWLVGCPFFAALPPIGISTMVSVCLPMDISDLQYNSLVNLYLA 540
 474 QLRHAASVWLVGCPFFAALPPIGISTMVSVCLPMDISDLQYNSLVNLYLA 533
 541 FVYICGCTHTLVNRPNTYVSSSSDTKAKRMATLFTDFLCHAPISFFAISAISKVLPL 600
 534 FVYICGCTHTLVNRPNTYVSSSSDTKAKRMATLFTDFLCHAPISFFAISAISKVLPL 593
 601 ITVSKAKILLVLPYNSCANPLVAIPTKFRFRDFFILLKFCGYEMOQIYRTTSSA 660
 594 ITVSKAKILLVLPYNSCANPLVAIPTKFRFRDFFILLKFCGYEMOQIYRTTSSA 653
 651 THNFKHSCSSAPRVN--SVYLVNHNSSON 692
 654 GHISHPANGCPPTPRVINGANTCLVPLSHLAQN 687

RESULT 10
 FSHR-CHICK STANDARD; PRT: 693 AA.
 AC P79763; Q90719;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Follicle stimulating hormone receptor precursor (FSH-R) (Follicotropin receptor).
 GN Gallus gallus (Chicken).
 OS Chordata; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Gallinae; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae.
 OX NCBI-TaxID=9031;
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97473503; PubMed=9332357;
 RA Wakabayashi N., Suzuki A., Hoshino H., Nishimori K., Mizuno S.;
 RT "The cDNA cloning and transient expression of a chicken gene encoding
 RL a follicle-stimulating hormone receptor.";
 RN Gene 197:121-127(1997).
 RP SEQUENCE FROM N.A.
 RC STRAIN=White Leghorn;
 RA MEDLINE=97057887; PubMed=8902217;
 RT "You S., Bridgman J.F., Foster D.N., Johnson A.L.;
 FT Characterization of the chicken follicle-stimulating hormone
 FT of cFSH-R messenger complementary deoxyribonucleic acid, and expression
 RL Biol. Reprod. 55:1053-1062(1996).
 CC -1- FUNCTION: RECEPTOR FOR FOLLICLE STIMULATING HORMONE. THE ACTIVITY
 CC OF THIS RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE
 CC ADENYLATE CYCLASE.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 CC FSH/FSH SUBFAMILY.
 CC -1- SIMILARITY: CONTAINS 7 LEUCINE-RICH REPEATS (LRR).
 CC

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CC EMBL: D87871; BAA13487.1; .
 CC EMBL: U51097; AAC60030.1; .
 CC HSP: P23945; 1XUN.
 DR InterPro: IPR000276; GPCR_Rhodopn.
 DR InterPro: IPR001611; LRR.
 DR InterPro: IPR000372; LRR_Nterm.
 DR Pfam: PF00001; 7tm_1; 1.
 DR Pfam: PF00560; LRR; 1.
 DR PRINTS: PR00237; GPCRHHOOPS.
 DR SMART: SM00113; LRRNT; 1.
 DR PROSITE: PS0022; G-PROTEIN_RECEP_F1_1; 1.
 DR PROSITE: PS0022; G-PROTEIN_RECEP_F2_1; 1.
 KW G-Protein coupled receptor, 7 transmembrane, Glycoprotein; Signal;
 KW Phosphorylation; Repeat; Leucine-rich repeat.
 FT SIGNAL 1 17 POTENTIAL STIMULATING HORMONE RECEPTOR.
 FT CHAIN 18 693 EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 18 366 1 (POTENTIAL).
 FT TRANSMEM 367 387 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 388 398 2 (POTENTIAL).
 FT TRANSMEM 399 421 EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 422 443 3 (POTENTIAL).
 FT TRANSMEM 444 465 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 466 485 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 486 508 4 (POTENTIAL).
 FT DOMAIN 509 528 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 529 550 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 551 567 5 (POTENTIAL).
 FT TRANSMEM 568 598 EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 599 630 6 (POTENTIAL).
 FT TRANSMEM 631 653 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 654 687 7 (POTENTIAL).
 FT REPEAT 45 68 LRR 1.
 FT REPEAT 69 93 LRR 2.
 FT REPEAT 95 118 LRR 3.
 FT REPEAT 119 143 LRR 4.
 FT REPEAT 168 192 LRR 5.
 FT REPEAT 193 216 LRR 6.
 FT REPEAT 218 240 LRR 7.
 FT DISULFID 442 517 .BY SIMILARITY.
 FT CARBOHYD 47 47 N-LINKED (GLCNAC... (POTENTIAL).
 FT CARBOHYD 151 151 N-LINKED (GLCNAC... (POTENTIAL).
 FT CARBOHYD 152 152 N-LINKED (GLCNAC... (POTENTIAL).
 FT CARBOHYD 268 268 N-LINKED (GLCNAC... (POTENTIAL).
 FT CONFLICT 88 88 C > A (IN REF. 2).
 FT CONFLICT 140 140 R > R (IN REF. 2).
 FT CONFLICT 174 174 I > T (IN REF. 2).
 FT CONFLICT 191 191 N > S (IN REF. 2).
 FT CONFLICT 329 329 V > L (IN REF. 2).
 .SQ SEQUENCE 693 AA; 78697 MW; 46F9859635A1BDC CRC64;

Query Match 72.5%; Score 2605.5; DB 1; Length 693;
 Best Local Similarity 72.9%; Pred. No. 2.9e-159;
 Matches 304; Conservative 72; Mismatches 112; Indels 3; Gaps 2;
 QY 1 MALLVSLAFITGSGCHWCHCSNRVFLQDSKVTIPTDPRNAELRFLVTKLV 60
 DB 1 MSIGTCLLLIASCSCCHTCLSGRIFQIEIKYVOLPHDIPNATLRFVTKMRY 60
 QY 61 IPKSGFAGFQLEKISQNVLEVYADVSNKPKLRIERKANKLLINPEAFQMLP 120
 DB 61 IPKGAFTGLJDLKLEISQDALEIEGWFSSFLKLEIRKANKLKKIDQADAPQLP 120
 QY 121 SLRYLLSNTGKHPAVHKTSQKQVLSQKVLDDIDNINIHIVARNSPGSLSPESVILWLSKN 180
 DB 121 SLRYLLSNTGKHPAVHKTSQKQVLSQKVLDDIDNINIHIVARNSPGSLSPESVILWLSKN 180

Db	55	RLSLTYLPKIVIPSOQPRGUNEVIKIEISODSLSEKIEANAFDNLNLNSELIONKWL	114
Qy	110	YINPEAFONPFSRLYLLISNTGIKHLPVAKIQSLQ-KVLIDIOQNIHIVARNSEGL	168
Db	115	HIEAGAPTNPRLKYLSCIGNTGIKHPDVTKIFSEFNFILEICDNLHITIPRPAFGM	174
Qy	169	SFSPVILWLSKNGIEETHNCAFNGTQJDELNLSNDDNLEELPNDVFOCASGPVILDSRT	228
Db	175	NNESITUKLYNGFEEETOSHAFNNTTJISLEKENARLEKMHNDAFRGATGPSILDISST	234
Qy	229	KVHSLPHRGLENKLLRARSPYRKLLPNLDKFTLMEASLTYPHSCCAFANLKRQISEL	288
Db	235	KLQALPTYGLESIQTLATSSYLKKLPUSREKFTNLLDATLTPSHCCAFRNL-----	287
Qy	289	HPCTNKSILRQDIDDMTOIGDQRVSLDIDDESYG---KGSMDMYNEFDYDLCNEVDVTC	345
Db	288	-PTNEQNFSPSIFKNFSKOCESSTARPPNNETLYSAIFAESLSGDWYDYGCLPKT-LQC	345
Qy	346	SPRPDAENPCEDINGNLRVLWIFISILATIGNTTVLVLTTSQYKLTVPFRFLMCNLAF	405
Db	346	AEPDAENPCEDINGYNFLRVLIWLINLATIGNTVFLVLTTSYKLTVPFRFLMCNLSE	405
Qy	406	ADLCIGYVLLLIASVDIHTKSQYHNYAIDWOTGAGCDAAGFTTFVASELSVYTLTAITLE	465
Db	406	ADFCMGLYVLLLIASVDAQTKQYNYHAIWOTGSGCSAAGFTTFVASELSVYTLTAITLE	465
Qy	466	RWHTITHAMOLECKVOLRHAASVMVLGWTFAAALFPFIFGSISSYMKVSYICLPMDDISPL	525
Db	466	RWHTITVAIQDLKRLKHALPVMGLWGLFSTLIAPLVGVSNTYMKVSYICLPMDDVESTL	525
Qy	526	SQLYVMALLVNLVLAFFVYCCGYTHIYLTVRNPTIVSSSDTKIAKRMATLIFTDFLCMA	585
Db	526	SOVYILTILNLVMAFIICACYIKIYFAVQNPCLMATNKDTKIAKNKAVLIFTDTGMA	585
Qy	586	PISFPATASLKVPLITVTSKAKILLVLPYPIVNSCANPFLYALFTKNFRDRFILLSKCC	645
Db	586	PISFPATSAFVKVPLITVTSKVLVLPYPIVNSCANPFLYALFTKAFDFELLISKCC	645
Qy	646	YEMOQAYRTTSSATHNFHARKSHCSS	673
Db	646	KYRAELYRRK-----DFSAYISNCKN	667

, RESULT 13

LSHR_MOUSE	STANDARD;	PRT;	700 AA..
ID	LSHR_MOUSE		
AC	P30730;		
DT	01-APR-1993 (Rel. 25, Created)		
DT	01-APR-1993 (Rel. 25, Last sequence update)		
DT	16-OCT-2001 (Rel. 40, Last annotation update)		
DE	Lutropin-choriogonadotropic hormone precursor (LH/CG-R)		
DE	(LSH-R) (Luteinizing hormone receptor)		
GN	LHCGR OR LHR.		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
OX	NCBI_TaxID=10090;		
[1]			
RN	SEQUENCE FROM N.A.		
RP			
RX	MEDLINE=92165799; PubMed=1311310;		
RA	Gudermann T., Birnbaumer M., Birnbaumer L.;		
RT	"Evidence for dual coupling of the murine luteinizing hormone		
RT	receptor to adenylyl cyclase and phosphoinositide breakdown and Ca2+		
RT	mobilization. Studies with the cloned murine luteinizing hormone		
RT	receptor expressed in L cells.";		
RL	J. Biol. Chem. 267:4479-4488(1992).		
RN	[2]		
RN	SEQUENCE OF 1-58 FROM N.A.		
RP			
RX	MEDLINE=93093308; PubMed=1459341;		
RA	Huhtaniemi I.T., Eskola V., Pakarinen P., Matikainen T., Sprengel R.;		
RT	"The murine luteinizing hormone and follicle-stimulating hormone		
RT	receptor genes: transcription initiation sites, putative promoter		

```
OY 103 EKANLLXINPFAOWLPISLYLLISNGIKULPAVHQLQSLQVLLDQDNHINIVA 161
DB 110 ONTKULLIPECAFWLPKLYLSICNTGIRLIDNSKISSFENFLEICDNLIITIP 169
OY 162 RNSPGLSIPESVILKSKNGTEEHNCANGTDLNLSNNNLEELPNDVFOGASCPY 221
DB 170 GNAPOGMNNESTLKLYNGPEVOSHAFNGTTLISLEKKNIVLEKMSHSGTFOGATPS 229
OY 222 ILDIRTKVHSLPHNGLKLLKLRARSTYRLKLPNDKFTVLMKASLYPSHCCAFANL 281
DB 230 ILVDSSTKQALPGLSGLSIOTLATSSYSKLTPSRKFTSLVATLYPSHCCAFANL 289
OY 282 KROISELHPICNKSILRODDIMTOIGDQVSLDDDEPSYG---KGSOMMYNEFYDOLCN 338
DB 290 PKR-----SQNPSFISFENFSQCESTVEARENNETLYSAIFENELSGMDYDFCS 341
OY 339 EYVDVTCGSRDPAKPCDNGYHNLVILWFLSILATGNTVTVLVITSTQKLTVPFR 398
DB 342 PKT-LOCTPEPAPNCEIDNAGTFLVRLVILNLTALNLTALNLTALNLTALNLTALN 400
OY 399 LACNLAFADLCIGITLLIASVSDIHTKSOYHVAIDWOTGACDAGGFTVPASELSVYT 458
DB 401 LACNLSPADPCMGILLLIASVSDQTKQYINHAIDWOTGSCGSAAGFTVPASELSVYT 460
OY 459 LTAITLERHTITHAMOLECIVOLRHAASVWLVGTFAPAAALPFIPIGSSYMKVSIQCLP 518
DB 461 LTVITLERHTITVAOLDOQLRLRHATPMLGGWIFSTLMAATLPLVGVSSYMKVSIQCLP 520
OY 519 MDIDSPASQLYVVALVNLVAFVVICCTHYLYTVRNPTIVSSSDTKIARMTATLIF 578
DB 521 MDVSTLSQVITLSILLNAVAFVVIACVTRYIPAVONPELTAPNKOTKIARKMAILIF 580
OY 579 TDFLCAPISFPAISALSVLTYSKATLLVLPYDINSCANPFLIATFNKFRPFFI 638
DB 581 TDFTCAPISFPAISALSVLTYSKATLLVLPYDINSCANPFLIATFNKFRPFFI 640
OY 639 LLSKPGCVENQOITRTSSA-----TINPARKS-----MCS--SAPRV 677
DB 641 LLSRPGCKHRAELRYRKEPSACTFNSANGFPSPSKPSOAAKLISIVHCQOPTPRV 697

RESULT 14
LSHR_RAT
ID AC P16235: P70646; 063807; 063808; 063809;
DT 01-APR-1990 (Rel. 14, Created)
DI 02-APR-1990 (Rel. 14, Last sequence update)
DE LSH-RAT (Luteinizing hormone receptor precursor (LH/CG-R)
DE (LSH-R) (Luteinizing hormone receptor).
CN LSHR
OS Rattus norvegicus (Rat).
OC Eukaryote; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-89332512; PubMed-2502842;
RA Rosenblatt N., Nikolics K., Segaloff D.L., Seeburg P.H.;
RA "Lutropin-choriogonadotropin receptor: an unusual member of the G
protein-coupled receptor family.";
RA Science 245:494-499(1989).
RP SEQUENCE FROM N.A. AND ALTERNATIVE SPLICING.
RC STRAIN-Sprague-Dawley; TISSUE-Ovary;
RX MEDLINE-93347604; PubMed-1353463;
RA AasLanki J.T., Pietila E.M., Lakkakorpi J.T., Rajaniemi H.J.;
RA "Expression of the LH/CG receptor gene in rat ovarian tissue is
regulated by an extensive alternative splicing of the primary
transcript.";
RL Mol. Cell. Endocrinol. 84:127-135(1992).
RN [3]

RP SEQUENCE FROM N.A.
RX MEDLINE-91209270; PubMed-2019252;
RA Koo Y.B., Slaughter R.G., Ji T.H.;
RA "Structure of the luteinizing hormone receptor gene and multiple
exons of the coding sequence."
RL Endocrinology 128:2297-2308(1991).
RN [4]
RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
RX MEDLINE-91006819; PubMed-1976554;
RA Bernard M.P., Myers R.V., Moyle W.R.;
RA "Cloning of rat lutropin (LH) receptor analogs lacking the soybean
lectin domain.";
RL Mol. Cell. Endocrinol. 71:R19-R23(1990).
RN [5]
RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
RX MEDLINE-91126285; PubMed-2281186;
RA Segaloff D.L., Sprengel R., Nikolics K., Ascoli M.;
RA "Structure of the lutropin/choriogonadotropin receptor.";
RL Recent Prog. Horm. Res. 46:261-303(1990).
RN [6]
RP SEQUENCE OF 295-700 FROM N.A.
RX MEDLINE-91060531; PubMed-2174034;
RA Tsai-Morris C.H., Buckle E., Wang W., Dufau M.L.;
RA "Intronic nature of the rat luteinizing hormone receptor gene defines
a soluble receptor subtypes with hormone binding activity.";
RL J. Biol. Chem. 265:19385-19388(1990).
RN [7]
RP SEQUENCE OF 27-37.
RX MEDLINE-89174723; PubMed-2925659;
RA Roche P.C., Ryan R.J.;
RA "Purification, characterization, and amino-terminal sequence of rat
ovarian receptor for luteinizing hormone/human chorogonadotropin.";
RL J. Biol. Chem. 264:4636-4641(1989).
RN [8]
RP LUTEINIZATION.
RX MEDLINE-91332007; PubMed-1714448;
RA Ji T.H., Koo Y.B.
RA "Asp183 in the second transmembrane domain of the lutropin receptor
is important for high affinity hormone binding and cAMP production.";
RL J. Biol. Chem. 266:14953-14957(1991).
CC -1- FUNCTION: RECEPTOR FOR LUTROPIN-CHORIOGONADOTROPIC HORMONE.
CC THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G PROTEINS WHICH
CC ACTIVATE ADENYLATE CYCLASE.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- ALTERNATIVE PRODUCTS: AT LEAST 11 ISOFORMS WHICH DIFFER IN
CC SUBCELLULAR LOCATION ARE PRODUCED BY ALTERNATIVE SPLICING
CC OF THE SAME GENE.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -1- PSY/LSH/TSH SUBFAMILY.
CC -1- SIMILARITY: CONTAINS 7 LEUCINE-RICH REPEATS (LRR).
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CC -----
CC EXBL: M26199; AAA1528.1;
CC EXBL: M61212; AAA1527.1;
CC EXBL: M61211; AAA1527.1; JOINED.
CC EXBL: S40803; AAB22680.1;
CC EXBL: S40787; AAB22680.1; JOINED.
CC EXBL: S40903; AAB22680.1; JOINED.
CC EXBL: S40905; AAB22680.1; JOINED.
CC EXBL: S40907; AAB22680.1; JOINED.
CC EXBL: S40909; AAB22680.1; JOINED.
CC EXBL: S40918; AAB22680.1; JOINED.
CC EXBL: S40920; AAB22680.1; JOINED.
CC EXBL: S40795; AAB22680.1; JOINED.
CC EXBL: S40798; AAB22680.1; JOINED.
```

FT	TRANSMEM	487	509	4 (POTENTIAL).	
FT	DOMAIN	510	529	EXTRACELLULAR (POTENTIAL).	
FT	TRANSMEM	530	551	5 (POTENTIAL).	
FT	DOMAIN	552	574	CYTOPLASMIC (POTENTIAL).	
FT	TRANSMEM	575	598	6 (POTENTIAL).	
FT	DOMAIN	599	609	EXTRACELLULAR (POTENTIAL).	
FT	TRANSMEM	610	631	7 (POTENTIAL).	
FT	DOMAIN	632	700	CYTOPLASMIC (POTENTIAL).	
FT	REPEAT	52	75	LRR 1.	
FT	REPEAT	126	150	LRR 2.	
FT	REPEAT	152	175	LRR 3.	
FT	REPEAT	176	200	LRR 4.	
FT	REPEAT	202	224	LRR 5.	
FT	REPEAT	225	248	LRR 6.	
FT	REPEAT	250	271	LRR 7.	
FT	DISULFID	443	518	BY SIMILARITY.	
FT	CARBOHYD	103	103	N-LINKED (GLCNAC. . .) (POTENTIAL).	
FT	CARBOHYD	178	178	N-LINKED (GLCNAC. . .) (POTENTIAL).	
FT	CARBOHYD	199	199	N-LINKED (GLCNAC. . .) (POTENTIAL).	
FT	CARBOHYD	295	295	N-LINKED (GLCNAC. . .) (POTENTIAL).	
FT	CARBOHYD	303	303	N-LINKED (GLCNAC. . .) (POTENTIAL).	
FT	CARBOHYD	317	317	N-LINKED (GLCNAC. . .) (POTENTIAL).	
FT	VARSPLIC	83	132	MISSING (IN ISOFORM 1950).	
FT	VARSPLIC	133	157	MISSING (IN ISOFORM 1759).	
Query Match 50.08; Score 1797; DB 1; Length 700;					
Best Local Similarity 56.58; Pred. No. 1.3e-107;					
Matches 359; Conservative 105; Mismatches 149; Indels 22; Gaps 7;					
Qy	45	PRNAIELRFLVTKL--RVIEKGFAGFGDLEKIEISONDVLEIVTEADVFNLPKLHEIRI	102		
Db	51	PRAGL-ARLSYTLPVKVIQSAFRLGVVVKIEISQSDSLERIANAFNLLNSELLI	109		
Qy	103	EKANNNLYINPEAFQNPLPSRLYLISNITGIKHPAVHKIOSLO-KVLLDIQDNINIHVA	161		
Db	110	QNTKNLLYIEPGAFTNPLRLKYLISICNTGIRTLPDVTKISSEFNFLEICDNLHITIP	169		
Qy	162	RNSPMGLSFESVILWLSKNGIEETHNCAFNGTQDELNLDNNNLELPLNDVFGASGPV	221		
Db	170	GNAFQGMNNEVSITLKLXNGFEEVQSHAFNGTLLISLEKENIYLEKMHGSAFGATGPS	229		
Qy	222	ILDISRTKVLHSLPNHGLNKLKARSTYRLKKLPNLDKFTLMEASLTYPSHCCAPANL	281		
Db	230	ILDISSTKLQALPSHGLSITQTLIALSSYSLKTLPSKEKETSLLVATLTYPSHCCAPRN	289		
Qy	282	KQITSELHPICNKSILRQDIDMTQIGQRVSLIDDEPSYG---KGSMDMYNEFDYDLN	338		
Db	290	PKK-----EQNFSFISFENFSKQESTVRKADNETLYSAIFEENELSGWDYDYGCS	341		
Qy	339	EVDVDTCKPKDAFNPCEIDMGYNILRVLLWFTSILAITGNTTVLVVLTTSQYKLTVPFR	398		
Db	342	PKT--LQCAPEDAFNPCEIDMGYAFRLWLWILNLAIFGNLTVLVLLTSRYKLTVPFR	400		
Qy	399	LMCNLAFADLCIGTYLLLIASVDIHTKSYHNVAIDMQTGAGCDAAAGFFTVFASLSVYT	458		
Db	401	LMCNLSPADCMGLYLLLIASVDSOTKGOYVNHAIIDMQTGSCGCAAGFFTVFASLSVYT	460		
Qy	459	LTAITLERWHTITHAMOLEKVQLRHAASVWVLGWTFAFAAALPIPIFGISYMKVSLCP	518		
Db	461	LTVTILERWHTITVAVQDQKLRHAIPMLGGWLFSTLIATMPLVGSINMYKVSICLP	520		
Qy	519	MDIDSPLSOLYVMALLNVLNLAFFVVICGTYHIYLTVRNPTTVSSSDTKIARMTLIF	578		
Db	521	MDVESTSQVYISILINVLNVAFFVICACYIRIYFAVONPELTAPNKDTHIAKMKAILF	580		
Qy	579	TDFLCMAPIFFFAISLKVPLITVSKAKILLVLFPYINSCANPELYAIFTKNFRDDEFI	638		
Db	581	TDFTCMAPIFFFAISAAFKVPLITVTSKILLVLFPVNSCANPFLYAITTKAFQDFLL	640		
Qy	639	LLSKEFGCEMOAQIYRTTETSATHNPHARKSHCSS	673		
Db	641	LLSRFGCKRRAELYRRK-----EFSAYTSNCKN	669		

RESULT 15
LSHR HUMAN STANDARD; PRT: 699 AA.
AC P2388;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Lutropin-chorionadotropin hormone receptor precursor (LH/CG-R)
DE (LSH-R) (luteinizing hormone receptor).
GN LHCR OR LHRH OR LCR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID:9606;
PC TISSUE-Brain; N.A.
PC TISSUE-Ovary;
RX MEDLINE-9105934; PubMed-224890;
RA Minegishi T., Nakamura K., Takahara Y., Miyamoto K., Hasegawa Y.,
RA Ibuki Y., Igarashi M.,
RL Biochem. Biophys. Res. Commun. 172:1049-1054(1990).
RN [2]
RN SEQUENCE FROM N.A.
RC TISSUE-Ovary;
RX MEDLINE-9201781; PubMed-1922095;
RA Jia X.-C., Oikawa M., Bo M., Tanaka T., My T., Boime I., Hauch A.J.W.;
RA "Expression of human luteinizing hormone (LH) receptor: interaction
RT with LH and chorionic gonadotropin from human but not equine, rat,
RT and ovine species.";
RL Mol. Endocrinol. 5:759-768(1991).
RN [3]
RN SEQUENCE FROM N.A.
RC TISSUE-Thyroid;
RX MEDLINE-91155962; PubMed-2393030;
RA Frazier A.L., Robbins L.S., Scott P.J., Sprengel R., Segaloff D.L.,
RA Cone R.D.;
RT "Isolation of TSH and LH/CG receptor cDNAs from human thyroid:
RT regulation by tissue specific splicing.";
RL Mol. Endocrinol. 4:1264-1276(1990).
RN [4]
RN 3D-STRUCTURE MODELING OF 51-232.
RX MEDLINE-96363672; PubMed-8747461;
RA Jiang X., Dreano M., Buckler D.R., Cheng S., Ythier A.; Wu H.,
RA Hendrickson W.A.; el Teyar N.;
RT "Structural predictions for the ligand-binding region of glycoprotein
RT hormone receptors and the nature of hormone-receptor interactions.";
RL Structure 3:1341-1353(1995).
RN [5]
RN VARIANT FMPP GLY-578.
RX MEDLINE-94019815; PubMed-7692306;
RA Shenker A., Laue L., Kosugi S., Merendino J.J. Jr., Minegishi T.,
RA Cutler G.B. Jr.;
RT "A constitutively activating mutation of the luteinizing hormone
RT receptor in familial male precocious puberty.";
RL Nature 365:652-654(1993).
RN [6]
RN VARIANTS FMPP ILE-571 AND GLY-578.
RX MEDLINE-94108425; PubMed-8281137;
RA Kremer H., Mariman E., Otten B.J., Moll G.W. Jr., Stoeltinga G.B.A.,
RA Wit J.M., Jansen M., Drop S.L., Paas B., Ropers H.-H., Brunner H.G.;
RT "Coregulation of missense mutations of the luteinizing hormone
RT receptor gene with clinical manifestations of limited precocious puberty.";
RL Hum. Mol. Genet. 2:1177-1182(1993).
RN [7]
RN VARIANT FMPP ILE-577.
RX MEDLINE-95276728; PubMed-7757065;
RA Kosugi S., van Dop C., Geffner M.E., Rabl W., Carel J.-C.,
RA Chaussain J.-L., Mori T., Merendino J.J. Jr., Shenker A.;
RT "Characterization of heterogeneous mutations causing constitutive
RT activation of the luteinizing hormone receptor in familial male
RT precocious puberty.";
RL Hum. Mol. Genet. 4:183-188(1995).
RN [8]
RN VARIANT FMPP VAL-572.
RX MEDLINE-9522804; PubMed-7714085;
RA Yamada K., Saji M., Hatake A., Moriya N., Okuno A., Kohn L.D.,
RA Cutler G.B. Jr.;
RT "A new constitutively activating point mutation in the luteinizing
RT hormone/chorionadotropin receptor gene in cases of male-limited
RT precocious puberty.";
RL J. Clin. Endocrinol. Metab. 80:1162-1168(1995).
RN [9]
RN VARIANT FMPP VAL-568.
RX MEDLINE-95555560; PubMed-7629248;
RA Latronico A.C., Anastasi J., Arnold I.J., Mendonca B.B., Domenice S.,
RA Albano M.C., Zachman K., Wajchenberg B.L., Tsigos C.;
RT "A novel mutation of the luteinizing hormone receptor gene causing
RT male gonadotropin-independent precocious puberty.";
RL J. Clin. Endocrinol. Metab. 80:2490-2494(1995).
RN [10]
RN VARIANT LCH PRO-593.
RX MEDLINE-95235561; PubMed-7719343;
RA Kremer H., Kraaij R., Toledo S.P.A., Post M., Fridman J.B.,
RA Hayashida C.Y., van Reen H.G.,
RA Themmen A.P.N., Brunner H.G.;
RT "Male pseudohermaphroditism due to a homozygous missense mutation of
RT the luteinizing hormone receptor gene.";
RL Nat. Genet. 9:160-164(1995).
RN [11]
RN VARIANT FMPP ILE-577.
RX MEDLINE-96233936; PubMed-8829636;
RA Cocco S., Meloni A., Marini M.G., Cao A., Mol P.;
RT "A missense (T577I) mutation in the luteinizing hormone receptor gene
RT associated with familial male-limited precocious puberty.";
RL Hum. Mutat. 7:164-166(1996).
RN [12]
RN VARIANT FMPP THR-398.
RX MEDLINE-97083378; PubMed-8929952;
RA Evans B.J., Bernal J., Smith P.J., Clayton P.E., Gregory J.M.;
RT "A new point mutation in the luteinizing hormone receptor gene in
RT familial and sporadic male limited precocious puberty: genotype does
RT not always correlate with phenotype.";
RL J. Med. Genet. 33:143-147(1996).
RN [13]
RN VARIANT LCH TYR-616.
RX MEDLINE-96157015; PubMed-8559204;
RA Latronico A.C., Anastasi J., Arnold I.J.P., Rapaport R., Mendonca B.B.,
RA Bloise W., Castro M., Tsigos C., Chrousos G.P.;
RT "Brief report: testicular and ovarian resistance to luteinizing
RT hormone caused by inactivating mutations of the luteinizing
RT hormone-receptor gene.";
RL N. Engl. J. Med. 334:507-512(1996).
RN [14]
RN VARIANT LCH ARG-131.
RX MEDLINE-97358168; PubMed-9215288;
RA Misrahi M., Meduri G., Pissard S., Bouvattier C., Beau I.,
RA Loosfelt H., Jollivet A., Rapaport R., Milgrom E., Bougneres P.;
RT "Comparison of immunocytochemical and molecular features with the
RT phenotype in a case of incomplete male pseudohermaphroditism
RT associated with a mutation of the luteinizing hormone receptor.";
RL J. Clin. Endocrinol. Metab. 82:2159-2165(1997).
RN [15]
RN VARIANTS LEU-GLN-13 INS; SER-284 AND ASN-306.
RA Wu S.-M., Jose M., Hallermeier K., Rennert O.M., Chan W.-Y.;
RT "Polymorphisms in the coding exons of the human luteinizing hormone
RT receptor gene.";
RL Hum. Mutat. 11:333-334(1998).
RN [16]
RN VARIANT FMPP VAL-373.
RX MEDLINE-98128689; PubMed-9467560;
RA Gromell J., Pertsch C.-J., Simoni M., Nordhoff V., Sippell W.G.,
RA Mieschlag E., Saxena B.B.;
RT "A mutation in the first transmembrane domain of the lutropin receptor
RT causes male precocious puberty.";

[illegible]

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OM protein - protein search, using sw model

Run on: June 16, 2003, 12:58:36 : Search time 43.5347 seconds
(without alignments)
3275.191 Million cell updates/sec

Title: US-09-877-804-6

Perfect score: 3594
Sequence: 1 WALLVSLAFGTGSCGHH.....SAPRVNYSVLPLNHSN 692

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671560

Minimum DB seq length: 0

Maximum Match 100%

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

SPTREMBL_21.*

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phase.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_rvirus.*
- 16: sp_bacteriap.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3560	99.1	688	11	Q64183
2	3144.5	87.5	695	11	Q8R428
3	2507	69.8	696	13	Q9DGF5
4	1979	55.1	673	13	Q9DGP8
5	1901.5	52.9	410	4	Q16223
6	1801.5	51.3	762	13	Q8R784
7	1803.5	50.3	662	13	Q8R936
8	1802	50.1	662	13	Q15936
9	1776	49.4	699	4	Q14751
10	1776	49.4	701	13	Q9DSC5
11	1685	46.9	701	13	Q9DSC5
12	1676	46.6	763	6	Q8R6A4
13	1670.5	46.5	764	6	Q8R6S6
14	1670.5	46.5	764	6	Q8R6P9
15	1658.5	46.1	601	13	Q42500
16	1653.5	46.0	764	11	Q9D697

ALIGNMENTS

RESULT 1

Q64183 Q64183 PRELIMINARY; PRT; 688 AA.
AC Q64183.
DT 01-NOV-1996 (TREMBLrel_01, Created)
DT 01-NOV-1996 (TREMBLrel_01, Last sequence update)
DT 01-DEC-2001 (TREMBLrel_19, Last annotation update)
DE Follicle-stimulating hormone receptor.
OS Rattus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10110;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-92149579; PubMed-173873;
RA Heckert L.L., Daley I.J., Griswold M.D.;
RT Structural organization of the follicle-stimulating hormone receptor gene.
FL Mol. Endocrinol. 6:70-80(1992).
DR EMBL; S81198; AAB21415.2; JOINED.
DR EMBL; S81117; AAB21415.2; JOINED.
DR EMBL; S81119; AAB21415.2; JOINED.
DR EMBL; S81121; AAB21415.2; JOINED.
DR EMBL; S81171; AAB21415.2; JOINED.
DR EMBL; S81174; AAB21415.2; JOINED.
DR EMBL; S81176; AAB21415.2; JOINED.
DR EMBL; S81183; AAB21415.2; JOINED.
DR EMBL; S81185; AAB21415.2; JOINED.
DR EMBL; S81194; AAB21415.2; JOINED.
DR HSSP; P23945; LXUN.
DR InterPro; IPR000276; GPCR_Rhodopn.
DR InterPro; IPR001611; LRR.
DR InterPro; IPR000272; LRR_Mterm.
DR Pfam; PF00000; LRR_1.
DR Pfam; PF00560; LRR_3.
DR Pfam; PF01462; LRRNT_1.
DR SMART; SM00013; LRRNT.
DR PROSITE; PS00237; G_PROTEIN_RECP_FL1; UNKNOWN_1.
DR PROSITE; PS0262; G_PROTEIN_RECP_FL2; 1.

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Q92650 oncorhynchu
Q9265

KW Receptor. 688 AA; 77341 MW; 441F0D9E7D01DF18 CRC64;
SQ SEQUENCE 99.1%; Score 3560; DB 11; Length 688;
Query Match Best Local Similarity 99.3%; Pred. No. 1.4e-256;
Matches 687; Conservative 0; Mismatches 1; Indels 4; Gaps 1;

QY 1 MALLVSLAFLGTGSGCHHMLCHCNRVFLQDSKVTEIPTDLPNATLREVLTKLRV 60
DB 1 MALLVSLAFLGTGSGCHHMLCHCNRVFLQDSKVTEIPTDLPNATLREVLTKLRV 60
QY 61 IPKGSFAGDLEKIEISQNDVLEADVFNPLKHEIRIEKANNLLYINPEAFONLP 120
DB 61 IPKGSFAGDLEKIEISQNDVLEADVFNPLKHEIRIEKANNLLYINPEAFONLP 120
QY 121 SLRYLLISNTGKHLPAVHKIOSLQKVLDDIQQNINIHIVARNSPFGLSFESVILWLSKN 180
DB 121 SLRYLLISNTGKHLPAVHKIOSLQKVLDDIQQNINIHIVARNSPFGLSFESVILWLSKN 180
QY 181 GIEEIHNCFAFNGTQDDELNLSDNNLELNDVDFQASGVPVLDISRTKVHSLPNHGLN 240
DB 177 GIEEIHNCFAFNGTQDDELNLSDNNLELNDVDFQASGVPVLDISRTKVHSLPNHGLN 236
QY 241 LKKLRARSTYRLKLPNLDKFTVLTMEASLTYPHCCAFANLKRQISELHPICNKSILROD 300
DB 237 LKKLRARSTYRLKLPNLDKFTVLTMEASLTYPHCCAFANLKRQISELHPICNKSILROD 296
QY 301 IDDMTOIGDQSVSLIDDEPSYKGSDDMYNEFDYDLCNEVDVDTCPKPDAPNCPEDIM 360
DB 297 IDDMTOIGDQSVSLIDDEPSYKGSDDMYNEFDYDLCNEVDVDTCPKPDAPNCPEDIM 356
QY 361 YNLRVLWIFISILAITGNTVLTTSQYKLTVPFLMCNLAFLADLCIGIYLLIASV 420
DB 357 YNLRVLWIFISILAITGNTVLTTSQYKLTVPFLMCNLAFLADLCIGIYLLIASV 416
QY 421 DIHTKSOYHNYAIDMOTGAGDAAGFTVFASELSVYTLTATLERWHITTHAMOLECKV 480
DB 417 DIHTKSOYHNYAIDMOTGAGDAAGFTVFASELSVYTLTATLERWHITTHAMOLECKV 476
QY 481 QLRHAASVMVLGWTFAFAALPFIIGISSYKMKVSIKLPMDIDSPISQLYVMALLVNLVA 540
DB 477 QLRHAASVMVLGWTFAFAALPFIIGISSYKMKVSIKLPMDIDSPISQLYVMALLVNLVA 536
QY 541 FVVICGCTHYLTVRNPTIVSSSDTKIAKRNATLIFTDFLCMAPISEFASISLKVPL 600
DB 537 FVVICGCTHYLTVRNPTIVSSSDTKIAKRNATLIFTDFLCMAPISEFASISLKVPL 596
QY 601 ITVSKAKILLVLPINSCANPFLYAIFTKNFRDRDFILLSKFGCYEMQAQIYRTTSSA 660
DB 597 ITVSKAKILLVLPINSCANPFLYAIFTKNFRDRDFILLSKFGCYEMQAQIYRTTSSA 656
QY 661 THNFHARKSHCSSAPRVTSYVLPVPLNHSSQN 692
DB 657 THNFHARKSHCSSAPRVTSYVLPVPLNHSSQN 688

RESULT 2
Q8R428 PRELIMINARY; PRT; 695 AA.
AC Q8R428;
DT 01-JUN-2002 (T-EMBLrel. 21, Created)
DT 01-JUN-2002 (T-EMBLrel. 21, Last sequence update)
DE Follicle stimulating hormone receptor.
GN FSHR.
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
OX NCBI_TaxID=10141;
RN [1]
RP SEQUENCE FROM N.A.
RA SUZUKI O.;

RT "Guinea pig follicle stimulating hormone receptor."
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY082514; AAL92577.1;
KW Receptor.
SQ SEQUENCE 695 AA; 77838 MW; 9A3ECF419C45227B CRC64;
Query Match 87.5%; Score 3144.5; DB 11; Length 695;
Best Local Similarity 87.1%; Pred. No. 1.2e-225;
Matches 605; Conservative 38; Mismatches 49; Indels 3; Gaps 2;

QY 1 MALLVSLAFLGTGSGCHHMLCHCNRVFLQDSKVTEIPTDLPNATLREVLTKLRV 60
DB 1 MALLVSLAFLGTGSGCHHMLCHCNRVFLQDSKVTEIPTDLPNATLREVLTKLRV 60
QY 61 IPKGSFAGDLEKIEISQNDVLEADVFNPLKHEIRIEKANNLLYINPEAFONLP 120
DB 61 IPKGSFAGDLEKIEISQNDVLEADVFNPLKHEIRIEKANNLLYINPEAFONLP 120
QY 121 SLRYLLISNTGKHLPAVHKIOSLQKVLDDIQQNINIHIVARNSPFGLSFESVILWLSKN 180
DB 121 SLRYLLISNTGKHLPAVHKIOSLQKVLDDIQQNINIHIVARNSPFGLSFESVILWLSKN 180
QY 181 GIEEIHNCFAFNGTQDDELNLSDNNLELNDVDFQASGVPVLDISRTKVHSLPNHGLN 240
DB 181 GIEEIHNCFAFNGTQDDELNLSDNNLELNDVDFQASGVPVLDISRTKVHSLPNHGLN 240
QY 241 LKKLRARSTYRLKLPNLDKFTVLTMEASLTYPHCCAFANLKRQISELHPICNKSILROD 300
DB 241 LKKLRARSTYRLKLPNLDKFTVLTMEASLTYPHCCAFANLKRQISELHPICNKSILROD 300
QY 301 IDDMTOIGDQSVSLIDDEPSYKGSDDMYNEFDYDLCNEVDVDTCPKPDAPNCPEDIM 359
DB 301 VMDITQAGAQSVSLAEDEFSYSGRFDYAEFDYDLCNEVDVDTCPKPDAPNCPEDIM 360
QY 360 GYNILRVLWIFISILAITGNTVLTTSQYKLTVPFLMCNLAFLADLCIGIYLLIASV 419
DB 361 GYNILRVLWIFISILAITGNTVLTTSQYKLTVPFLMCNLAFLADLCIGIYLLIASV 420
QY 420 VDIHTKSOYHNYAIDMOTGAGDAAGFTVFASELSVYTLTATLERWHITTHAMOLECKV 479
DB 421 VDVHTRTLYHNYAIDMOTGAGDAAGFTVFASELSVYTLTATLERWHITTHAMOLECKV 480
QY 480 VQLRHAASVMVLGWTFAFAALPFIIGISSYKMKVSIKLPMDIDSPISQLYVMALLVNLVA 539
DB 481 VQLRHAASVMVLGWTFAFAALPFIIGISSYKMKVSIKLPMDIDSPISQLYVMALLVNLVA 540
QY 540 AFVVICGCTHYLTVRNPTIVSSSDTKIAKRNATLIFTDFLCMAPISEFASISLKVPL 599
DB 541 AFVVICGCTHYLTVRNPTIVSSSDTKIAKRNATLIFTDFLCMAPISEFASISLKVPL 600
QY 600 LITVSKAKILLVLPINSCANPFLYAIFTKNFRDRDFILLSKFGCYEMQAQIYRTTSS 659
DB 601 LITVSKAKILLVLPINSCANPFLYAIFTKNFRDRDFILLSKFGCYEMQAQIYRTTSS 660
QY 660 ATHNFHARKSHCSSAPRVTSYVLPVPLNHSSQN 692
DB 661 TANHSHPRNGHSSSVSRVTNGSSYIILAPLNHLAQN 695

RESULT 3
Q9DGF5 PRELIMINARY; PRT; 696 AA.
AC Q9DGF5;
DT 01-MAR-2001 (T-EMBLrel. 16, Created)
DT 01-MAR-2001 (T-EMBLrel. 16, Last sequence update)
DT 01-JUN-2002 (T-EMBLrel. 21, Last annotation update)
DE Follicle-stimulating hormone receptor precursor.
OS Cynops pyrrhogaster (Japanese common newt).
OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Caudata; Salamandroidae; Salamandridae; Cynops.
OX NCBI_TaxID=8330;
RN [1]
RP SEQUENCE FROM N.A.

TISSUE-TESTIS; PubMed-10944452;
RA Nakayama Y., Yamamoto T., Oba Y., Nagahama Y., Abe S.-I.:
RT "Molecular cloning, functional characterization, and gene expression
of a follicle-stimulating hormone receptor in the testis of newt
Cynops pyrrhogaster.";
RL Biochem. Biophys. Res. Commun. 275:121-128(2000).
DR HSP: P23945; 1XUN.
DR EMBL: AB005587; BAB13501.1; .
DR XREF: P23945; 1XUN.
DR InterPro: IPR000276; GPCR_Rhodopsin.
DR InterPro: IPR001611; LRR.
DR Pfam: PF00560; LRR; 2.
DR Pfam: PF00560; LRR; 1.
DR SMART: SM00013; GPCR_Rhodopsin.
DR PROSITE: PS00237; G-PROTEIN_RECEP_FL_1; UNKNOWN_1.
DR PROSITE: PS0262; G-PROTEIN_RECEP_FL_2; 1.
KW Receptor; Signal.
FT SIGNAL 1 17 POTENTIAL.
FT CHAIN 18 696 POTENTIAL.
SQ SEQUENCE 696 AA; 78633 MW; 179A6FC800B71E57 CRC64;
Query Match 69.8%; Score 2507; DB 13; Length 696;
Best Local Similarity 70.5%; Pred. No. 3.3e-178;
Matches 490; Conservative 84; Mismatches 113; Indels 8; Gaps 5;
OY 1 MALLVSLAFATGCGCHWLCNCSNRVFLCDSKVTETPTDLPNNAIELRVTLKRV 60
DB 1 MSIAIICLLAVGSSPCHP-VCRCLARVFCQESHVQIPDIPRNSTELRVTLKRV 59
OY 61 IPKSGFAGDELEKIEISONDVLEIADVFNPLKHEIRIEKANNLLYINPEAFON 120
DB 60 IPKASGFEDVNEIISONDVLEIADVFNPLKHEIRIEKANNLLYINPEAFON 119
OY 121 SLAVLLISNTGKILPAVHKISQLOKVLVDODNINHYVARNSPAGLSFESVILMLS 180
DB 120 SLKVLISNTGILQVPAVSKIRSFHSYVLLQVDNINRIHUKSFAGLSSESITRLNKN 179
OY 181 GEEITHNCAFNCTOLDLNLSDNNHLEPNDFOGASGPVILDSRTKYVHSLPNGLN 240
DB 180 GEEITHNCAFNCTOLDLNLSDNNHLEPNDFOGASGPVILDSRTKYVHSLPNGLN 239
OY 241 LKKLRARSTYRLKLPDLKPFVTLMEASLTPSHCCAFANLKRQISELHPICNKSILROD 300
DB 240 IKKPRAFNTPKLPDLKPFVTLMEASLTPSHCCAFANLKRQISELHPICNKSILROD 299
OY 301 IDDMTOIGD-ORVSLIDDESPYSGSDM--EPDYP--LCHNEVDVTCSPKPAFNP 355
DB 300 SAEKPEKHLRSNEDLSYSGPSYSLVENCDEFNYILCNEVDHYICFPKPAFNP 359
OY 356 EDIMGNILRVLPISLITATGNTVVLVLTTSQYKLTVPFRLMCLNLAFAOLCIGIYLL 415
DB 360 EDIMGNILRVLPISLITATGNTVVLVLTTSQYKLTVPFRLMCLNLAFAOLCIGIYLL 419
OY 416 LIASVDIHTKSOYHNTAIDMOTGACCAAGFFTFVASELSVYTLTALTLEWHHTTHAMQ 475
DB 420 LIASVDIHTKSOYHNTAIDMOTGACCAAGFFTFVASELSVYTLTALTLEWHHTTHAMQ 479
OY 476 LCKVQLRHAASVYVGLTTPAALAFPIFGISSTMYKVSICLPMIDSPLSQLYNALLY 535
DB 480 LCKVQLRHAASVYVGLTTPAALAFPIFGISSTMYKVSICLPMIDSPLSQLYNALLY 539
OY 536 LNVLPVWICCGTHYLYTVRNPVTSSSDTKAKRMATLITDPLCMAPISFALSAS 595
DB 540 LNVCAPIICACIGIYLYTVRNPVYVNSDTRAKRMALITDPLCMAPISFALSAS 599
OY 596 LKVLPTVSKAKILLVYLPVINSKANPLVAFKTRDFEILLKFGCYEKQAIYRT 655
DB 600 LKVLPTVSKAKILLVYLPVINSKANPLVAFKTRDFEILLKFGCYEKQAIYRT 659
OY 656 ETSSTANTFARKSHCSNAPR--VTNSVYLVPLNR 680
DB 655 ETSSTANTFARKSHCSNAPR--VTNSVYLVPLNR 680

660 ETSSSLNHSNHRNGHYVPAPKYSASHTLVPLNN 694
DB 656 ETSSSLNHSNHRNGHYVPAPKYSASHTLVPLNN 694
RESULT 4
O90MP8
ID O90MP8 PRELIMINARY; PRT: 673 AA.
AC O90MP8
DT 01-DEC-2001 (TRENBLRel. 19, Created)
DT 01-DEC-2001 (TRENBLRel. 19, Last sequence update)
DT 01-JUN-2002 (TRENBLRel. 21, Last annotation update)
DE FSH receptor.
OS FSH RECEPTOR.
GN Podarcis sicula.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Scincomorpha; Lacertoides;
OC Lacertidae; Podarcis.
OX NCBI_TaxID:63484;
RN [1]
RC SEQUENCE FROM N.A.
RX NEDJNEC21459565; PubMed-11574163;
RA Borrelli L., De Stasio B., Parigi G., Filosa S.;
RT "Molecular cloning, sequence and expression of follicle-stimulating
hormone receptor in the lizard Podarcis sicula.";
RL EMBL: AJ292553; CAC82173.1; .
DR InterPro: IPR000276; GPCR_Rhodopsin.
DR InterPro: IPR001611; LRR.
DR Pfam: PF00001; 7tm_1; 1.
DR Pfam: PF00560; LRR; 2.
DR PROSITE: PS00237; G-PROTEIN_RECEP_FL_1; UNKNOWN_1.
DR PROSITE: PS0262; G-PROTEIN_RECEP_FL_2; 1.
KW Receptor.
SQ SEQUENCE 673 AA; 76288 MW; 688994C8B5F67B5 CRC64;
Query Match 55.1%; Score 1979; DB 13; Length 673;
Best Local Similarity 59.5%; Pred. No. 6.3e-139;
Matches 414; Conservative 81; Mismatches 151; Indels 50; Gaps 12;
OY 8 LLALFLGTCGCHWLCNCSNRVFLCDSKVTETPTDLPNNAIELRVTLKRVIP--- 62
DB 11 LLLALLGSGSG--HPTCQPLDNLMTCDKSKVTQVPTQSERHG-----TGIPPHON 59
OY 63 ----KGSFAGFGLEKIEISONDVLEIADVFNPLKHEIRIEKANNLLYINPEAFON 118
DB 60 KHTERAFVGLDEVEKIEISONDALGTIESNVFSLPKLYEIIIEKANHLVTDYAFON 119
OY 119 LPSRYLLISMTGKILPAVHKISQLOKVLVDODNINHYVARNSPAGLSFESVILMLS 178
DB 120 LPSRYLLISMTGKILPAVHKISQLOKVLVDODNINHYVARNSPAGLSFESVILMLS 179
OY 179 KNGTEETHNCAFNCTOLDLNLSDNNHLEPNDFOGASGPVILDSRTKYVHSLPNGL 238
DB 180 KNGTEETHNCAFNCTOLDLNLSDNNHLEPNDFOGASGPVILDSRTKYVHSLPNGL 239
OY 239 ENLKKLRARSTYRLKLPDLKPFVTLMEASLTPSHCCAFANLKRQISELHPICNKSILR 298
DB 240 EKINKLRARSTYRLKLPDLKPFVTLMEASLTPSHCCAFANLKRQISELHPICNKSILR 299
OY 299 ODIDDMTOIGDORVSLIDDESPYSGSDM--MYNEFDY--DLCHNEVDVTCSPKPAFNP 355
DB 300 LQTD-----GTFDLDDEHDYQSLCKEEVEYICFPKPAFNP 338
OY 356 EDIMGNILRVLPISLITATGNTVVLVLTTSQYKLTVPFRLMCLNLAFAOLCIGIYLL 415
DB 339 EDIMGNILRVLPISLITATGNTVVLVLTTSQYKLTVPFRLMCLNLAFAOLCIGIYLL 398
OY 416 LIASVDIHTKSOYHNTAIDMOTGACCAAGFFTFVASELSVYTLTALTLEWHHTTHAMQ 475
DB 399 LIATKDIQTSQYHNTAIDMOTGACCAAGFFTFVASELSVYTLTALTLEWHHTTHAMQ 457
OY 476 LCKVQLRHAASVYVGLTTPAALAFPIFGISSTMYKVSICLPMIDSPLSQLYNALLY 535
DB 475 LCKVQLRHAASVYVGLTTPAALAFPIFGISSTMYKVSICLPMIDSPLSQLYNALLY 535

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Db 458 LNKVRFQAVAPMLVGMFAFTVAIPVQVSSYMKVSLCLPMDIETPPCQAYINFLV 517
Qy 536 LNVAFVWICGCTHYLYVRNPTIVSSSDTKIAKRMATLFTDFLCMAPISFFAISAS 595
Db 518 LNLAFLLIISTYISITVTRTNISSNDTKIAKRMATLFTDFLCMAPISFFAISAS 577
Qy 596 LKPLITVSKAKILLVLYFPINSCAN-PFLYAIFTKNFRDRPFILLSKFCGYEMOQAIYR 654
Db 578 LKPLITVSKAKILLVLYFPINRPTVPVRH--LHOEFFQDFILLSKFCGLCEKQAIYR 635
Qy 655 TETSTAHNPHARKSHCSSAPRTN--SYVLVPLNH 688
Db 636 TETSTVPTSHMKNHGCTPASKASEGPAVALVPLNY 671

RESULT 5
Q16225 PRELIMINARY; PRT; 410 AA.
AC Q16225;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE Follicle-stimulating hormone receptor (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Gromoll J., Ried T., Holtgreve-Grez H., Nieschlag E., Gudermann T.;
RT "Localization of the human FSH receptor to chromosome 2 p21 using a
RT genonic probe comprising exon 10.";
RL J. Mol. Endocrinol. 12:265-271(1994).
DR EMBL; S73526; AAB32225.1;
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHOPOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
DR PROSITE; PSS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER
SQ SEQUENCE 410 AA; 46008 MW; F345E029C16BC792 CRC64;

Query Match 52.98; Score 1901.5; DB 4; Length 410;
Best Local Similarity 89.58; Pred. No. 2e-133;
Matches 367; Conservative 15; Mismatches 25; Indels 3; Gaps 2;

Qy 286 SELHPICNKSILRQDIDMTQIGDQVSLIDD-EPYSGKSDMMYNEFDYDLCNEVDVT 344
Db 1 SELHPICNKSILRQVDYMTQTRQSSLAEDNESSYRGFDYTYEFDYDLCNEVDVT 60
Qy 345 CSPKPAFNPCEIDMGNYILRVLIWFTSLAIGNTVTLVLTYSQYKLVPRFLMCLNLA 404
Db 61 CSPKPAFNPCEIDMGNYILRVLIWFTSLAIGNTVTLVLTYSQYKLVPRFLMCLNLA 120
Qy 405 FADLCIGYLLLTASVDIHTKSOYHNYAIDMOTGAGCDAAGFTVFASLSVYTLTAITL 464
Db 121 FADLCIGYLLLTASVDIHTKSOYHNYAIDMOTGAGCDAAGFTVFASLSVYTLTAITL 180
Qy 465 ERWHTITHAMOLECKVQLRHAASVWVLGWTFAFAAALFPIFGISSYMKVSIPLMDIDSP 524
Db 181 ERWHTITHAMOLECKVQLRHAASVWVNGWIFAFAAALFPIFGISSYMKVSIPLMDIDSP 240
Qy 525 LSQLYVMALLVNLVAFVWICGCTHYLYVRNPTIVSSSDTKIAKRMATLFTDFLCM 584
Db 241 LSQLYVMALLVNLVAFVWICGCTHYLYVRNPTIVSSSDTKIAKRMATLFTDFLCM 300
Qy 585 APISFFAISASLKVPLITVSKAKILLVLYFPINSCANPFLYAIFTKNFRDRPFILLSKFG 644
Db 301 APISFFAISASLKVPLITVSKAKILLVLYFPINSCANPFLYAIFTKNFRDRPFILLSKFG 360
Qy 645 CYENQAIYRTETSSATHNFHARKSHCSSAPRTV--NSYVLVPLNHSSQN 692
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Db 361 CYENQAIYRTETSSATHNFHARKSHCSSAPRTVSGTSLVPLSHLAQN 410

RESULT 6
Q98T84 PRELIMINARY; PRT; 662 AA.
AC Q98T84;
DT 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
DE Follicle-stimulating hormone receptor precursor.
OS Ictalurus punctatus (Channel catfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Siluriformes;
OC Ictaluridae; Ictalurus.
OX NCBI_TaxID=7998;
RN [1]
RP SEQUENCE FROM N.A.
RA Kumar R.S., Ijiri S., Trant J.M.;
RT "Molecular Biology of Channel Catfish Gonadotropin Receptors: 2. cDNA
RT Cloning, Functional Expression, and Seasonal Gene Expression of the
RT Follicle-Stimulating Hormone Receptor.";
RL Biol. Reprod. 0:0-0(2001).
DR EMBL; AF285182; AAK16067.1;
DR HSSP; P23945; 1XUN.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR InterPro; IPR001611; LRR.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHOPOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
DR PROSITE; PSS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor; Signal.
FT SIGNAL
SQ SEQUENCE 662 AA; 74846 MW; DC179F07A2CADEED CRC64;

Query Match 51.38; Score 1844; DB 13; Length 662;
Best Local Similarity 54.28; Pred. No. 6.9e-129;
Matches 361; Conservative 110; Mismatches 163; Indels 32; Gaps 6;

Qy 1 MALLVSLLAFLGTGS-GCHHWLCHCSNRVFLCDSKVTEIPTDLPNATLRFVLTCLR 59
Db 2 MCFILSWLMHAGMCMCLGSAVLANTGTSFCLGSKGVHOMPHIPKNTYVEIKLRIL 61
Qy 60 VIPKGFAGFDLEKIEISONDVLEADVFNLSPLKHEIRIEKANNLLYINPEAFONL 119
Db 62 MLPSSAMSSLDLKLRLVSENGVLQRIEAYAFANLTKEBITTTKSNLVCMDRHTFWGL 121
Qy 120 PSLRYLLISNTGKHLPAVHKIOSLO-KVLLDQDNIHINIVARNSPMGLSFESVI-LWL 177
Db 122 PKLRYLTISNTGTLVLPDFSKVSAAFELFDLEDNMHIEVIPSNAPAGTSGITELRL 181
Qy 178 SKNGIEIHCNFAEQGLDELNLSDNNLELNDVFOGASGPVILDSRTKVSLSLPHNG 237
Db 182 TKNGIEVDNENAGTKIEKFLMGQQLKRIINYAFAGAGPLVLDISRTASSLPENM 241
Qy 238 LEMKLRARSTYRLKPLNLDKFTVLMESALYPSHCCAFANLKRIOISELHPTCNKSL 297
Db 242 LRRLKLLIATSVYSLRWLPNLEIFTELTQANLTYPSHCCAFKFNKSEKNRLCNDSTI 301
Qy 298 RODIDDWTQIGDQVSLIDDEPSYKGSMDMYNEFDYDLCNEVDVTCSKPAFNPCE 357
Db 302 R-----NOEP-----YFEEHCKDVIEVCYPEPDAFNPCE 333
Qy 358 IMGNYILRVLIWFTSLAIGNTVTLVLTYSQYKLVPRFLMCLNLAFAADLCIGYLLLI 417
Db 334 IMGFTLRVLNFIISVLAVLGNFTVLLVLSSTKLTVPFLMCHLAFADFCMGLYLLII 393
Qy 418 ASVDIHTKSOYHNYAIDMOTGAGCDAAGFTVFASLSVYTLTAITLERWHTITHAMOLE 477
Db 394 GSVDLQTRSHYNYGIEWQTGVCGTAGFTLVFASLSVYTLTAITLERWHTITHAMRLE 453
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DR EMBL: X84755; CA59234.1; JOINED.
DR EMBL: X84756; CA59234.1; JOINED.
DR EMBL: X84757; CA59234.1; JOINED.
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DR EMBL: X84759; CA59234.1; JOINED.
DR EMBL: X84760; CA59234.1; JOINED.
DR EMBL: X84761; CA59234.1; JOINED.
DR EMBL: X84762; CA59234.1; JOINED.
DR EMBL: X84763; CA59234.1; JOINED.
DR EMBL: AP082076; AAC98291.1; -.
DR HSP: P22888; 1LUT.
DR InterPro: IPR000276; GPCR_Rhodopsin.
DR InterPro: IPR001611; LRR.
DR InterPro: IPR000372; LRR_Nterm.
DR Pfam: PF00001; 7tm_1; 1.
DR Pfam: PF00560; LRR; 3.
DR SMART: SMO0013; LRRNT; 1.
DR PROSITE: PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
DR PROSITE: PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
SQ
SEQUENCE 701 AA: 78757 MW: 659FF5BABC409DA CRC64;
Query Match 49.4%; Score 1776; DB 4; Length 701;
Best Local Similarity 55.4%; Pred. No. 8.5e-124;
Matches 349; Conservative 107; Mismatches 148; Indels 26; Gaps 6;
QY 55 LTKL-----RVIPKGFAGFDGKLEKIEISONDVLEYEADVFNLPKLHEIRKANN 107
DB 53 LTRSLAYLPVKVPSQAFGLNEVKEISQISDLERTEANAFNLNLSELITQTKN 112
QY 108 LYTNPAPQNLPSGLYLLSNGLKHPVKHI-QSLQKVLDDIQNNIHIVARNSP 166
DB 113 LTRPQNPQNLPSGLYLLSNGLKHPVKHI-QSLQKVLDDIQNNIHIVARNSP 166
QY 167 GUSPEVILNLSKNGTEINGCAWCTQDELNSDNNLELPLNDVPOGASCPVLDIS 226
DB 173 GNNESYTLKLYNGFEVOSHAPNTTSLKLNKLVLEKHGAPGACGPKTLDIS 232
QY 227 RTKVSLNPHRGLNKLARSTYRLKPLNDRFVTLMEASLYTPSHCCAFANLKRQIS 286
DB 233 STKQALPSYGLESIQRLIATSYSLKPLPSREFVYNLEATLYPSHCCAFNRL- 287
QY 287 ELRPICKNSILRODDMTQIGDQSVSLDDPSYK---GSDMMYNFEVDYLCNEVDV 343
DB 288 ---PTKQNPFSHSISNFKQCESTYRVKSNKLYSSMLAESLSDWDYEGCLPKTP- 343
QY 344 TCSPPDAPNCPEDINGTNIHLVLIWPIISLAITGNTVLYLTTSQTKLTPVPLMNL 403
DB 344 RCPEDPAPNCPEDINGTNIHLVLIWPIISLAITGNTVLYLTTSQTKLTPVPLMNL 403
QY 404 AFADLCIGIYLLIASVDIHTKSOYHNYADMTGACDMAAGFTVFASELSVYTLTAT 463
DB 404 SFADPCNGLYLLIASVDQTKGYNHAIQDWTGSGCSTAGFTVFASELSVYTLTAT 463
QY 464 LERHHTITHAMOLECKVOLRHAASVYVGLWTFAPFAALPPIFGISYMKVSYCLPMDIS 523
DB 464 LERHHTITHAMOLECKVOLRHAASVYVGLWTFAPFAALPPIFGISYMKVSYCLPMDIS 523
QY 524 PLSQLYVALLVNLVAFVYVCCYTHIYLTVRNPTIVSSSSOTKIARMAATLIFTDPLC 583
DB 524 TISQYITLILVNLVAFVYVCCYTHIYLTVRNPTIVSSSSOTKIARMAATLIFTDPLC 583
QY 584 MAPISPPATSAKLVPLTVTSKAKTLLVPLTINSCANPFLKATPKRPPDPTLLSKP 643
DB 584 MAPISPPATSAKLVPLTVTSKAKTLLVPLTINSCANPFLKATPKRPPDPTLLSKP 643
QY 644 GYENQAOIYRTSSANTNPHARKSHCSS 673
DB 644 GCKKRAELYRK-----DPSATTSCKN 667
RESULT 11
Q9DCC6
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QY 611 VLFYFINSKANFLYAIETKFNRRDFFILLSKFGCYEMQAIYRTETSS 659
DB 622 VLFYFINSKSNFLYAFYFTRNRDFFLLAAREGLFKTRAIYRTETSS 670

RESULT 12
Q9BGN4 PRELIMINARY: PRT: 763 AA.
AC Q9BGN4:
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Thyrotropin receptor.
OS Fells silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Fells.
OX NCBI_TaxID=9685;
RN
RP SEQUENCE FROM N.A.
RA Nguyen L.Q., Karamanoglu Arseven O., Gerber H., Stein B.S.,
RA Jameson J.L., Kopp P.;
RT "Cloning of the cat thyrotropin receptor and evidence against an
RT autoimmune etiology of feline hyperthyroidism.";
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF218264; AAK00133.1;
DR HSSP; P16473; 1XUM.
DR InterPro: IPR00276; GPCR_Rhodopsn.
DR InterPro: IPR001611; LRR.
DR Pfam; PF00001; 7tm_1; 1.
DR Pfam; PF00360; LRR; 1.
DR PRINTS; PR00237; GPCR_Rhodopsn.
DR PROSITE; PS00237; G_PROTEIN_RECEP_FL_1; UNKNOWN_1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_FL_2; 1.
DR Receptor.
SQ SEQUENCE 763 AA; 86588 MW; 937F60A140487D60 CRC64;

Query Match 46.6%; Score 1676; DB 6; Length 763;
Best Local Similarity 46.9%; Pred. No. 2.6e-116;
Matches 352; Conservative 113; Mismatches 213; Indels 72; Gaps 12;

QY 4 LLSVLLAFGLTGGCHHMLCHCSN----RVFLQDSKVTEIPDLPNRAIELRFLVTKLR 59
DB 11 LLSLPSRLSG-KRGKCPSPCECHQEDDFRV-TCKD--IHRIPS-LPPSTQTLKFIEHLK 65
QY 60 VIPKGSFAGDGLKLEIEISQNDVLEIADVFNLPKLHEIRKANNLLYNPEAFQNL 119
DB 66 TIPSRAFNLPNIRIYLSIDATLQRLSHSFYNLSKMTHEIRNTRSLTYIDPGALKEL 125
QY 120 PSRLYLISNTGKIKHLPVAVHKIQSLQK-VLLDIDQNNIHIIVARNFMSGLSPESVILWS 178
DB 126 PLKLFGLIGNTGLGVFDLTQVYSTDFVILEITDNPYMTSIPANAFQGLCNETLTKLY 185
QY 179 KNGIEIHNCFAFGDLEKIEISQNDVLEIADVFNLPKLHEIRKANNLLYNPEAFQNL 237
DB 186 NNGFTSIQHAFTNGTKLDAVILNKNKYLTATDQAFGVYSGTLLDVSYTSVTLPSKG 245
QY 238 LNLKILRARSYRLKLNLDKLVFLMEASLTYPSCHCACAFANLKRQISELHP-ICNKSI 296
DB 246 LEHLKELIARNTWTLKPLTUSFLTLRADLSYPSHCACAFNKKIRGILFESFMCNDS 305
QY 297 LRQ-----DIDMTQIGDQVSLDDPSYCKGSDMW----- 329
DB 306 IRSLRQKSVNALNGPFDQEEYELGDSHAGYKDNKSFQDTRSNHYVFFEQDILGF 365
QY 330 -----NEFDYDLCEVNDVTCSPKPAFNPCEDIMGYNLRVLIWFISI 373
DB 366 GQELKNPQEBTLOAFDSHYDYTVCGGNEDMVCPTKPSDEFNCPEDIMGYNLRVLIWFISI 425
QY 374 LAITGNTVVLVLTTSQYKLTVPFLMCLNLAFLADLCIGYLLLIASVDHTSKQYINYAI 433
DB 426 LALLGNVFLVLIITLTHYKLTVPFLMCLNLAFLADLCIGYLLLIASVDHTSKQYINYAI 485
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QY 434 DMQTGAGCDAGFTTFVASELSVYTLTALTILRWHTITHAMOLECKVQLRHAASVVLGW 493
DB 486 DMQTGPGCNAAGFTTFVASELSVYTLTALTILRWHTITFAMLRDKMRLRHAYAVMGW 545
QY 494 TFAFAAALPPIFGISSYKVSICLPMDDSPLSQLYVMALLVNLVAFVVGCGYTHIYL 553
DB 546 VCCFLALLPLVGISSYKVSICLPMDDTPTLALAYIILVLLNINVAFTIVGSCYKVIYI 605
QY 554 TVRNPTIVSSSDTKIAKRMATLIFTDFLCMAPISEFAISASLKVPILTVSKAKILLVLP 613
DB 606 TVRNFOYNTGDKDTIAKRNVLIFTDFCMAPISFYALSALMKRPLITVTNSKILLVLP 665
QY 614 YPINSKANFLYAIETKFNRRDFFILLSKFGCYEMQAIYR-----TETSSATH 662
DB 666 YPINSKANFLYAIETKFNRRDFFILLSKFGCYEMQAIYR-----TETSSATH 662
QY 663 NFHARKSHCCSAPRVNYSVPLNHSN 692
DB 726 NMR-----QSLPNMODDYELLENSHLTPN 749

RESULT 13
Q9BG56 PRELIMINARY: PRT: 764 AA.
AC Q9BG56:
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Thyroid-stimulating hormone receptor.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RA Melen L.B., McNamara E.M., Hennen G.P., Igout A.;
RT "Porcine thyroid stimulating hormone receptor (TSHR) mRNA.";
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF338249; AAK09510.1;
DR HSSP; P16473; 1XUM.
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR InterPro: IPR001611; LRR.
DR Pfam; PF00001; 7tm_1; 1.
DR Pfam; PF00360; LRR; 1.
DR PRINTS; PR00237; GPCR_Rhodopsn.
DR PROSITE; PS00237; G_PROTEIN_RECEP_FL_1; UNKNOWN_1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_FL_2; 1.
DR Receptor.
SQ SEQUENCE 764 AA; 86643 MW; 1E8E8BDB617E7052 CRC64;

Query Match 46.5%; Score 1670.5; DB 6; Length 764;
Best Local Similarity 46.8%; Pred. No. 6.7e-116;
Matches 352; Conservative 115; Mismatches 208; Indels 77; Gaps 14;

QY 3 LLSVLLAFGLTGGCHHMLCHCSN----RVFLQDSKVTEIPDLPNRAIELRFLV 55
DB 6 LLSVLLAFGLTGGCHHMLCHCSN----RVFLQDSKVTEIPDLPNRAIELRFLV 61
QY 56 TKLRVIPKGSFAGDLEKIEISQNDVLEIADVFNLPKLHEIRKANNLLYNPEA 115
DB 62 THLKTIPSRAFNLPNIRIYLSIDATLQRLSHSFYNLSKMTHEIRNTRSLTYINPGA 121
QY 116 FQNLPSRLYLISNTGKIKHLPVAVHKIQSLQK-VLLDIDQNNIHIIVARNFMSGLSPESVI 174
DB 122 LKDLPLKLFGLIGNTGLGVFDLTQVYSTDFVILEITDNPYMTSIPANAFQGLCNETLT 181
QY 175 LNLKILRARSYRLKLNLDKLVFLMEASLTYPSCHCACAFANLKRQISELHP-ICNKSI 233
DB 182 LKLNNGFTSIQHAFTNGTKLDAVILNKNKYLTATDQAFGVYSGTLLDVSYTSVTL 241
QY 234 PNHGLENLKILRARSYRLKLNLDKLVFLMEASLTYPSCHCACAFANLKRQISELHP-IC 292
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[illegible]

	Matches	330;	Conservative	99;	Mismatches	118;	Indels	47;	Gaps	8;
QY	102	IEKANNLLYINPEAFONLPSRLYLTISNTGKHLPAVHKIQSLQ-KVLLDIOODNINIHV	160							
Db	2	ILNTRNLLHIEDGAPNLPRLAYLSICNTGIEFFDLTOIFSEAHFILEICDNLHMTYI	61							
QY	161	ARNSPFGLSFESVILWLSKNGIEEIHNCAPNGTQDDELNLSNNNLEELPNDVFCASGP	220							
Db	62	PONAFQGMNESITLKYKNGFEDIHSHAFNGTKLNQILKDNKLNRRTHNDALRGATGP	121							
QY	221	VILDISRTKVVHSLPNHGLNKLKRLARSTYRLKLPNLDKFVTLMEASLTYSCHCAPAN	280							
Db	122	DVLDISSTALESLPSYGLEAIOVLNAESSYSLKRLPPLDKFSLSLEAVLTYPSSHCCAFRN	181							
QY	281	LK--RQISELHPICN-----KSLRODIDDM-----TOIGDQVSLID-DEPSYKGK	324							
Db	182	LATERKONMSLIFDNFSKCESIVRTTSEIFYRDASFNTSLGQRKSTRTHEQPKI---	238							
QY	325	SDMYNEFDYDLCNEVVDVTCSPKPDAPNCPEDIMGNILRVLIWIFISILAITGNTVLV	384							
Db	239	-----LTCPEPDAPNCPEDILGYSFLRVLIWIFINILAGNLIVLL	280							
QY	385	VLTTSQYKLTVPRLMCLNAPADLCIGIYLLIASVDIHTKSOYHNYAIDMOTGAGCDA	444							
Db	281	VLITSHYKLMVPRLMCLNLFADFCMGLYLVLIASVDAQTSGQYVNHAIYWTGSGCSTA	340							
QY	445	GFETVFASELSVYTLTATLTERWHITTHAMOLECKVOLRHAASVMVLGWTFAFAALFPI	504							
Db	341	GFETVFASELSVYTLTATLTERWHITTYAMQDLRQLRHLRAVLIMLGGWVFSILITAVLPL	400							
QY	505	FGISSYMKVSIKLPMDIDSPLSQLYVMALLVLNLAFAVVICGYTHIYLTVRNPTIVSS	564							
Db	401	LGVSVMKVSIKLPMDIETGLSQAYILLILVLNNAFAVVICACYIKIYIYAVQNPELYAN	460							
QY	565	SDTKIAKRMATLIFTDFLCMAISFPAISASLKVPLITVSKAKILLVLFPINSCANPFL	624							
Db	461	KDTKIAKRMATLIFTDFTCMAISFPAISAFKVPPLITVTSKILLVLFPVNSCANPFL	520							
QY	625	YAIFTKRRDRFFILLSKFCGYEMOAOIYRTETSSATHNFARKSHC-----SSAP	675							
Db	521	YAIFTKAFORDFLLMSKLGCCCKSRAEICR-----MNYFSAYTSNCKNGSSAP	568							

Search completed: June 16, 2003, 13:35:54
 Job time : 47.5347 secs

GenCore version 5.1.6
Copyright (C) 1993 - 2003 CompuGen Ltd.
OK protein - protein search, using sw model
Run on: June 16, 2003, 11:37:21 : Search time 46.4155 Seconds
(without alignments)
1937.804 Million cell updates/sec.
Title: US-09-877-804-7
Perfect score: 3516
Sequence: 1 CHRMCHCSNVPFLCQSKV.....SAPRYTNSVLYVPLNHSO 675
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 908470 seqs, 133250620 residues 908470
Total number of hits satisfying chosen parameters:
Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3511	99.9	692	11	Rat testicular lut
2	3511	99.9	692	11	Rat testicular lut
3	3454	98.2	695	14	N-terminal of LH r
4	3445	98.0	695	14	N-terminal of LH r
5	3441	97.9	696	14	N-terminal of LH r
6	3268.5	93.0	696	14	N-terminal of LH r
7	3194.5	90.9	696	14	N-terminal of LH r
8	3169.5	90.1	695	14	FSH receptor. Hom
9	3169.5	90.1	695	18	FSH receptor. Hom
10	3164.5	90.0	695	13	FSHR. Homo sapien

11	3151.5	89.6	634	14	AA193520	N-terminal of LH r
12	3109.5	88.4	696	14	AA193513	N-terminal of LH r
13	3109.5	88.4	696	14	AA193521	N-terminal of LH r
14	3036.5	86.4	620	14	AA193522	N-terminal of LH r
15	2941	86.7	889	14	AA193509	N-terminal of LH r
16	2842	85.7	703	14	AA193505	N-terminal of LH r
17	2831	84.5	703	14	AA193514	N-terminal of LH r
18	2632.5	74.9	690	14	AA193514	N-terminal of LH r
19	2552.5	72.6	699	14	AA193515	N-terminal of LH r
20	2474	70.4	692	14	AA193503	N-terminal of LH r
21	2354	67.0	697	14	AA193508	N-terminal of LH r
22	2276	64.7	706	14	AA193504	N-terminal of LH r
23	2189.5	62.3	699	14	AA193517	N-terminal of LH r
24	2075.5	59.0	693	14	AA193510	N-terminal of LH r
25	2043.5	58.1	699	14	AA193512	N-terminal of LH r
26	1941	55.2	700	14	AA193516	N-terminal of LH r
27	1940	55.2	700	14	AA193511	N-terminal of LH r
28	1901.5	54.1	410	22	AA193518	Human follicle sti
29	1816	51.6	650	14	AA193518	N-terminal of LH r
30	1797	51.1	700	11	AA193518	Rat ovarian lutein
31	1787	51.1	702	14	AA193518	N-terminal of LH r
32	1787	51.1	702	14	AA193518	N-terminal of LH r
33	1783	51.0	705	14	AA193518	N-terminal of LH r
34	1778	50.6	699	13	AA193518	Sequence of luteal
35	1756.5	50.0	685	12	AA193518	Human testis
36	1690.5	48.1	679	19	AA193518	Human testis
37	1650.5	46.9	714	12	AA193518	Human testis
38	1648	46.9	764	12	AA193518	Human TSH Receptor
39	1642.5	46.7	764	12	AA193518	Human thyroid sti
40	1641.5	46.7	764	12	AA193518	Human thyroid sti
41	1638.5	46.6	764	22	AA193518	Non-endogenous hum
42	1638.5	46.6	764	23	AA193518	Mouse thyroid sti
43	1638	46.6	756	12	AA193518	Human TSH Receptor
44	1637.5	46.6	764	12	AA193518	Human thyroid sti
45	1637.5	46.6	764	22	AA193518	Non-endogenous hum

ALIGNMENTS

RESULT 1
AA193518
ID AA193518 standard; protein; 692 AA.
AC AA193518
DT 26-FEB-1991 (first entry)
DE Rat testicular luteinising hormone/choriogonadotropin receptor.
DE LH/CG receptor: FSH receptor; TSH receptor; fertility; breast cancer;
DE prostate cancer; thyroid cancer; osteoporosis; Graves disease;
DE polycystic ovarian disease; vasomotor instability.
OS Rattus rattus.
PN WO3013643-A.
PD 15-NOV-1990.
PF 04-MAY-1990; 90WO-US02488.
PR 05-MAY-1989; 89US-0347683.
PR (GETH) GENENTECH INC.
PR Mikolics K, McFarland KC, Segaloff DL, Seeburg PH;
PR WPI, 1990-361478/48.
PR N-PSUB; AAQ06634.
PR Pharmaceutical compsn. contg. hormone receptor mol. - used for
PR treating fertility, breast-and prostate-cancer and osteoporosis.

PT etc.
XX Disclosure; fig 6; 78pp; English.
XX
CC This rat testicular follicle-stimulating hormone (FSH) receptor.
CC This receptor is useful in a pharmaceutical compen. for treating
CC e.g. breast-, prostate- and thyroid cancer, fertility, osteopor-
CC osis, vasomotor instability and polycystic ovarian disease.
CC LH/CG- or TSH-receptors can also be used, to treat e.g. Graves
CC disease. Abs can be used to inhibit receptor binding and for imag-
CC ing and therapy... See also AAR08015-23, AAR08035-36 and AAR06633.
XX
SQ Sequence 692 AA;
Query Match 99.9%; Score 3513; DB 11; Length 692;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 674; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 CHWLCHCSNRVFLCQDSKVTEIPTDLPRAIELRFLVTLKLRVLPKGSFAGFGDLEKIEI 60
DB 18 CHWLCHCSNRVFLCQDSKVTEIPTDLPRAIELRFLVTLKLRVLPKGSFAGFGDLEKIEI 77
QY 61 SONDVLEIADVFSLPKLHEIRIEKANNLLINPEAFONLPSRLYLLISNTGIKHLPA 120
DB 78 SONDVLEIADVFSLPKLHEIRIEKANNLLINPEAFONLPSRLYLLISNTGIKHLPA 137
QY 121 VHRIQSLQKVLDDQDNIHIVARNSEFGLSFESVTLWLSKNGIEIHNCAFNGLTOLDE 180
DB 138 VHRIQSLQKVLDDQDNIHIVARNSEFGLSFESVTLWLSKNGIEIHNCAFNGLTOLDE 197
QY 181 LNLSDNNLEELPNDVFGAGSGPVILDISRTKVHSLPNHGLENLKLRARSTYRLKKLPN 240
DB 198 LNLSDNNLEELPNDVFGAGSGPVILDISRTKVHSLPNHGLENLKLRARSTYRLKKLPN 257
QY 241 LDRFVTLMEASLYPSHCCAFANLKRQISELHPICNKSILRQIDDMTQIGDQVSLIDD 300
DB 258 LDRFVTLMEASLYPSHCCAFANLKRQISELHPICNKSILRQIDDMTQIGDQVSLIDD 317
QY 301 EPSYKGSDMYNEFDYDLGNEVDVTCSPKPAFNPCEIDIMGNILRVLIWFISILAIT 360
DB 318 EPSYKGSDMYNEFDYDLGNEVDVTCSPKPAFNPCEIDIMGNILRVLIWFISILAIT 377
QY 361 GNTTVLVLTSTQYKLTVPRLMCLNLAFAADLCIGIYLLIASVDIHTKSOYHNYAIDWQT 420
DB 378 GNTTVLVLTSTQYKLTVPRLMCLNLAFAADLCIGIYLLIASVDIHTKSOYHNYAIDWQT 437
QY 421 GAGCDAAGFTVFASLSVYTLTAITLERWHTITHAMOLECKVOLRHAASVWVLGWTFAF 480
DB 438 GAGCDAAGFTVFASLSVYTLTAITLERWHTITHAMOLECKVOLRHAASVWVLGWTFAF 497
QY 481 AAALFTPIFGISSYMKVSIKLPMDIDSPLSQLYVALLVNLVAFVVICGCTHYLYTVRN 540
DB 498 AAALFTPIFGISSYMKVSIKLPMDIDSPLSQLYVALLVNLVAFVVICGCTHYLYTVRN 557
QY 541 PTIVSSSDTKIAKRWATLIFTDFLCMAPIISFAISASLKVPILITVSKAKILLVLPYIN 600
DB 558 PTIVSSSDTKIAKRWATLIFTDFLCMAPIISFAISASLKVPILITVSKAKILLVLPYIN 617
QY 601 SCANPFLYALFTKNERDRFPILLKFCGYEQMAQIYETETSSATHNPHARKSHCSSAPRV 660
DB 618 SCANPFLYALFTKNERDRFPILLKFCGYEQMAQIYETETSSATHNPHARKSHCSSAPRV 677
QY 661 TNSVLYVPLNHSNQN 675
DB 678 TNSVLYVPLNHSNQN 692
RESULT 2
AAR30506
ID AAR30506 standard; protein; 695 AA.
XX
AC AAR30506;
XX

10-MAY-1993 (first entry)
DE N-terminal of LH receptor/FSH receptor chimaera #15.
XX
KW Follicle stimulating hormone receptor; luteinising hormone receptor;
KW human chorionic gonadotrophin; glycoprotein hormone receptor;
KW chimaera; chimera.
XX
OS Chimaeric; homo sapiens.
XX
PN WO9222667-A.
XX
PD 23-DEC-1992.
XX
PF 12-JUN-1992; 92WO-US04987.
XX
PR 14-JUN-1991; 91US-0715911.
XX
PA (UYNE-) UNIV NEW JERSEY.
PI Bernard M, Moyle WR, Myers R;
XX
XX WPI: 1993-018150/02.
XX
XX Glyco:protein hormone receptor analogues - having binding
XX affinity to human chorionic gonadotrophin, luteinising and
XX follicle stimulating hormones, useful in bio:immunoassays
XX
XX Examples; Fig 12: 103pp; English.
XX
XX This sequence represents the N-terminal of a novel protein having a
XX binding affinity for human chorionic gonadotrophin (hCG), luteinising
XX hormone (LH), and follicle stimulating hormone (FSH). The protein
XX itself is a chimaera having residues from both the FSH receptor,
XX and LH receptor. The receptor analogues can be used in bio:immunoassays
XX for the simultaneous detection of both LH (or hCG) and FSH as
XX well as their ratio of biological activities. The analogues can also
XX be used for raising, purifying and assaying antibodies to the
XX analogues. Coding sequence for the chimaera was produced by two step
XX PCR.
SQ Sequence 695 AA;
Query Match 99.9%; Score 3511; DB 14; Length 695;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 674; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 CHWLCHCSNRVFLCQDSKVTEIPTDLPRAIELRFLVTLKLRVLPKGSFAGFGDLEKIEI 60
DB 18 CHWLCHCSNRVFLCQDSKVTEIPTDLPRAIELRFLVTLKLRVLPKGSFAGFGDLEKIEI 77
QY 61 SONDVLEIADVFSLPKLHEIRIEKANNLLINPEAFONLPSRLYLLISNTGIKHLPA 120
DB 78 SONDVLEIADVFSLPKLHEIRIEKANNLLINPEAFONLPSRLYLLISNTGIKHLPA 137
QY 121 VHRIQSLQKVLDDQDNIHIVARNSEFGLSFESVTLWLSKNGIEIHNCAFNGLTOLDE 180
DB 138 VHRIQSLQKVLDDQDNIHIVARNSEFGLSFESVTLWLSKNGIEIHNCAFNGLTOLDE 197
QY 181 LNLSDNNLEELPNDVFGAGSGPVILDISRTKVHSLPNHGLENLKLRARSTYRLKKLPN 240
DB 198 LNLSDNNLEELPNDVFGAGSGPVILDISRTKVHSLPNHGLENLKLRARSTYRLKKLPN 257
QY 241 LDRFVTLMEASLYPSHCCAFANLKRQISELHPICNKSILRQIDDMTQIGDQVSLIDD 300
DB 258 LDRFVTLMEASLYPSHCCAFANLKRQISELHPICNKSILRQIDDMTQIGDQVSLIDD 317
QY 301 EPSYKGSDMYNEFDYDLGNEVDVTCSPKPAFNPCEIDIMGNILRVLIWFISILAIT 360
DB 318 EPSYKGSDMYNEFDYDLGNEVDVTCSPKPAFNPCEIDIMGNILRVLIWFISILAIT 377
QY 361 GNTTVLVLTSTQYKLTVPRLMCLNLAFAADLCIGIYLLIASVDIHTKSOYHNYAIDWQT 420
DB 378 GNTTVLVLTSTQYKLTVPRLMCLNLAFAADLCIGIYLLIASVDIHTKSOYHNYAIDWQT 437
QY 421 GAGCDAAGFTVFASLSVYTLTAITLERWHTITHAMOLECKVOLRHAASVWVLGWTFAF 480
DB 438 GAGCDAAGFTVFASLSVYTLTAITLERWHTITHAMOLECKVOLRHAASVWVLGWTFAF 497
QY 481 AAALFTPIFGISSYMKVSIKLPMDIDSPLSQLYVALLVNLVAFVVICGCTHYLYTVRN 540
DB 498 AAALFTPIFGISSYMKVSIKLPMDIDSPLSQLYVALLVNLVAFVVICGCTHYLYTVRN 557
QY 541 PTIVSSSDTKIAKRWATLIFTDFLCMAPIISFAISASLKVPILITVSKAKILLVLPYIN 600
DB 558 PTIVSSSDTKIAKRWATLIFTDFLCMAPIISFAISASLKVPILITVSKAKILLVLPYIN 617
QY 601 SCANPFLYALFTKNERDRFPILLKFCGYEQMAQIYETETSSATHNPHARKSHCSSAPRV 660
DB 618 SCANPFLYALFTKNERDRFPILLKFCGYEQMAQIYETETSSATHNPHARKSHCSSAPRV 677
QY 661 TNSVLYVPLNHSNQN 675
DB 678 TNSVLYVPLNHSNQN 692

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Db 378 GNTVLVLTTSQKLTVPRLMCLNADLCIGYLLIASVDIHTKSOYHNYAIDMOT 437
Oy 421 GAGDAAGFFTVFASLSVYTLTAITLERHHTITHAMQLECKVOLRHAASVWVLTGTFAP 480
Db 438 GAGDAAGFFTVFASLSVYTLTAITLERHHTITHAMQLECKVOLRHAASVWVLTGTFAP 497
Oy 481 AALPPIFGISSYMKVSYICLPMIDISPLQYVWALLVLAFFVYICGCTHYILTVRN 540
Db 498 AALPPIFGISSYMKVSYICLPMIDISPLQYVWALLVLAFFVYICGCTHYILTVRN 557
Oy 541 PTIVSSSDTKIARMAATLIFTDFLCMAPISFPAISASLKVPILTYSKAKILLVLPYIN 600
Db 558 PTIVSSSDTKIARMAATLIFTDFLCMAPISFPAISASLKVPILTYSKAKILLVLPYIN 617
Oy 601 SCANPFLYAIPTFNPRDFPILLSKFCYEMQAOIYRTTSSATHNPHARKSHCSSAPRV 660
Db 618 SCANPFLYAIPTFNPRDFPILLSKFCYEMQAOIYRTTSSATHNPHARKSHCSSAPRV 677
Oy 661 TNSYVLPVPLNHSOON 675
Db 678 TNSYVLPVPLNHSOON 692

RESULT 3
AAR30524 standard; protein; 695 AA.
XX
XX
XX
Oy 10-MAY-1993 (first entry)
XX
DE N-terminal of LH receptor/FSH receptor chimaera #33.
XX
KW Follicle stimulating hormone receptor; luteinising hormone receptor;
KW human chorionic gonadotrophin; glycoprotein hormone receptor;
XX chimaera; chimera.
XX
OS Chimaeric; homo sapiens.
XX
PN MO9222667-A.
XX
PD 23-DEC-1992.
XX
PR 12-JUN-1992; 92WO-US04987.
XX
PR 14-JUN-1991; 91US-0715911.
XX
PA (UTNE-) UNIV NEW JERSEY.
XX
PI Bernard M. Moyle MR, Myers R;
XX
DR MPI; 1993-018150/02.
XX
PT Glyco:protein hormone receptor analogues - having binding
PT affinity to human chorionic gonadotrophin, luteinising and
PT follicle stimulating hormones, useful in bio:immunoassays
XX
XX
XX Examples; Fig 12; 103pp; English.
XX
CC This sequence represents the N-terminal of a novel protein having a
CC binding affinity to human chorionic gonadotrophin (hCG), luteinising
CC hormone (LH), and follicle stimulating hormone (FSH). The protein
CC itself is a chimaera having residues from both the FSH receptor
CC and LH receptor. The receptor analogues can be used in bio:immunoassays
CC for the simultaneous detection of both LH (or hCG) and FSH as
CC well as their ratio of biological activities. The analogues can also
CC be used for raising, purifying and assaying antibodies to the
CC analogues. Coding sequence for the chimaera was produced by two step
CC PCR.
XX
XX Sequence 695 AA;
XX
XX
XX Query Match 98.21; Score 3454; DB 14; Length 695;

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Best Local Similarity 98.18; Pred. No. 0;
Matches 662; Conservative 6; Mismatches 7; Indels 0; Gaps 0;
Oy 1 CHHMLCHCSNRVFLQDSKVTETPTDLP RNAI TELRFLVLT KLVIPKGSFAGGDELEKIEI 60
Db 18 CHHMLCHCSNRVFLQDSKVTETPTDLP RNAI TELRFLVLT KLVIPKGSFAGGDELEKIEI 77
Oy 61 SONOVLEVTEADVFNSLPKHEIRIEKANNLLYINPEAFQNLPSRLYLLISMTGKHLPA 120
Db 78 SONOVLEVTEADVFNSLPKHEIRIEKANNLLYINPEAFQNLPSRLYLLISMTGKHLPA 137
Oy 121 VHKTSQKLVLLDIOONINIHIVANSFNGLSFESVILMSKNGIEEIHNCAPNGTOLDE 180
Db 138 VHKTSQKLVLLDIOONIHHTIPGNAFQGNHNSVILMSKNGIEEIHNCAPNGTOLDE 197
Oy 181 LNLSDNNLLELNDVDFOGASGPVILDISRTKYNSLPNGLEENLKLBARSTYRLAKLPN 240
Db 198 LNLSDNNLLELNDVDFOGASGPVILDISRTKYNSLPNGLEENLKLBARSTYRLAKLPN 257
Oy 241 LDKFVTLMEASLTYPSCCAFNALKROISELHPICNKSILRODIDDMTOIGDORVSLIDD 300
Db 258 LDKFVTLMEASLTYPSCCAFNALKROISELHPICNKSILRODIDDMTOIGDORVSLIDD 317
Oy 301 EPSYKGSQDMYNEFDYDLCNEVDVTCSPKPDAPNCPEDIMGYNILRVLIWFIISLAIIT 360
Db 318 EPSYKGSQDMYNEFDYDLCNEVDVTCSPKPDAPNCPEDIMGYNILRVLIWFIISLAIIT 377
Oy 361 GNTVLVLTTSQKLTVPRLMCLNADLCIGYLLIASVDIHTKSOYHNYAIDMOT 420
Db 378 GNTVLVLTTSQKLTVPRLMCLNADLCIGYLLIASVDIHTKSOYHNYAIDMOT 437
Oy 421 GAGDAAGFFTVFASLSVYTLTAITLERHHTITHAMQLECKVOLRHAASVWVLTGTFAP 480
Db 438 GAGDAAGFFTVFASLSVYTLTAITLERHHTITHAMQLECKVOLRHAASVWVLTGTFAP 497
Oy 481 AALPPIFGISSYMKVSYICLPMIDISPLQYVWALLVLAFFVYICGCTHYILTVRN 540
Db 498 AALPPIFGISSYMKVSYICLPMIDISPLQYVWALLVLAFFVYICGCTHYILTVRN 557
Oy 541 PTIVSSSDTKIARMAATLIFTDFLCMAPISFPAISASLKVPILTYSKAKILLVLPYIN 600
Db 558 PTIVSSSDTKIARMAATLIFTDFLCMAPISFPAISASLKVPILTYSKAKILLVLPYIN 617
Oy 601 SCANPFLYAIPTFNPRDFPILLSKFCYEMQAOIYRTTSSATHNPHARKSHCSSAPRV 660
Db 618 SCANPFLYAIPTFNPRDFPILLSKFCYEMQAOIYRTTSSATHNPHARKSHCSSAPRV 677
Oy 661 TNSYVLPVPLNHSOON 675
Db 678 TNSYVLPVPLNHSOON 692

RESULT 4
AAR30525
ID AAR30525 standard; protein; 695 AA.
XX
XX
XX AAR30525;
XX
XX 10-MAY-1993 (first entry)
XX
XX N-terminal of LH receptor/FSH receptor chimaera #34.
XX
XX Follicle stimulating hormone receptor; luteinising hormone receptor;
XX human chorionic gonadotrophin; glycoprotein hormone receptor;
XX chimaera; chimera.
XX
XX Chimaeric; homo sapiens.
XX
XX MO9222667-A.
XX
XX 23-DEC-1992.
XX
XX 12-JUN-1992; 92WO-US04987.

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XX PR 14-JUN-1991; 91US-0715911.
XX PA (UYNE-) UNIV NEW JERSEY.
XX PI Bernard M, Moyle WR, Myers R;
XX XX WPI; 1993-018150/02.
XX DR
XX XX Glyco:protein hormone receptor analogues - having binding
XX PT affinity to human chorionic gonadotrophin (hCG), luteinising
XX PT follicle stimulating hormones, useful in bio:immunoassays
XX XX
XX PS Examples; Fig 12; 103pp; English.
XX XX
XX CC This sequence represents the N-terminal of a novel protein having a
XX CC binding affinity for human chorionic gonadotrophin (hCG), luteinising
XX CC hormone (LH), and follicle stimulating hormone (FSH). The protein
XX CC itself is a chimera having residues from both the FSH receptor,
XX CC and LH receptor. The receptor analogues can be used in bioimmunoassays
XX CC for the simultaneous detection of both LH (or hCG) and FSH as
XX CC well as their ratio of biological activities. The analogues can also
XX CC be used for raising, purifying and assaying antibodies to the
XX CC analogues. Coding sequence for the chimera was produced by two step
XX CC PCR.
XX XX
XX SQ Sequence 695 AA;

Query Match 98.0%; Score 3445; DB 14; Length 695;
Best Local Similarity 98.4%; Pred. No. 0;
Matches 664; Conservative 2; Mismatches 9; Indels 0; Gaps 0;

QY 1 CHHWLCHCSNRVFLCQDSKVTETPTDLPRAIELRVLTPLKRVIPKGSFAGDLEKIEI 60
DB 18 CHHWLCHCSNRVFLCQDSKVTETPTDLPRAIELRVLTPLKRVIPKGSFAGDLEKIEI 77
QY 61 SONDVLEIADVFSNLPKLHEIRIEKANNLLYINPEAFONLPSRLYLLISNTGIKHLPA 120
DB 78 SONDVLEIADVFSNLPKLHEIRIEKANNLLYINPEAFONLPSRLYLLISNTGIKHLPA 137
QY 121 VHKLQSLQVLLDIQDNIHIVARNSEFMGLSPFESVILWLSKNGIEEIHNCFAFNGTQDLE 180
DB 138 VHKLQSLQVLLDIQDNIHIVARNSEFMGLSPFESVILWLSKNGIEEIHNCFAFNGTQDLE 197
QY 181 LNLSDNNLEELPNDVFOGASGVILDISRTKVHSLPNHGLENLKRLARSTYRLKLPN 240
DB 198 LNLSDNNLEELPNDVFOGASGVILDISRTKVHSLPNHGLENLKRLARSTYRLKLPN 257
QY 241 LDKFVTLMEASLTYPSSHCCAFANLKRQISELHPICKNSILRODIDDMTOIGDQVSLIDD 300
DB 258 LDKFVTLMEASLTYPSSHCCAFANLKRQISELHPICKNSILRODIDDMTOIGDQVSLIDD 317
QY 301 EPSYKSGSDMYNEFDYDLCNEVVDVTCSPKDAFNPCEIDIMGYNLRVILNFIISLAIT 360
DB 318 EPSYKSGSDMYNEFDYDLCNEVVDVTCSPKDAFNPCEIDIMGYNLRVILNFIISLAIT 377
QY 361 GNTTVLWLTTSQYKLTVPFLMCNLFADLCIGIYLLIASVDIHTKSOYHNYADWQT 420
DB 378 GNTTVLWLTTSQYKLTVPFLMCNLFADLCIGIYLLIASVDIHTKSOYHNYADWQT 437
QY 421 GACCDAAAGFTVPASLSVYTTAITLERWHTTHAMOLECKVOLRAHASVMVLGWTFFAF 480
DB 438 GACCDAAAGFTVPASLSVYTTAITLERWHTTHAMOLECKVOLRAHASVMVLGWTFFAF 497
QY 481 AALFPFIFGSSYMKYSICLPMIDSPLSQYVALLVNLVAFVVICGCTHYILTVRN 540
DB 498 AALFPFIFGSSYMKYSICLPMIDSPLSQYVALLVNLVAFVVICGCTHYILTVRN 557
QY 541 PTIVSSSDTKIAKRNATLIFTDFLCMAPISSFAISASLKVPLITVSKAKILLVLFPYIN 600
DB 558 PTIVSSSDTKIAKRNATLIFTDFLCMAPISSFAISASLKVPLITVSKAKILLVLFPYIN 617
QY 601 SCANPELYAIFTKNFRDFILLSKFCGYEMOQIYRTTSSATHNFARKSCSSAPRV 660

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DB 618 SCANPELYAIFTKNFRDFILLSKFCGYEMOQIYRTTSSATHNFARKSCSSAPRV 677
QY 661 TNSYVLVPLNHSSQN 675
DB 678 TNSYVLVPLNHSSQN 692

RESULT 5
AAR30523
ID AAR30523 standard; protein: 696 AA.
XX AC AAR30523;
XX DT 10-MAY-1993 (first entry)
XX DE N-terminal of LH receptor/FSH receptor chimera #32.
XX KW Follicle stimulating hormone receptor; luteinising hormone receptor;
XX KW human chorionic gonadotrophin; glycoprotein hormone receptor;
XX KW chimera: chimera.
XX OS Chimaeric: homo sapiens.
XX PN W09222667-A.
XX PD 23-DEC-1992.
XX PF 12-JUN-1992; 92WO-US04987.
XX PR 14-JUN-1991; 91US-0715911.
XX PA (UYNE-) UNIV NEW JERSEY.
XX PI Bernard M, Moyle WR, Myers R;
XX XX WPI; 1993-018150/02.
XX DR Glyco:protein hormone receptor analogues - having binding
XX PT affinity to human chorionic gonadotrophin, luteinising and
XX PT follicle stimulating hormones, useful in bio:immunoassays
XX PS Examples; Fig 12; 103pp; English.
XX XX
XX CC This sequence represents the N-terminal of a novel protein having a
XX CC binding affinity for human chorionic gonadotrophin (hCG), luteinising
XX CC hormone (LH), and follicle stimulating hormone (FSH). The protein
XX CC itself is a chimera having residues from both the FSH receptor,
XX CC and LH receptor. The receptor analogues can be used in bioimmunoassays
XX CC for the simultaneous detection of both LH (or hCG) and FSH as
XX CC well as their ratio of biological activities. The analogues can also
XX CC be used for raising, purifying and assaying antibodies to the
XX CC analogues. Coding sequence for the chimera was produced by two step
XX CC PCR.
XX XX
XX SQ Sequence 696 AA;

Query Match 97.9%; Score 3441.5; DB 14; Length 696;
Best Local Similarity 98.1%; Pred. No. 0;
Matches 663; Conservative 4; Mismatches 8; Indels 1; Gaps 1;

QY 1 CHHWLCHCSNRVFLCQDSKVTETPTDLPRAIELRVLTPLKRVIPKGSFAGDLEKIEI 60
DB 18 CHHWLCHCSNRVFLCQDSKVTETPTDLPRAIELRVLTPLKRVIPKGSFAGDLEKIEI 77
QY 61 SONDVLEIADVFSNLPKLHEIRIEKANNLLYINPEAFONLPSRLYLLISNTGIKHLPA 120
DB 78 SONDVLEIADVFSNLPKLHEIRIEKANNLLYINPEAFONLPSRLYLLISNTGIRLTPD 137
QY 121 VHKLQSLQVLLDIQDNIHIVARNSEFMGLSPFESVILWLSKNGIEEIHNCFAFNGTQD 179
DB 138 VTKISSEFNFLEIQDNIHIVARNSEFMGLSPFESVILWLSKNGIEEIHNCFAFNGTQD 197

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XX DE N-terminal of LH receptor/FSH receptor chimera #35.
 XX KW Follicle stimulating hormone receptor; luteinising hormone receptor;
 XX KW human chorionic gonadotrophin; glycoprotein hormone receptor;
 XX KW chimera; chimera.
 XX OS Chimeraic; homo sapiens.
 XX PN W09222667-A.
 XX PD 23-DEC-1992.
 XX PF 12-JUN-1992; 92WO-US04987.
 XX PR 14-JUN-1991; 91US-0715911.
 XX PA (UYNE-) UNIV NEW JERSEY.
 XX PI Bernard M, Moyle WR, Myers R;
 XX DR WPI; 1993-018150/02.
 XX KW Glyco:protein hormone receptor analogues - having binding
 XX PT affinity to human chorionic gonadotrophin, luteinising and
 XX PT follicle stimulating hormones, useful in bio:immunoassays
 XX PS Examples; Fig 12; 103pp; English.
 XX KW This sequence represents the N-terminal of a novel protein having a
 CC binding affinity for human chorionic gonadotrophin (hCG), luteinising
 CC hormone (LH), and follicle stimulating hormone (FSH). The protein
 CC itself is a chimera having residues from both the FSH receptor,
 CC and LH receptor. The receptor analogues can be used in bioimmunoassays
 CC for the simultaneous detection of both LH (or hCG) and FSH as
 CC well as their ratio of biological activities. The analogues can also
 CC be used for raising, purifying and assaying antibodies to the
 CC analogues. Coding sequence for the chimera was produced by two step
 CC PCR.
 XX SQ Sequence 696 AA;
 Query Match 90.9%; Score 3194.5; DB 14; Length 696;
 Best Local Similarity 91.6%; Pred. No. 1.5e-298;
 Matches 619; Conservative 17; Mismatches 39; Indels 1; Gaps 1;
 QY 1 CHHWLCHCSNRVFLQDSKVTEIPTDLPNRIELRVLTUKLRVTPKGSFAGDLEKIEI 60
 DB 18 CHHWLCHCSNRVFLQDSKVTEIPTDLPNRIELRVLTUKLRVTPKGSFAGDLEKIEI 77
 QY 61 SONDVLEIADVFENLPLKHEIRTEKANNLLYINPEAFONLPSRLYLISNTGKHLPA 120
 DB 78 SOSDSLRIEAFANFONLNLSELLONTKNLLYIEPGAFTNLPRLKYLISNTGRTLPD 137
 QY 121 VHKIQSLQ-KVLLDQDNINIHIVARNFGLSFESVILMSKNGIEETHNCAFGTOLD 179
 DB 138 VTKISSENFLEICDNLHITIPGNAPQGNNEVTLKLYNGFEEVQSHAFNGTOLD 197
 QY 180 ELNLSNNLEELPNDVFOGASGPVILDSRTKVHSLPNHGLENLKLRARSTYRLKLP 239
 DB 198 ELNLSNNLEELPNDVFOGASGPVILDSRTKVHSLPNHGLENLKLRARSTYRLKLP 257
 QY 240 NLDKFTVLEASITPESHCCAFANLKRQISELHPICNKSILRQDDIMDTQIGQORVSLID 299
 DB 258 NLDKFTVLEASITPESHCCAFANLKRQISELHPICNKSILRQDDIMDTQIGQORVSLID 317
 QY 300 DEPSYKSGSDMYNEFDYDLNCEVVDVTCSPKPAFNPCEINGYNILRVLIWFISILAI 359
 DB 318 DEPSYKSGSDMYNEFDYDLNCEVVDVTCSPKPAFNPCEINGYNILRVLIWFISILAI 377
 QY 360 TGNVTVLVLTTSQYKLTVPRLFMCLNAPADICIGIYLLIASVDIHTKSOYHNAIDNQ 419
 DB 378 TGNVTVLVLTTSQYKLTVPRLFMCLNAPADICIGIYLLIASVDIHTKSOYHNAIDNQ 437

QY 420 TGAGCDAAGFTTVFASSELVSYTLTAITLERWHTITHAMOLECKVQLRHAASVMVLTGTF 479
 DB 438 TGAGCDAAGFTTVFASSELVSYTLTAITLERWHTITHAMOLECKVQLRHAASVMVLTGTF 497
 QY 480 FAALPPIFGISSYMKVSIICLPMDIDSPLSQLYVMALLVNLVAFVVICGTHIYLTVR 539
 DB 498 FAALPPIFGISSYMKVSIICLPMDIDSPLSQLYVMALLVNLVAFVVICGTHIYLTVR 557
 QY 540 NPTIVSSSDTKIAKRMTATLIFTDFLCMAPIISFPAISASLKVPPLITVSKAKILLVLPYPI 599
 DB 558 NPTIVSSSDTKIAKRMTATLIFTDFLCMAPIISFPAISASLKVPPLITVSKAKILLVLPYPI 617
 QY 600 NSCANPELYAIFTKNFRDRDFILLSKFCGYEMOQIYRTETSSATHNFHARKSHCSAPR 659
 DB 618 NSCANPELYAIFTKNFRDRDFILLSKFCGYEMOQIYRTETSSATHNFHARKSHCSAPR 677
 QY 660 VTNSYVLVPLNHHSSON 675
 DB 678 VTNSYVLVPLNHHSSON 693
 RESULT 8
 AAR42082
 ID AAR42082 standard; Protein; 695 AA.
 XX AC AAR42082;
 XX DT 05-MAY-1994 (first entry)
 XX DE FSH receptor.
 XX KW FSH; receptor; follicle stimulating hormone; GST;
 KW glutathione-S-transferase; primer; PCR; amplification;
 KW polymerase chain reaction; probe; antibody; overstimulation.
 XX OS Homo sapiens.
 XX PN W09320199-A.
 XX PD 14-OCT-1993.
 XX PF 29-MAR-1993; 93WO-EP00780.
 XX PR 30-MAR-1992; 92EP-0200886.
 XX PA (ALKU) AKZO NV.
 XX PI De Leeuw R, Dijkema R;
 DR WPI; 1993-336907/42.
 XX N-PSDB; AAQ50013.
 PT New follicle stimulating hormone receptor - and derived
 PT antibodies, anti-idiotypic antibodies, and transfected cells,
 PT useful e.g. in diagnosis and as antidote for FSH overstimulation
 XX Claim 7; Page 20-23; 42pp; English.
 CC The primers given in AAQ50029-34 were used in the cloning of GST-FSH-
 CC R1, GST-FSH-R2 and GST-FSH-R3 fusion protein constructs.
 CC Screening of the human testis cDNA library with a hFSH-R specific
 CC probe resulted in five recombinant phages positive in hybridisation.
 CC Sequence analysis was performed of the 2222 bp fragment of pGEM32c1
 CC (AAQ50013).
 XX SQ Sequence 695 AA;
 Query Match 90.1%; Score 3169.5; DB 14; Length 695;
 Best Local Similarity 89.5%; Pred. No. 3.9e-296;
 Matches 607; Conservative 31; Mismatches 37; Indels 3; Gaps 2;
 QY 1 CHHWLCHCSNRVFLQDSKVTEIPTDLPNRIELRVLTUKLRVTPKGSFAGDLEKIEI 60

DB 18 CHIRCHCHNRVFLCQSKVTEIPSDLPNNAELAFVLTAKVIOKAFSGFDLEKIEI 77
OY 61 SONDVLEVIEADVFSNLPKLEHRIEKANLLYINPEAFONLPSPYLLISNTGKHLPA 120
DB 78 SONDVLEVIEADVFSNLPKLEHRIEKANLLYINPEAFONLPYLLISNTGKHLPD 137
OY 121 VHKIOSLOKVLIDODINIHIVARNSPGLSFESVILWLSKNGIEIHNCAPNGTOLDE 180
DB 138 VHKIHSLOKVLIDODINIHIVARNSPGLSFESVILWLSKNGIEIHNCAPNGTOLDE 197
OY 181 LNSDNNLLELPNDVPHGASCPVILDSRTKHSPLNGLNKLKLRARSTYLNKLUPT 240
DB 258 LKLVALMEASLTTPSHCCAFANRRROISELHPICNKSILROEDVYNTOTRCQSSLAED 317
OY 301 -EPSTYKSGDMYNEFDYDLCNEVVDVTCSPKDPAPNCPEDIMGYNILRVLINFISILAI 359
DB 318 NESYSRGFDMTYTEFDYDLCNEVVDVTCSPKDPAPNCPEDIMGYNILRVLINFISILAI 377
OY 360 TGNITVVLVLTTSQKLTVPRLMCLNAPADLCIGIYLLIASVDIHTKSQYHNYAIDMQ 419
DB 438 TGACDAAAGFTTVPFASLSVYTLTAITLERHHTITHAMOLECKVQLRHAASVYMGWIFA 497
OY 480 FAALPFIPIGSSYKVSICLPMDIDPSLSQLYVALLVNLVAFVYVIGCYTHILTVR 539
DB 498 FAALPFIPIGSSYKVSICLPMDIDPSLSQLYVALLVNLVAFVYVIGCYTHILTVR 557
OY 540 NPTIVSSSDTKAKRMATLIFTDFLCHAPISFFAISASLKVPLITYSKAKILLVLPFI 599
DB 558 NPNTIVSSSDTKAKRMATLIFTDFLCHAPISFFAISASLKVPLITYSKAKILLVLPFI 617
OY 600 NSCANPFIYAIPTKRNPRDFPILLSKGCYEMOQAIYRTTSSATHNPHARKHSCSAPR 659
DB 618 NSCANPFIYAIPTKRNPRDFPILLSKGCYEMOQAIYRTTSSATHNPHARKHSCSAPR 677
OY 660 VTN--SYVLVPLNHSOON 675
DB 678 VTNGSTYILVPLSHLAQN 695

RESULT 9
ID AAM14782 standard; Protein; 695 AA.
AC AAM14782;
DT 20-JUN-1997 (first entry)
DE FSH receptor.
XX Follicle stimulating hormone receptor; FSH receptor;
KW ovarian dysgenesis; hypergonadotropic hypogonadism; diagnosis.
XX Homo sapiens.
PN WO9711194-A1.
XX 27-MAR-1997.
PD 20-SEP-1996; 96WO-F100501.
PP 20-SEP-1995; 95US-0531070.
PR (UYHE-) UNIV HELSINKI LICENSING LTD OY.
PA
XX

PI Altomaeki K, De La Chapelle A, Huhtaniemi I;
XX WPI: 1997-202900/18.
DR N-PSDB: AAT63181.
XX
CC Diagnosis of ovarian dysgenesis and carriers from DNA abnormalities
CC - by amplifying DNA including follicle stimulating hormone receptor
CC allele(s), i.e. codon 189, cleaving fragments, and examination
XX
PS Disclosure: Page 18-21: 43pp: English.
XX
CC The human follicle stimulating hormone (FSH) receptor (AAM14782)
CC is a G-protein coupled transmembrane receptor. A mutation in the
CC fshr gene (see also AAT63181) is associated with ovarian dysgenesis,
CC and methods for provided for the diagnosis of this disorder.
XX
SO Sequence 695 AA;
Query Match 90.18; Score 3169.5; DB 18; Length 695;
Best Local Similarity 89.34; Pred. No. 3; 9e-296;
Matches 607; Conservative 31; Mismatches 37; Indels 3; Gaps 2;
OY 1 CHIRCHCHNRVFLCQSKVTEIPSDLPNNAELAFVLTAKVIOKAFSGFDLEKIEI 60
DB 18 CHIRCHCHNRVFLCQSKVTEIPSDLPNNAELAFVLTAKVIOKAFSGFDLEKIEI 77
OY 61 SONDVLEVIEADVFSNLPKLEHRIEKANLLYINPEAFONLPSPYLLISNTGKHLPA 120
DB 78 SONDVLEVIEADVFSNLPKLEHRIEKANLLYINPEAFONLPYLLISNTGKHLPD 137
OY 121 VHKIOSLOKVLIDODINIHIVARNSPGLSFESVILWLSKNGIEIHNCAPNGTOLDE 180
DB 138 VHKIHSLOKVLIDODINIHIVARNSPGLSFESVILWLSKNGIEIHNCAPNGTOLDE 197
OY 181 LNSDNNLLELPNDVPHGASCPVILDSRTKHSPLNGLNKLKLRARSTYLNKLUPT 240
DB 258 LKLVALMEASLTTPSHCCAFANRRROISELHPICNKSILROEDVYNTOTRCQSSLAED 317
OY 301 -EPSTYKSGDMYNEFDYDLCNEVVDVTCSPKDPAPNCPEDIMGYNILRVLINFISILAI 359
DB 318 NESYSRGFDMTYTEFDYDLCNEVVDVTCSPKDPAPNCPEDIMGYNILRVLINFISILAI 377
OY 360 TGNITVVLVLTTSQKLTVPRLMCLNAPADLCIGIYLLIASVDIHTKSQYHNYAIDMQ 419
DB 438 TGACDAAAGFTTVPFASLSVYTLTAITLERHHTITHAMOLECKVQLRHAASVYMGWIFA 497
OY 480 FAALPFIPIGSSYKVSICLPMDIDPSLSQLYVALLVNLVAFVYVIGCYTHILTVR 539
DB 498 FAALPFIPIGSSYKVSICLPMDIDPSLSQLYVALLVNLVAFVYVIGCYTHILTVR 557
OY 540 NPTIVSSSDTKAKRMATLIFTDFLCHAPISFFAISASLKVPLITYSKAKILLVLPFI 599
DB 558 NPNTIVSSSDTKAKRMATLIFTDFLCHAPISFFAISASLKVPLITYSKAKILLVLPFI 617
OY 600 NSCANPFIYAIPTKRNPRDFPILLSKGCYEMOQAIYRTTSSATHNPHARKHSCSAPR 659
DB 618 NSCANPFIYAIPTKRNPRDFPILLSKGCYEMOQAIYRTTSSATHNPHARKHSCSAPR 677
OY 660 VTN--SYVLVPLNHSOON 675
DB 678 VTNGSTYILVPLSHLAQN 695
RESULT 10
AAR27558

AA027558 standard; Protein: 695 AA.

AA027558;

04-MAR-1993 (first entry)

FSHR.

Human; follicle stimulating hormone receptor; maturation; spermatogenesis; birth control.

Homo sapiens.

Key Location/Qualifiers

Peptide 1..17

Protein /note= "signal peptide"

Domain /note= "mature hFSHR "

Domain /note= "N-terminal extracellular domain"

Domain /note= "transmembrane domain"

Domain /note= "transmembrane region I"

Domain /note= "transmembrane region II"

Domain /note= "transmembrane region III"

Domain /note= "transmembrane region IV"

Domain /note= "transmembrane region V"

Domain /note= "transmembrane region VI"

Domain /note= "transmembrane region VII"

Domain /note= "C-terminal intracellular domain"

W09216620-A.

01-OCT-1992.

02-JAN-1992; 92WO-US00122.

15-MAR-1991; 91US-0670085.

(ISTF) ARS APPL RES SYST HOLDING NV.

Cheng SVI, Kelton CA, Nugent NP, Schweickhardt RL;

WT: 1992-349206/42.

N-PSDB: AAQ29377.

Pure human FSH receptor, fragments and mutants - for preventing

follicle growth, maturation and spermatogenesis, also for use of

appropriate cell lines for bio-assays of FSH

Claim 2; Page 25; 48pp; English.

The protein sequence of human follicle stimulating hormone receptor

(FSHR) was deduced from the DNA sequence obtd. by screening a lambda

gt11 cDNA library constructed from RNA extracted from human testis

with a rat FSHR cDNA clone as a probe. hFSHR binds to FSH to reduce

endogenous FSH bioactivity, in females to prevent follicle growth and

maturation and in males to prevent spermatogenesis, i.e. as a birth

control agent. hFSHR may be used in assays for detection of FSH

bioactivity and in x-ray crystallographic analysis to develop molecular

models useful in defining the tertiary structure of the hormone binding

domains of hFSHR. This will aid the design of peptides with FSH

(ant)agonist activity.

Sequence 695 AA;

Query Match	90.0%	Score 3164.5	DB 13	Length 695
Best Local Similarity	89.4%	Pred. No. 1.2e-295		
Matches 606	Conservative 32	Mismatches 37	Indels 3	Gaps 2
QY	1	CHWLCHCSNRVFLCQDSKVTEIPDLPRNAIELRFLVTLKLRVLPKGSFAGFGDLEKIEI	60	
DB	18	CHHRICHCSNRVFLCQDSKVTEIPSDLPNRNAIELRFLVTLKLRVLPKGSFAGFGDLEKIEI	77	
QY	61	SQNDVLEIVADVFSLNPKLHEIRIEKANNLLYINPEAFQNLPSLRLLISNTGTHLPA	120	
DB	78	SQNVLEIVADVFSLNPKLHEIRIEKANNLLYINPEAFQNLPSLRLLISNTGTHLPA	137	
QY	121	VHKIQSLQKVLDDIQQNINIHIVARNSEFMGLSFESVILWLSKNGIEEIHNCAPNGTQIDE	180	
DB	138	VHKIQSLQKVLDDIQQNINIHIVARNSEFMGLSFESVILWLSKNGIEEIHNCAPNGTQIDE	197	
QY	181	LNLSDDNNLELPNDVFOGASGPVLDISRTKVHSLPNHGLENLKLRARSTYRLKLLPN	240	
DB	198	LNLSDDNNLELPNDVFOGASGPVLDISRTKVHSLPNHGLENLKLRARSTYRLKLLPN	257	
QY	241	LDRFVTLMEASLTYPSCCAAFANLKRQISELHPICNKSILRQDIDDDMTQIGDQVSLTDD	300	
DB	258	LEKLVALMEASLTYPSCCAAFANLKRQISELHPICNKSILRQDIDDDMTQIGDQVSLTDD	317	
QY	301	-EPSYKSGSDMYNEFDYDLCNEVVOVTCSPKPAFNPCEIDIMGYNLRVLWIFISILAI	359	
DB	318	NESSYSGDFMTYEFDYDLCNEVVOVTCSPKPAFNPCEIDIMGYNLRVLWIFISILAI	377	
QY	360	TGNTTVLVLTTSQYKLTVPFELMCNLAFAADLCIGIYLLLTASVDIHTKSOYHNYADMQ	419	
DB	378	TGNTTVLVLTTSQYKLTVPFELMCNLAFAADLCIGIYLLLTASVDIHTKSOYHNYADMQ	437	
QY	420	TGAGCDAAGFTTFASELSVTTTALTITLERMHTITHAMQLECKVQLRHAASVMVLGWTFA	479	
DB	438	TGAGCDAAGFTTFASELSVTTTALTITLERMHTITHAMQLECKVQLRHAASVMVLGWTFA	497	
QY	480	FAAALPFIIGISSYMKVSYICLPMDIDSPLSQLYWALLVNLVAFVVCYTHIYLTVR	539	
DB	498	FAAALPFIIGISSYMKVSYICLPMDIDSPLSQLYWALLVNLVAFVVCYTHIYLTVR	557	
QY	540	NPTIVSSSDTKIAKRMATLIFTDFLCMAPISTFAISASLKVPLITVSKAKILLVLPVI	599	
DB	558	NPNIVSSSDTKIAKRMATLIFTDFLCMAPISTFAISASLKVPLITVSKAKILLVLPVI	617	
QY	600	NSCANPELYAIFTKNFRDRFFILLSKGCEYEMQAQIYRTTSSATHNPHARKSHCSSAPR	659	
DB	618	NSCANPELYAIFTKNFRDRFFILLSKGCEYEMQAQIYRTTSSATHNPHARKSHCSSAPR	677	
QY	660	VTN--SYVLYPLNHSSON 675		
DB	678	VTNGSTYILVPLSHLAQN 695		

RESULT 11

AA030520

ID AA030520 standard; protein: 634 AA.

XX

AA030520;

XX

10-MAY-1993 (first entry)

DT

XX

N-terminal of LH receptor/FSH receptor chimera #29.

DE

XX

Follicle stimulating hormone receptor; luteinising hormone receptor;

human chorionic gonadotrophin; glycoprotein hormone receptor;

chimera; chimera.

XX

Chimeraic; homo sapiens.

OS

XX

W09222667-A.

XX

23-DEC-1992.

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XX 12-JUN-1992; 92MO-US04987.
XX 14-JUN-1991; 91US-0715911.
XX (UYNE-) UNIV NEW JERSEY.
XX Bernard M. Moyle WR. Myers R;
XX WPI; 1993-018150/02.
XX
XX Glyco:protein hormone receptor analogues - having binding
XX affinity to human chorionic gonadotrophin, luteinising and
XX follicle stimulating hormones, useful in bio:immunoassays
XX
XX Examples; Fig 12; 103pp: English.
XX
XX This sequence represents the N-terminal of a novel protein having a
XX binding affinity for human chorionic gonadotrophin (hCG), luteinising
XX hormone (LH), and follicle stimulating hormone (FSH). The protein
XX itself is a chimera having residues from both the FSH receptor
XX and LH receptor. The receptor analogues can be used in bio:immunoassays
XX for the simultaneous detection of both LH (or hCG) and FSH as
XX well as their ratio of biological activities. The analogues can also
XX be used for raising, purifying and assaying antibodies to the
XX analogues. Coding sequence for the chimera was produced by two step
XX PCR.
XX
XX Sequence 634 AA:
XX
Query Match 89.6%; Score 3151.5; DB 14; Length 634;
Best Local Similarity 90.8%; Pred. No. 1.8e-294;
Matches 613; Conservative 0; Mismatches 1; Indels 61; Gaps 1;
OY 1 CHHILCHSRRVFLCDSKVTETPTDLPNNALFVLTPLKRVIPKGSFAGFGLKIEI 60
DB 18 CHHILCHSRRVFLCDSKVTETPTDLPNNALFVLTPLKRVIPKGSFAGFGLKIEI 77
OY 61 SONDVLEYEADVSNLPKHEIRIEKANLLYINPEAFONLPSRLYLLISMTGKHLPA 120
DB 78 SONDVLEYEADVSNLPKHEIRIEKANLLYINPEAFONLPSRLYLLISMTGKHLPA 137
OY 131 VHKIOSLQKYLQDODNINIHIVARNSPMGLSFESVILMSKNGIEIHNCAFNCTOLDE 180
DB 138 VHKIOSLQKYLQDODNINIHIVARNSPMGLSFESVILMSKNGIEIHNCAFNCTOLDE 197
OY 181 LNLSDNNLEELPNDVPOGASGPVILDISRTKRVHSLPNHGLENLKLRARSTYRLKLPN 240
DB 198 LNLSDNNLEELPNDVPOGASGPVILDISRTKRVHSLPNHGLENLKLRARSTYRLKLPN 223
OY 241 LDKFVTLMEASLTTPSCCNFANLKRQISELHPICNKSILRODIDMTQICDORVSLDD 300
DB 224 -----ISELHPICNKSILRODIDMTQICDORVSLDD 256
OY 301 EPSYKGSDDMTNEPDYDLCEVNVYVTCSPKPAFNCEDIMGTNLRVLWISTLAIT 360
DB 257 EPSYKGSDDMTNEPDYDLCEVNVYVTCSPKPAFNCEDIMGTNLRVLWISTLAIT 316
OY 361 GNTTVLVYLTTSQYKLVPRFLCNLAFADLCIGYLLLTASVDIHTKSQYHNYADWQT 420
DB 317 GNTTVLVYLTTSQYKLVPRFLCNLAFADLCIGYLLLTASVDIHTKSQYHNYADWQT 376
OY 421 GACDAGFTTFVASELSVYTLTAITLERWHITTHAMOLECKVOLRRHAAVYVLGNTFAP 480
DB 377 GACDAGFTTFVASELSVYTLTAITLERWHITTHAMOLECKVOLRRHAAVYVLGNTFAP 436
OY 481 AALAPPTFGISSTKRVISGLPMDISPLQSDSOLYVYLLVNLAVYLCCTTHYLYVRN 540
DB 437 AALAPPTFGISSTKRVISGLPMDISPLQSDSOLYVYLLVNLAVYLCCTTHYLYVRN 496
OY 541 PTVVSSSDTKIARMATLITPTDFLCMAPISPFAISAKVPLITYSKATLLVLYPTIN 600
DB 497 PTVVSSSDTKIARMATLITPTDFLCMAPISPFAISAKVPLITYSKATLLVLYPTIN 556

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OY 601 SCANFLYAIFTRNFRROFFILLSKFCYEMOAGIYRTETSSATRNPHARKSHCSSAPRV 660
DB 557 SCANFLYAIFTRNFRROFFILLSKFCYEMOAGIYRTETSSATRNPHARKSHCSSAPRV 616
OY 661 TNSYVLVPLAHSSQN 675
DB 617 TNSYVLVPLAHSSQN 631
XX
XX RESULT 12
XX AAR30513
XX ID AAR30513 standard; protein; 696 AA.
XX AC AAR30513;
XX DT 10-MAY-1993 (first entry)
XX DE N-terminal of LH receptor/FSH receptor chimera #22.
XX KW Follicle stimulating hormone receptor; luteinising hormone receptor;
XX human chorionic gonadotrophin; glycoprotein hormone receptor;
XX chimera; chimera.
XX OS Chimeraic; homo sapiens.
XX PN W09222667-A.
XX PD 23-DEC-1992.
XX PF 12-JUN-1992; 92MO-US04987.
XX PR 14-JUN-1991; 91US-0715911.
XX (UYNE-) UNIV NEW JERSEY.
XX Bernard M. Moyle WR. Myers R;
XX WPI; 1993-018150/02.
XX Glyco:protein hormone receptor analogues - having binding
XX affinity to human chorionic gonadotrophin, luteinising and
XX follicle stimulating hormones, useful in bio:immunoassays
XX
XX Examples; Fig 12; 103pp: English.
XX
XX This sequence represents the N-terminal of a novel protein having a
XX binding affinity for human chorionic gonadotrophin (hCG), luteinising
XX hormone (LH), and follicle stimulating hormone (FSH). The protein
XX itself is a chimera having residues from both the FSH receptor
XX and LH receptor. The receptor analogues can be used in bio:immunoassays
XX for the simultaneous detection of both LH (or hCG) and FSH as
XX well as their ratio of biological activities. The analogues can also
XX be used for raising, purifying and assaying antibodies to the
XX analogues. Coding sequence for the chimera was produced by two step
XX PCR.
XX
XX Sequence 696 AA:
XX
Query Match 88.4%; Score 3109.5; DB 14; Length 696;
Best Local Similarity 89.3%; Pred. No. 2.3e-290;
Matches 604; Conservative 22; Mismatches 49; Indels 1; Gaps 1;
OY 1 CHHILCHSRRVFLCDSKVTETPTDLPNNALFVLTPLKRVIPKGSFAGFGLKIEI 60
DB 18 CHHILCHSRRVFLCDSKVTETPTDLPNNALFVLTPLKRVIPKGSFAGFGLKIEI 77
OY 61 SONDVLEYEADVSNLPKHEIRIEKANLLYINPEAFONLPSRLYLLISMTGKHLPA 120
DB 78 SONDVLEYEADVSNLPKHEIRIEKANLLYINPEAFONLPSRLYLLISMTGKHLPA 137
OY 121 VHKIOSLQ-KVLLDIDONINIHIVARNSPMGLSFESVILMSKNGIEIHNCAFNCTOLD 179
DB 121 VHKIOSLQ-KVLLDIDONINIHIVARNSPMGLSFESVILMSKNGIEIHNCAFNCTOLD 179

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Db 138 VTKISSSEFNFILEICNDLHITTPGNFAQGMNNESTYTKLYGNGFEVQSHAFNGTTLI 197
 QY 180 ELNLSNNLEELPNDFOGASGPVILDSRTKVSHPNHLNGLNKKLRARSTYRKLKLP 239
 Db 198 SLEKENIYLEKMHSAFOGATGPVILDSRTKVSHPNHLNGLNKKLRARSTYRKLKLP 257
 QY 240 NLDKFVTLMEASLTYPSSHCAAFANLKRQISELHPICNKSILRQIDDMTQIGDQVSLID 299
 Db 258 NLDKFVTLMEASLTYPSSHCAAFANLKRQISELHPICNKSILRQIDDMTQIGDQVSLID 317
 QY 300 DEPSYKGSDDMYNEFDYDLCLNEVDVTCSPKPDAPNCPEDINGYNILRVLIWFIILAI 359
 Db 318 DEPSYKGSDDMYNEFDYDLCLNEVDVTCSPKPDAPNCPEDINGYNILRVLIWFIILAI 377
 QY 360 TGNITVLVLTTSQYKLTVPFRLMCLNLAFLADLCIGIYLLLIASVDIHTKSOYHNYAIDMQ 419
 Db 378 TGNITVLVLTTSQYKLTVPFRLMCLNLAFLADLCIGIYLLLIASVDIHTKSOYHNYAIDMQ 437
 QY 420 TGAGCDAAGFTVFASLSVYTLTATLERWHITTHAMOLECKVQLRHAASVMVLGWTF 479
 Db 438 TGAGCDAAGFTVFASLSVYTLTATLERWHITTHAMOLECKVQLRHAASVMVLGWTF 497
 QY 480 FFAALFPFIIGISSYMKVSIKLPMDIDSPLSQLYMALLVNLVLAFFVVICGCTHYIYTVR 539
 Db 498 FFAALFPFIIGISSYMKVSIKLPMDIDSPLSQLYMALLVNLVLAFFVVICGCTHYIYTVR 557
 QY 540 NPTIVSSSDTKIAKRMATLIPTDFLCMAPISEFAISASLKVPLITVSKAKILLVLFYPI 599
 Db 558 NPTIVSSSDTKIAKRMATLIPTDFLCMAPISEFAISASLKVPLITVSKAKILLVLFYPI 617
 QY 600 NSCANPFLYAIFTKNFRDFFILLSKFGCYEQMAQIYRTTSSATHNFHARKSHCSAPR 659
 Db 618 NSCANPFLYAIFTKNFRDFFILLSKFGCYEQMAQIYRTTSSATHNFHARKSHCSAPR 677
 QY 660 VTNSYVLVPLNHSQN 675
 Db 678 VTNSYVLVPLNHSQN 693

RESULT 13

AAR30521
 ID AAR30521 standard; protein: 696 AA.

XX AC AAR30521;

XX DT 10-MAY-1993. (first entry)

XX DE N-terminal of LH receptor/FSH receptor chimaera #30.

XX KW Follicle stimulating hormone receptor; luteinising hormone receptor;
 KW human chorionic gonadotrophin; glycoprotein hormone receptor;
 KW chimaera; chimera.

XX OS Chimeric; homo sapiens.

XX PN W09222667-A.

XX PD 23-DEC-1992.

XX PF 12-JUN-1992; 92WO-US04987.

XX PR 14-JUN-1991; 91US-0715911.

XX PA (UYNE-) UNIV NEW JERSEY.

XX PI Bernard M, Moyle WR, Myers R;

XX PF; 1993-018150/02.

XX Glyco:protein hormone receptor analogues - having binding
 PT affinity to human chorionic gonadotrophin, luteinising and
 PT follicle stimulating hormones, useful in bio:immunoassays
 XX

PS Examples: Fig 12; 103pp; English.

XX This sequence represents the N-terminal of a novel protein having a
 CC binding affinity for human chorionic gonadotrophin (hCG), luteinising
 CC hormone (LH), and follicle stimulating hormone (FSH). The protein
 CC itself is a chimaera having residues from both the FSH receptor,
 CC and LH receptor. The receptor analogues can be used in immunoassays
 CC for the simultaneous detection of both LH (or hCG) and FSH as
 CC well as their ratio of biological activities. The analogues can also
 CC be used for raising, purifying and assaying antibodies to the
 CC analogues. Coding sequence for the chimaera was produced by two step
 CC PCR.

SQ Sequence 696 AA;

Query Match 88.4%; Score 3109.5; DB 14; Length 696;
 Best Local Similarity 89.3%; Pred. No. 2.3e-290;
 Matches 604; Conservative 22; Mismatches 49; Indels 1; Gaps 1;

QY 1 CHWLCHCSNRVFLCODSKVTEIPTDLPRNAIELRFLVTLKLRVLPKGSFAGFGDLEKIEI 60
 Db 18 CHWLCHCSNRVFLCODSKVTEIPTDLPRNAIELRFLVTLKLRVLPKGSFAGFGDLEKIEI 77
 QY 61 SQNDVLEIVADVFSNLPKLHEIRIEKANNLLVINPEAFQNLPSRLYLLISNTGIKHLPA 120
 Db 78 SQSDSLERIEANAFDNLNLSSELLIQNTKNLLYIEGAPTNLPRLKYLISICNTGIRLPD 137
 QY 121 VHKIQSLQ-KVLLDIQDNIHIVARNSPMGLSFESVILWLSKNGIEEINCAFNPGTOLD 179
 Db 138 VTKISSSEFNFILEICNDLHITTPGNFAQGMNNESTYTKLYGNGFEVQSHAFNGTTLI 197
 QY 180 ELNLSNNLEELPNDFOGASGPVILDSRTKVSHPNHLNGLNKKLRARSTYRKLKLP 239
 Db 198 SLEKENIYLEKMHSAFOGATGPVILDSRTKVSHPNHLNGLNKKLRARSTYRKLKLP 257
 QY 240 NLDKFVTLMEASLTYPSSHCAAFANLKRQISELHPICNKSILRQIDDMTQIGDQVSLID 299
 Db 258 NLDKFVTLMEASLTYPSSHCAAFANLKRQISELHPICNKSILRQIDDMTQIGDQVSLID 317
 QY 300 DEPSYKGSDDMYNEFDYDLCLNEVDVTCSPKPDAPNCPEDINGYNILRVLIWFIILAI 359
 Db 318 DEPSYKGSDDMYNEFDYDLCLNEVDVTCSPKPDAPNCPEDINGYNILRVLIWFIILAI 377
 QY 360 TGNITVLVLTTSQYKLTVPFRLMCLNLAFLADLCIGIYLLLIASVDIHTKSOYHNYAIDMQ 419
 Db 378 TGNITVLVLTTSQYKLTVPFRLMCLNLAFLADLCIGIYLLLIASVDIHTKSOYHNYAIDMQ 437
 QY 420 TGAGCDAAGFTVFASLSVYTLTATLERWHITTHAMOLECKVQLRHAASVMVLGWTF 479
 Db 438 TGAGCDAAGFTVFASLSVYTLTATLERWHITTHAMOLECKVQLRHAASVMVLGWTF 497
 QY 480 FFAALFPFIIGISSYMKVSIKLPMDIDSPLSQLYMALLVNLVLAFFVVICGCTHYIYTVR 539
 Db 498 FFAALFPFIIGISSYMKVSIKLPMDIDSPLSQLYMALLVNLVLAFFVVICGCTHYIYTVR 557
 QY 540 NPTIVSSSDTKIAKRMATLIPTDFLCMAPISEFAISASLKVPLITVSKAKILLVLFYPI 599
 Db 558 NPTIVSSSDTKIAKRMATLIPTDFLCMAPISEFAISASLKVPLITVSKAKILLVLFYPI 617
 QY 600 NSCANPFLYAIFTKNFRDFFILLSKFGCYEQMAQIYRTTSSATHNFHARKSHCSAPR 659
 Db 618 NSCANPFLYAIFTKNFRDFFILLSKFGCYEQMAQIYRTTSSATHNFHARKSHCSAPR 677
 QY 660 VTNSYVLVPLNHSQN 675
 Db 678 VTNSYVLVPLNHSQN 693

RESULT 14

AAR30522
 ID AAR30522 standard; protein: 620 AA.

XX AC AAR30522;

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XX 10-MAY-1993 (first entry)
XX N-terminal of LH receptor/FSH receptor chimera #31.
XX Follicle stimulating hormone receptor; lutelinising hormone receptor;
XX human chorionic gonadotrophin; glycoprotein hormone receptor;
XX chimera; chimera.
XX Chimeraic; homo sapiens.
XX OS W09222667-A.
XX PD 23-DEC-1992.
XX PF 12-JUN-1992; 92WO-US04987.
XX PR 14-JUN-1991; 91US-0715911.
XX PA (UYNE-) UNIV NEW JERSEY.
XX PI Bernard M, Moyle WR, Myers R;
XX WPI; 1993-018150/02.
XX Glyco:protein hormone receptor analogues - having binding
XX affinity to human chorionic gonadotrophin, lutelinising and
XX follicle stimulating hormones, useful in bio:immunoassays
XX Examples; Fig 12; 103pp; English.
XX This sequence represents the N-terminal of a novel protein having a
XX binding affinity for human chorionic gonadotrophin (hCG), lutelinising
XX hormone (LH), and follicle stimulating hormone (FSH). The protein
XX itself is a chimera having residues from both the FSH receptor,
XX and LH receptor. The receptor analogues can be used in bio:immunoassays
XX for the simultaneous detection of both LH (or hCG) and FSH as
XX well as their ratio of biological activities. The analogues can also
XX be used for raising, purifying and assaying antibodies to the
XX analogues. Coding sequence for the chimera was produced by two step
XX PCR.
XX Sequence 620 AA;
XX
XX Query Match 86.4%; Score 3036.5; DB 14; Length 620;
XX Best Local Similarity 87.74; Pred. No. 2.le-283;
XX Matches 592; Conservative 1; Mismatches 7; Indels 75; Gaps 1;
XX
XX QY 1 CHHNLCHSNRVFLCDSKVTEIPTDLPNNALIEFLVTLKLVIPKGSFAGGLEKIEI 60
XX DB 18 CHHNLCHSNRVFLCDSKVTEIPTDLPNNALIEFLVTLKLVIPKGSFAGGLEKIEI 77
XX
XX QY 61 SONDVLEIADVFNPLKHEIRIEKANNLLIINPEAFONLPSLYLLISNTGKHLPA 120
XX DB 78 SONDVLEIADVFNPLKHEIRIEKANNLLIINPEAFONLPSLYLLISNTGKHLPA 137
XX
XX QY 121 VHKGISLQKVLDDIQDNNIHIVARNSEFGLSPESVYLWLSKNGIEIHCNFAFNGTOLDE 180
XX DB 138 VHKGISLQKVLDD----- 150
XX
XX QY 181 LKLSDDNNLZELPDVPOGASGVILDISRTKVHSLPNHGLNKLKLRARSTYELKKLPN 240
XX DB 151 -----SRTKVHSLPNHGLNKLKLRARSTYELKKLPN 182
XX
XX QY 241 LQKPYTLAEASLTYSHCCAFANLKRQISELHPICNKSILLRODIDDTQIGDORVSLDD 300
XX DB 183 LQKPYTLAEASLTYSHCCAFANLKRQISELHPICNKSILLRODIDDTQIGDORVSLDD 242
XX
XX QY 301 EPSYVGSGDDMYNEFDYDLCNVEDVTCSPKPAFNPCCEDIMCYNHLRVLWFLPISLAI 360
XX DB 243 EPSYVGSGDDMYNEFDYDLCNVEDVTCSPKPAFNPCCEDIMCYNHLRVLWFLPISLAI 302
XX
XX QY 361 GNTTVLVLTTSQTKLVNPRFLMCLNLAFLADLCIGYLLLIASVDIHTKSOYHNTAIDMQ 420

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DB 303 GNTTVLVLTTSQTKLVNPRFLMCLNLAFLADLCIGYLLLIASVDIHTKSOYHNTAIDMQ 362
QY 421 GAGCDAAGEFTVFASLSVYTLTAITLERHHTITHAMQLECKVOLRHAASVWVLCMTFAP 480
DB 363 GAGCDAAGEFTVFASLSVYTLTAITLERHHTITHAMQLECKVOLRHAASVWVLCMTFAP 422
QY 481 AALPPIFGISYKVSICLPMIDISPLSOLYVALLVNLVAFVVICGCTHYIYLVN 540
DB 423 AALPPIFGISYKVSICLPMIDISPLSOLYVALLVNLVAFVVICGCTHYIYLVN 482
QY 541 PTIVSSSDTKIAKRMATLIPTDFLCHAPISFAISLUSKLYPLTVSKAKILLVLPYIN 600
DB 483 PTIVSSSDTKIAKRMATLIPTDFLCHAPISFAISLUSKLYPLTVSKAKILLVLPYIN 542
QY 601 SCANPFLYALFTKWRDFRFFILLKFGCYEQAOIYRTTSSATHNPHARKSHCSSAPRV 660
DB 543 SCANPFLYALFTKWRDFRFFILLKFGCYEQAOIYRTTSSATHNPHARKSHCSSAPRV 602
QY 661 TNSYVLVPLNHSQN 675
DB 603 TNSYVLVPLNHSQN 617
XX
XX RESULT 15
XX AAR30509
XX ID AAR30509 standard; protein: 689 AA.
XX AC AAR30509;
XX DT 10-MAY-1993 (first entry)
XX DE N-terminal of LH receptor/FSH receptor chimera #18.
XX KW Follicle stimulating hormone receptor; lutelinising hormone receptor;
XX human chorionic gonadotrophin; glycoprotein hormone receptor;
XX chimera; chimera.
XX OS Chimeraic; homo sapiens.
XX PN W09222667-A.
XX PD 23-DEC-1992.
XX PF 12-JUN-1992; 92WO-US04987.
XX PR 14-JUN-1991; 91US-0715911.
XX PA (UYNE-) UNIV NEW JERSEY.
XX PI Bernard M, Moyle WR, Myers R;
XX WPI; 1993-018150/02.
XX Glyco:protein hormone receptor analogues - having binding
XX affinity to human chorionic gonadotrophin, lutelinising and
XX follicle stimulating hormones, useful in bio:immunoassays
XX Examples; Fig 12; 103pp; English.
XX This sequence represents the N-terminal of a novel protein having a
XX binding affinity for human chorionic gonadotrophin (hCG), lutelinising
XX hormone (LH), and follicle stimulating hormone (FSH). The protein
XX itself is a chimera having residues from both the FSH receptor,
XX and LH receptor. The receptor analogues can be used in bio:immunoassays
XX for the simultaneous detection of both LH (or hCG) and FSH as
XX well as their ratio of biological activities. The analogues can also
XX be used for raising, purifying and assaying antibodies to the
XX analogues. Coding sequence for the chimera was produced by two step
XX PCR.
XX Sequence 689 AA;
XX

```

Query Match 86.3%; Score 3034; DB 14; Length 689;
Best Local Similarity 87.0%; Pred. No. 4.4e-283;
Matches 590; Conservative 32; Mismatches 44; Indels 12; Gaps 3;

QY 1 CHHWLCHCSNRVFLCDSKVTEIPTDLPRNAIELRFLVTKLRVLPKGSFAGFGDLEKIEI 60
DB 18 CHHWLCHCSNRVFLCDSKVTEIPTDLPRNAIELRFLVTKLRVLPKGSFAGFGDLEKIEI 77
QY 61 SONDVLEIADVFNLPKLHEIRIEKANNLLYINPEAFONLPRLYLLISNTGKHLPA 120
DB 78 SONDVLEIADVFNLPKLHEIRIEKANNLLYINPEAFONLPRLYLLISNTGKHLPA 137
QY 121 VHKIOSLQKVLDDIODNINIHIVARNFPMGLSFESVILWLSKNGIEEIHNCFAFNGTOLDE 180
DB 138 VHKIOSLQKVLDDIODNINIHIVARNFPMGLSFESVILWLSKNGIEEIHNCFAFNGTOLDE 197
QY 181 LNLSDNNLEELPNDVFOGASGPVILDISRTKVHSLPNHGLENLKLRARSTYRKLKLPN 240
DB 198 LNLSDNNLEELPNDVFOGASGPVILDISRTKVHSLPNHGLENLKLRARSTYRKLKLPN 257
QY 241 LDKFVTLMEASLTYPHCHCAFANLKRQISELHPICNKSILRODIDDMTOIGDORYSLIDD 300
DB 258 KEKFTSLVATITYSHCCAFNLPK-----EQNFSFIFENFSKQCESTVRKADN 309
QY 301 EPSYG---KGDMMYNEFDYDLCNEVDVTCSPKPDAPNCPEDIMGYNILRVLIWFISIL 357
DB 310 ETLYSATFEENELSGWDYDYGCSPT-LQCAPEPDAPNCPEDIMGYAFRLVLIWFISTL 368
QY 358 AITGNTVLVLTTSQYKLTVPFLMCNLAFLADLCIGIYLLLIASVDIHTKSQYHNYAID 417
DB 369 AITGNTVLVLTTSQYKLTVPFLMCNLAFLADLCIGIYLLLIASVDIHTKSQYHNYAID 428
QY 418 WOTGAGDAAGFTVPASELSVYTLTATLERWHTITHAMOLECKVOLRHAASVMVLGWT 477
DB 429 WOTGAGDAAGFTVPASELSVYTLTATLERWHTITHAMOLECKVOLRHAASVMVLGWT 488
QY 478 FAFAAALPFIIGISSYMKVSIPLMDIDSPLSQLYVMALLVNLVLAFFVVCGYTHIYIT 537
DB 489 FAFAAALPFIIGISSYMKVSIPLMDIDSPLSQLYVMALLVNLVLAFFVVCGYTHIYIT 548
QY 538 VRNPTIVSSSDTKAKRMATLIPTDFLCMAPISFFAISASLKVPPLITVSKAKILLVLFY 597
DB 549 VRNPTIVSSSDTKAKRMATLIPTDFLCMAPISFFAISASLKVPPLITVSKAKILLVLFY 608
QY 598 PINSKANPLYAIFTKNFRDFFILLSKFGCYEMOQIYRTETSSATHNFHARKSHCSSA 657
DB 609 PINSKANPLYAIFTKNFRDFFILLSKFGCYEMOQIYRTETSSATHNFHARKSHCSSA 668
QY 658 PRVTNSYVLVPLNHSSQN 675
DB 669 PRVTNSYVLVPLNHSSQN 686

Search completed: June 16, 2003, 13:33:21
Job time : 48.4155 secs

Db 18 CHHWLCHCSNRVFLCQDSKVTEIPTDLPRAIELRVLTKLRVLPKGSFAGFDLEKIEI 77
QY 61 SONDVLEVEADVSNLPLKHEIRLEKANNLLYINPEAFONLPSRLYLLISNTGKHLPA 120
Db 78 SONDVLEVEADVSNLPLKHEIRLEKANNLLYINPEAFONLPSRLYLLISNTGKHLPA 137
QY 121 VHKIQSLQKVLDDIQDNIHIVARNSPMGLSFESVILWLSKNGIEEIHNCFAFNQTOLDE 180
Db 138 VHKIQSLQKVLDDIQDNIHIVARNSPMGLSFESVILWLSKNGIEEIHNCFAFNQTOLDE 197
QY 181 LNLSDNNLEELPNDVFOGASGVILDISRTKVHSLPNHGLNKKLRARSTYRLKKLPN 240
Db 198 LNLSDNNLEELPNDVFOGASGVILDISRTKVHSLPNHGLNKKLRARSTYRLKKLPN 257
QY 241 LKFTVLMASLTYPSSHCAFLNKLROISELHPICKNSILRODIDMTQIGDQVSLIDD 300
Db 258 LKFTVLMASLTYPSSHCAFLNKLROISELHPICKNSILRODIDMTQIGDQVSLIDD 317
QY 301 EPSYKSGSDMYNEFDYDLCNEVDVTCSPKPDAPNCPEDIMGYNLRLVLIWFISILAIT 360
Db 318 EPSYKSGSDMYNEFDYDLCNEVDVTCSPKPDAPNCPEDIMGYNLRLVLIWFISILAIT 377
QY 361 GNTTVLVLTTSOYKLTVPREFLMCNLAFADLCIGIYVLLIASVDIHTKSQYHNYAIDMOT 420
Db 378 GNTTVLVLTTSOYKLTVPREFLMCNLAFADLCIGIYVLLIASVDIHTKSQYHNYAIDMOT 437
QY 421 GAGCDAAGFTTFASELSVYTLTATLERWHITTHAMQLECKVOLRHAASVMVLGWTFAP 480
Db 438 GAGCDAAGFTTFASELSVYTLTATLERWHITTHAMQLECKVOLRHAASVMVLGWTFAP 497
QY 481 AAALPFIIGISSYMKVKSICLPMDIDSPLSQVMALLVNLVAFVVICGYTHIYLVN 540
Db 498 AAALPFIIGISSYMKVKSICLPMDIDSPLSQVMALLVNLVAFVVICGYTHIYLVN 557
QY 541 PTIVSSSDTKIAKRMATLIETDFLCMAPISFASASLKVPPLITVSKAKILLVLFYPIIN 600
Db 558 PTIVSSSDTKIAKRMATLIETDFLCMAPISFASASLKVPPLITVSKAKILLVLFYPIIN 617
QY 601 SCANPLXYAFTKFNRRDFILLKFGCYEQMAQIYRTTSSATHNFARKSHCSAPRV 660
Db 618 SCANPLXYAFTKFNRRDFILLKFGCYEQMAQIYRTTSSATHNFARKSHCSAPRV 677
QY 661 TNSYVLVPLNHSQN 675
Db 678 TNSYVLVPLNHSQN 692

RESULT 2
US-08-487-886-2
; Sequence 2, Application US/08487886
; Patent No. 5744448
; GENERAL INFORMATION:
; APPLICANT: Kelton, Christie Ann
; APPLICANT: Schweickhardt, Rene Lynn
; APPLICANT: Cheng, Shirley Vui Yen
; APPLICANT: Nugent, No. 5744448een Patrice
; TITLE OF INVENTION: Human Follicle Stimulating
; TITLE OF INVENTION: Hormone Receptor
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Stephan P. Williams,
; ADDRESSEE: Ares-Serono, Inc.
; STREET: Exchange Place, 37th floor
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" diskette, 1.44 MB, high density
; COMPUTER: IBM PS/2, model 55 SX
; OPERATING SYSTEM: MS-DOS version 4.0
; SOFTWARE: VAX/VMS Massill via Kermit to IBM MS-DOS
; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/487,886
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/670,085
; FILING DATE: 15-MAR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Williams, Stephan P.
; REGISTRATION NUMBER: 28546
; REFERENCE/DOCKET NUMBER: US/252
; TELEPHONE: (617) 723-1300
; TELEFAX: (617) 723-8923
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 695
; TYPE: Amino acid
; TOPOLOGY: Linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: signal sequence
; LOCATION: -17 to -1
; IDENTIFICATION METHOD: hydrophobic
; FEATURE:
; NAME/KEY: putative amino-terminal extracellular domain
; LOCATION: 1 to 349
; IDENTIFICATION METHOD: similarity with other
; IDENTIFICATION METHOD: dimeric glycoprotein receptor extracellular
; IDENTIFICATION METHOD: domains, hydrophilic
; FEATURE:
; NAME/KEY: transmembrane domain
; LOCATION: 350 to 613
; IDENTIFICATION METHOD: similarity to other G
; IDENTIFICATION METHOD: protein-coupled receptor transmembrane domains
; FEATURE:
; NAME/KEY: putative transmembrane region I
; LOCATION: 350 to 370
; IDENTIFICATION METHOD: similarity to other G
; IDENTIFICATION METHOD: protein-coupled receptor transmembrane regions,
; IDENTIFICATION METHOD: hydrophobic, about 20-23 amino acids in length
; FEATURE:
; NAME/KEY: putative transmembrane region II
; LOCATION: 382 to 404
; IDENTIFICATION METHOD: similarity to other G
; IDENTIFICATION METHOD: protein-coupled receptor transmembrane regions,
; IDENTIFICATION METHOD: hydrophobic, about 20-23 amino acids in length
; FEATURE:
; NAME/KEY: putative transmembrane region III
; LOCATION: 427 to 448
; IDENTIFICATION METHOD: similarity to other G
; IDENTIFICATION METHOD: protein-coupled receptor transmembrane regions,
; IDENTIFICATION METHOD: hydrophobic, about 20-23 amino acids in length
; FEATURE:
; NAME/KEY: putative transmembrane region IV
; LOCATION: 469 to 491
; IDENTIFICATION METHOD: similarity to other G
; IDENTIFICATION METHOD: protein-coupled receptor transmembrane regions,
; IDENTIFICATION METHOD: hydrophobic, about 20-23 amino acids in length
; FEATURE:
; NAME/KEY: putative transmembrane region V
; LOCATION: 512 to 533
; IDENTIFICATION METHOD: similarity to other G
; IDENTIFICATION METHOD: protein-coupled receptor transmembrane regions,
; IDENTIFICATION METHOD: hydrophobic, about 20-23 amino acids in length
; FEATURE:
; NAME/KEY: putative transmembrane region VI
; LOCATION: 557 to 580
; IDENTIFICATION METHOD: similarity to other G
; IDENTIFICATION METHOD: protein-coupled receptor transmembrane regions,
; IDENTIFICATION METHOD: hydrophobic, about 20-23 amino acids in length
; FEATURE:
; NAME/KEY: putative transmembrane region VII
; LOCATION: 592 to 613


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FEATURE:
; NAME/KEY: putative transmembrane region V
; LOCATION: 512 to 533
; IDENTIFICATION METHOD: similarity to other G
; IDENTIFICATION METHOD: protein-coupled receptor transmembrane regions,
; IDENTIFICATION METHOD: hydrophobic, about 20-23 amino acids in length
; FEATURE:
; NAME/KEY: putative transmembrane region VI
; LOCATION: 557 to 580
; IDENTIFICATION METHOD: similarity to other G
; IDENTIFICATION METHOD: protein-coupled receptor transmembrane regions,
; IDENTIFICATION METHOD: hydrophobic, about 20-23 amino acids in length
; FEATURE:
; NAME/KEY: putative transmembrane region VII
; LOCATION: 592 to 613
; IDENTIFICATION METHOD: similarity to other G
; IDENTIFICATION METHOD: protein-coupled receptor transmembrane regions,
; IDENTIFICATION METHOD: hydrophobic, about 20-23 amino acids in length
; FEATURE:
; NAME/KEY: putative carboxy-terminal intracellular
; NAME/KEY: domain
; LOCATION: 614 to 678
; US-08-482-855-2

Query Match          90.1%; Score 3169.5; DB 3; Length 695;
Best Local Similarity 89.5%; Pred. No. 4.4e-249;
Matches 607; Conservative 31; Mismatches 37; Indels 3; Gaps 2;

Qy 1 CHHWLCHS NRVLFCQDSKVTEIPTDLPRNAIELRFLVTLKLRVLPKGSFAGFGDLEKIEI 60
Db 18 CHHRICHCS NRVLFCQESKVTEIPSDLPNAIELRFLVTLKLRVLPKGSFAGFGDLEKIEI 77
Qy 61 SONDVLEIADVFNSLPKLEHRIEKANLLINPEAFONLPSRLYLLISNTGIRKHPA 120
Db 78 SONDVLEIADVFNSLPKLEHRIEKANLLINPEAFONLPSRLYLLISNTGIRKHPD 137
Qy 121 VHKIQSLQKVLDDIQDNNIHIIVARNFSGLSFESVILNLSKNGIEIHNCAPNGTOLDE 180
Db 138 VHKIHSLSQKVLDDIQDNNIHIIVARNFSGLSFESVILNLSKNGIEIHNCAPNGTOLDE 197
Qy 181 LNFSDNNLEELPNDVFOGASGVILDISTKTVHSLPNHGLENNKLRARSTYRLKKLPN 240
Db 198 LNFSDNNLEELPNDVFOGASGVILDISTKTVHSLPNHGLENNKLRARSTYRLKKLPD 257
Qy 241 LDGFVTLMEASLYPSHCCAFANLKRQISELHPICNKSILRQDIDDMTQIGDQVSLIDD 300
Db 258 LEKLVAMEASLYPSHCCAFANWRQISELHPICNKSILRQVVDYMTQTRGQRSSLAED 317
Qy 301 -EPSYKSGSDMYNEFDYDLCNEVDVTCSPKDPAPNCPEDIMGYNILRLVLIWFISLAI 359
Db 318 NESSYSGFDMTTEFDYDLCNEVDVTCSPKDPAPNCPEDIMGYNILRLVLIWFISLAI 377
Qy 360 TGNITVLVLTTSQYKLTVPFLMCNLAFAADICIGIYLLIASVDIHTKSOYHNYAIDWQ 419
Db 378 TGNITVLVLTTSQYKLTVPFLMCNLAFAADICIGIYLLIASVDIHTKSOYHNYAIDWQ 437
Qy 420 TGACDAAAGFTVFASLSVYTLTALERWHHTITHAMOLECKVOLRHAASVVLGTFPA 479
Db 438 TGACDAAAGFTVFASLSVYTLTALERWHHTITHAMQJDCQVLRHAASVVMGWIFA 497
Qy 480 FAALPPIFGISSYMKVSYICLPMDIDSPLSQVMALLVNLVAFVVICGYTHIYLTVR 539
Db 498 FAALPPIFGISSYMKVSYICLPMDIDSPLSQVMALLVNLVAFVVICGYTHIYLTVR 557
Qy 540 NPITVSSSDTKAKRNATLITFDLCMAPISEFASLSKLVPLITVSKAKILLVLFYPI 599
Db 558 NPITVSSSDTKAKRNATLITFDLCMAPISEFASLSKLVPLITVSKAKILLVLFHPI 617
Qy 600 NSCANPLYAIFTKFNRRDFILLSKFGCYEMAQIYRTETSSATFNHARKSHCSAPR 659
Db 618 NSCANPLYAIFTKFNRRDFILLSKFGCYEMAQIYRTETSSATFNHARKSHCSAPR 677
Qy 660 VTN--SYVLPLNHSSQN 675.
```

```
Db 678 VTNGSYILVPLSHLAQN 695

RESULT 4
; GENERAL INFORMATION:
; APPLICANT: Kelton, Christie Ann
; Schwickhardt, Rene Lynn
; Cheng, Shirley Vui Yen
; Nugent, No. 637271leen Patrice
; TITLE OF INVENTION: Human Follicle Stimulating
; Hormone Receptor
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Stephan P. Williams,
; Ares-Serono, Inc.
; STREET: Exchange Place, 37th floor
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" diskette, 1.44 MB, high density
; COMPUTER: IBM PS/2, model 55 SX
; OPERATING SYSTEM: MS-DOS version 4.0
; SOFTWARE: VAX/VMS Massll via Kermit to IBM MS-DOS
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/474,986
; FILING DATE: 07-Jun-1995
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/670,085
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Williams, Stephan P.
; REGISTRATION NUMBER: 28546
; REFERENCE/DOCKET NUMBER: US/252
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 723-1300
; TELEFAX: (617) 723-8923
; LOCATION: 614 to 678
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
; US-08-474-986-2

Query Match          90.1%; Score 3169.5; DB 4; Length 695;
Best Local Similarity 89.5%; Pred. No. 4.4e-249;
Matches 607; Conservative 31; Mismatches 37; Indels 3; Gaps 2;

Qy 1 CHHWLCHS NRVLFCQDSKVTEIPTDLPRNAIELRFLVTLKLRVLPKGSFAGFGDLEKIEI 60
Db 18 CHHRICHCS NRVLFCQESKVTEIPSDLPNAIELRFLVTLKLRVLPKGSFAGFGDLEKIEI 77
Qy 61 SONDVLEIADVFNSLPKLEHRIEKANLLINPEAFONLPSRLYLLISNTGIRKHPA 120
Db 78 SONDVLEIADVFNSLPKLEHRIEKANLLINPEAFONLPSRLYLLISNTGIRKHPD 137
Qy 121 VHKIQSLQKVLDDIQDNNIHIIVARNFSGLSFESVILNLSKNGIEIHNCAPNGTOLDE 180
Db 138 VHKIHSLSQKVLDDIQDNNIHIIVARNFSGLSFESVILNLSKNGIEIHNCAPNGTOLDE 197
Qy 181 LNFSDNNLEELPNDVFOGASGVILDISTKTVHSLPNHGLENNKLRARSTYRLKKLPN 240
Db 198 LNFSDNNLEELPNDVFOGASGVILDISTKTVHSLPNHGLENNKLRARSTYRLKKLPD 257
Qy 241 LDGFVTLMEASLYPSHCCAFANLKRQISELHPICNKSILRQDIDDMTQIGDQVSLIDD 300
Db 258 LEKLVAMEASLYPSHCCAFANWRQISELHPICNKSILRQVVDYMTQTRGQRSSLAED 317
Qy 301 -EPSYKSGSDMYNEFDYDLCNEVDVTCSPKDPAPNCPEDIMGYNILRLVLIWFISLAI 359
Db 318 NESSYSGFDMTTEFDYDLCNEVDVTCSPKDPAPNCPEDIMGYNILRLVLIWFISLAI 377
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Qy 360 TGNVTVLVITTSOYKLTVPFLMKNLAPADLCIGIYLLIASVDIHTKSOYHVAIDQK 419
Db 378 TGNVTVLVITTSOYKLTVPFLMKNLAPADLCIGIYLLIASVDIHTKSOYHVAIDQK 437
Qy 420 TGAGCDAAGFTTVPFASLSVTTTATILRHHHTITHAMQLECKVOLRHAASVYVIGWTEA 479
Db 438 TGAGCDAAGFTTVPFASLSVTTTATILRHHHTITHAMQLECKVOLRHAASVYVIGWTEA 497
Qy 480 FMAALFPPIGISTMKVSYICUPMDIDSPLSQLYNALLVLYKLAFFVYICGCTHYIYTVR 539
Db 498 FMAALFPPIGISTMKVSYICUPMDIDSPLSQLYNALLVLYKLAFFVYICGCTHYIYTVR 557
Qy 540 NPTVSSSSDPTKIKAMATLPTDPLCHAPISFPAISASLKVPLTVSKAKILLVYPI 599
Db 558 NPTVSSSSDPTKIKAMATLPTDPLCHAPISFPAISASLKVPLTVSKAKILLVYPI 617
Qy 600 NSCANPFLTAITPNRPDPPTILLSCPCYEMQAIYRTSTSSATHARKSHCSSAPR 659
Db 618 NSCANPFLTAITPNRPDPPTILLSCPCYEMQAIYRTSTSSATHARKSHCSSAPR 677
Qy 660 VTN--STVLVPLNHSN 675
Db 678 VTNGSTVLVPLSHLAON 695

RESULT 5

US-07-757-3420-4
; Sequence 4, Application US/07/7573420
; Patent No. 4295079
; GENERAL INFORMATION:
; APPLICANT: IGARASHI, Masao
; INVENTOR: NINGISHI, Takashi
; NAME: KAMAMURA, Kazuo
; TITLE OF INVENTION: PROTEIN, DNA AND USE THEREOF
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &
; CUSHMAN
; STREET: 130 Water Street
; CITY: Boston
; STATE: Massachusetts
; ZIP: 02109
; COUNTRY: US

COMPUTER READABLE FORM:

; HARDWARE: 3.5 inch floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/757,3420
; FILING DATE: 10-Sep-1991
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: BUCKLEY, Linda M.
; REGISTRATION NUMBER: 31003
; REFERENCE/DOCKET NUMBER: 41226
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)523-3400
; TELEFAX: (617)523-6440
; TELE: 200291 STRE UR
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 696 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:

US-07-757-3420-4

Query Match 51.4%; Score 1807; DB 4; Length 696;
Best Local Similarity 57.6%; Pred.No.1.7e-138;
Matches 361; Conservative 98; Mismatches 142; Indels 26; Gaps 8;

Qy 28 PRNAIELRPVLTKL--RVIPKSGPAGFGDLEKIEISQNDVLEIVDAVFSNLPKLHEIRI 85
Db 47 PRAGLS-RUSLTITIKVYIPQSGPGLNEVYKILISQSDSLEKINAFDNILNLSLEI 105
Qy 86 EKXANLLYINPAPONLRYLLLSNTGIRKHPAVHKIOSLO-KVLLDIQDNIHIVA 144
Db 106 ONTKNLVYIEFGAFTNLPRLKYLISICNTGIRKLPDVTKIPSEFNPILLEICNLHITVP 165
Qy 145 RNSPMGLSPESVILMLNSKNGIEEINHCAPNGTQDELINLNNNNLEELPHNDVFCASGPV 204
Db 166 ANAFOGNNHESITLKLYGNGFEEIQSHAFNGTTLISLEKNAHLKKMHNDAFGARGPS 225
Qy 205 ILDISRTKVLPHGLNKLKLRARSTYRLKKLPNLDKFTVLMKASUTYPSHCCAPNL 264
Db 226 ILDISRTKQALSTGLSEIOTIATSYSLAKLPGRKFNLTLDATUTYPSHCCAPNL 285
Qy 265 --KRO-----ISELHPICNKSILQDIDDPFOIGORVSLIDDESYGKSGDMYNEFD 316
Db 286 PTKQNFSEFIPKNSKCESTARRPNNETL-----YSAFAB-----SELSDDMD 332
Qy 317 YDLNNEVVDVTCSPKDFAPNGEDIMGYNLRVLNFIHLAITGNTTVLVLTTSOYKL 376
Db 333 YGFCSPKT-LOCAPEPDAPNCPEDIMGYDFLVLNLIINLAINGNVTFLVLTSHYKL 391
Qy 377 TVPRLMCLNAPADLCIGIYLLIASVDIHTKSOYHVAIDQKTAGCDAAGFTTVPFASE 436
Db 392 TVPRLMCLNAPADLCIGIYLLIASVDIHTKSOYHVAIDQKTAGCDAAGFTTVPFASE 451
Qy 437 LSVYTLTATILRHHHTITHAMQLECKVOLRHAASVYVIGWTEAFAAALFPPIGISSYMKV 496
Db 452 LSVYTLTATILRHHHTITHAMQLECKVOLRHAASVYVIGWTEAFAAALFPPIGISSYMKV 511
Qy 497 STCLMDIDSPLSQLYNALLVLYKLAFFVYICGCTHYIYTVRNPVSSSDPTKIKAM 556
Db 512 STCLMDVETLSQVLTLLNVAFLIICNYIKYFAVQNPBLATKNTDITAKRM 571
Qy 557 ATLIPTDCHAPISFPAISASLKVPLTVSKAKILLVLYPVPINSCANPFLTAITPNR 616
Db 572 AVLIPTDCHAPISFPAISASLKVPLTVSKAKILLVLYPVPINSCANPFLTAITPNR 631
Qy 617 RDPFTLLSKFCYEMQAIYRTSTSSA 643
Db 632 RDPFTLLSKFCYEMQAIYRTSTSSA 658

RESULT 6

US-07-741-453A-60
; Sequence 60, Application US/07/741453A
; Patent No. 4295079
; GENERAL INFORMATION:
; APPLICANT: PARMENTIER, MARC
; APPLICANT: LIBERT, FREDERIC
; APPLICANT: DIMONT, JACQUES
; APPLICANT: VASSART, GILBERT
; TITLE OF INVENTION: POLYPEPTIDES HAVING THYROTROPIN-RECEPTOR
; TITLE OF INVENTION: ACTIVITY, NUCLEIC ACID SEQUENCES CODING FOR SUCH RECEPTORS
; TITLE OF INVENTION: AND POLYPEPTIDES, AND APPLICATIONS OF THESE POLYPEPTIDES
; NUMBER OF SEQUENCES: 62
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN DABRY & CUSHMAN
; STREET: 1615 L STREET, N.W.
; CITY: WASHINGTON, D.C.
; COUNTRY: U.S.A.
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/741,453A
; FILING DATE: 19911015
; CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: KOKULIS, PAUL N.
REGISTRATION NUMBER: 16773
REFERENCE/DOCKET NUMBER: 91913/1107/US/ST
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 861-3000
TELEFAX: (202) 822-0944
TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO: 60:
SEQUENCE CHARACTERISTICS:
LENGTH: 764 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-741-453A-60

Query Match 51.2%; Score 1799; DB 4; Length 764;
Best Local Similarity 51.9%; Pred. No. 8.7e-138;
Matches 377; Conservative 92; Mismatches 197; Indels 60; Gaps 10;

QY 6 CHCSN----RVFLQDSKVTETPTDLPNRAIELRVTLKRVIPKSGFAGDGLKIEIS 61
DB 29 CECHOEDEFV--TKCD--IHRIPT-LPPSTQTLKFTQTKTIPSRFNSLNPISRIYLS 84
QY 62 QNDVLEIADVFSLPKLHEIRIEKANNLLVINPEAFONLPSRLYLLISNTGIKHLPAV 121
DB 85 IDATLORLSEHFYLSKMTHEIRNTRSLTSDPAULKELPLKPLGIFNTGLGVFPDV 144
QY 122 HKIQSLQK-VLADIQDNIHIVARNSPMGLSFESVILWLSKNGIEEIHNCFAFGTQDLE 180
DB 145 TKVYSTDFVFILEITDNPYMASIPANAFQGLCNETLTLKLYNNGFTSIOGHAFNGTKLDA 204
QY 181 LNLSDNNLEELPNDVFOGA-SGPVILDSRTKVSHPNHLNKKLRARSTYRLKLP 239
DB 205 VTLNKKYLSAIDKDAFGVYSGTLLDDVSYTSVLTALPSKGLKELIARNTWTLLKLP 264
QY 240 NLDKFTVLEASLTYPSSHCCAFANLKRQISELHPI--CNKSILRO-----DI 284
DB 265 LSLFLHLTRADLSYPSHCCAFKQKKIRGILESIMCNESIRSLRQKSVNTLNGPFDQ 324
QY 285 DMTQIGDQVSLIDDEFSGYSGSDMY-----NE 314
DB 325 EYEEYLGDSHAGYKNSQFQDTSNSHYVFFEEQEDTLGFGQELKPNQEEITLQAFDSH 384
QY 315 FPDYDLNVEVDVTCSPKPAFNPCEIDMGYNILRVLWIFISILATGNTTVLVLTTSOY 374
DB 385 YDITVCGGNEDMVCTPKSDEFNPCEIDMGYKELRVVWFVSLALLGNVFLVLTSHY 444
QY 375 KLTVPFRFLMCLAFADLCIGIYLLIASVDIHTKSOYHNYAIDMTQAGCDAAAGFTVFA 434
DB 445 KLTVPFRFLMCLAFADFCIGIYLLIASVDIHTKSOYHNYAIDMTQAGCDAAAGFTVFA 504
QY 435 SELSVYTLTAITLERWHTTHAMQLECKVQLRHAASVMVGLWTFEFAAALPFIIGISSYM 494
DB 505 SELSVYTLTAITLERWHTTHAMQLDCKVQLRHAASVMVGMVIFAFAAALPFIIGISSYM 564
QY 495 KYVICLPMDIDPSLSQLYMALLVNLVAFVVICGYTHIYTVRNPTVSSSDTKIAK 554
DB 565 KYVICLPMDIDPSLSQLYMALLVNLVAFVVICGYTHIYTVRNPTVSSSDTKIAK 624
QY 555 RNATLIFTDLCAPISEFAISLKVPLITYSKAKILLVLPVNSCANPELYAIFTKN 614
DB 625 RNATLIFTDLCAPISEFAISLKVPLITYSKAKILLVLPVNSCANPELYAIFTKN 684
QY 615 FRDFPILLSKGCYEMOQAIIYRTETSSATHNF-----HARKSHCSSAPRVNTSVLPL 669
DB 685 FORDVILLSKGCYEMOQAIIYRTETSSATHNF-----HARKSHCSSAPRVNTSVLPL 744
QY 670 NHSSQN 675
DB 745 SHLTNP 750

RESULT 7

US-07-757-342D-3
Sequence 3, Application US/07757342D
Patent No. 6218509

GENERAL INFORMATION:

APPLICANT: IGARASHI, Masao
MINEGISHI, Takashi
NAKAMURA, Kazuto

TITLE OF INVENTION: PROTEIN, DNA AND USE THEREOF
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:

ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &
CUSHMAN

STREET: 130 Water Street
CITY: Boston
STATE: Massachusetts
COUNTRY: US
ZIP: 02109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA: US/07/757,342D

APPLICATION NUMBER: US/07/757,342D

FILING DATE: 10-Sep-1991

CLASSIFICATION: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: BUCKLEY, Linda M.

REGISTRATION NUMBER: 31003

REFERENCE/DOCKET NUMBER: 41226

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617)523-3400

TELEFAX: (617)523-6440

TELEX: 200291 STRE UR

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 700 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 3:

US-07-757-342D-3

Query Match 51.1%; Score 1797; DB 4; Length 700;

Best Local Similarity 56.5%; Pred. No. 1.1e-137;

Matches 359; Conservative 105; Mismatches 149; Indels 22; Gaps: 7;

QY 28 PRNATELRFVLTKL--RVIPKSGFAGDGLKIEISQNDVLEIADVFSLPKLHEIRI 85
DB 51 PRAGL-ARLSLTLYLVKVPISQAFRLNEVVKIEISQSDSLERIEANAFDNLNLSELLI 109
QY 86 EKANNLLYNPEAFONLPSRLYLLISNTGIKHLPAVHKIQSLQ-KVLLDIONINHIYA 144
DB 110 QNTKLLIYECAFNLPALKLTSLTNTGIRTPDVTKISSSEFNFILEICIONLHITTP 169
QY 145 RNSFMGLSFESVILWLSKNGIEEIHNCFAFGTQDLELNLSDNNLEELPNDVFOGASGV 204
DB 170 GNAFGMNNESVTLKLYNGPPEVQSHAFNGTTLISLEKNIYLEKHNSGAFQCATGFS 229
QY 205 ILDISRTKVSHPNHLNKKLRARSTYRLKKNLKNOKFVTLMEASLTYPSSHCCAFANL 264
DB 230 ILDISRTKVSHPNHLNKKLRARSTYRLKKNLKNOKFVTLMEASLTYPSSHCCAFANL 289
QY 265 KROISELHPICKNSLILRODIDMTQIGQVRSILIDDEPSYG---KGDMMYNEFVDYDLCN 321
DB 290 PKK-----EQNFSFISFENKQCESTVKKADNETLYSAIFEENELSGWDYDYGFS 341
QY 322 EYVDVTCSPKPAFNPCEIDMGYNILRVLWIFISILATGNTTVLVLTTSOYKLTVPFR 381
DB 342 PKT-LQCAPEPDAFNPCEIDMGYNILRVLWIFISILATGNTTVLVLTTSOYKLTVPFR 400

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QY 392 LACNAPALCIGIYLLIASVDIHTKSOYHNAIDMOTGAGCDAGFFTFVASELSVIT 441
DB 401 LACNAPALCIGIYLLIASVDIHTKSOYHNAIDMOTGAGCDAGFFTFVASELSVIT 450
QY 442 LTAITLERHHTITHAMOLECKVOLRHAASVVLGNTAFAPAAALFPIFGISSYMKVSVICLP 501
DB 461 LTVITLERHHTITHAMOLECKVOLRHAASVVLGNTAFAPAAALFPIFGISSYMKVSVICLP 520
QY 502 MDIDSPLOLYMALLVLAFLVYVCGCYTHIYLVNRPITVSSSSDTKIAKRMATLIF 561
DB 521 MDVSTLSOYVILSLILNVAVFYVACIYIRIFAVQNPFLTAPNKDKIAKRMATLIF 580
QY 562 TOPICNAPISFAISASUKVPLITVSKAKILLVLPYNSCANPFLYAITNFRDRDFTI 621
DB 581 TOPICNAPISFAISASUKVPLITVSKAKILLVLPYNSCANPFLYAITNFRDRDFTI 640
QY 622 LLSRECFEYMOAOIVTETTSATHNFAKHSKSS 656
DB 641 LLSRECFEYMOAOIVTETTSATHNFAKHSKSS 669

RESULT 8
US-07-757-342D-10
: Sequence 10, Application US/07757342D
: Patent No. 6218509
: GENERAL INFORMATION:
: APPLICANT: IGARASHI, Masao
: INVENTOR: IGARASHI, Masao
: TITLE OF INVENTION: PROTEIN, DNA AND USE THEREOF
: NAMES OF SEQUENCES: 10
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &
: STREET: 130 Water Street
: CITY: Boston
: STATE: Massachusetts
: COUNTRY: US
: ZIP: 02109
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent In Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/07/757,342D
: FILING DATE: 10-Sep-1991
: CLASSIFICATION: <Unknown>
: ATTORNEY/AGENT INFORMATION:
: NAME: BUCKLEY, Linda M.
: REGISTRATION NUMBER: 31003
: REFERENCE/DOCKET NUMBER: 41226
: TELEPHONE: (617)523-3400
: TELEFAX: (617)523-6440
: TELEX: 200291 STRE UR
: INFORMATION FOR SEQ ID NO: 10:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 674 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULAR WEIGHT: 74.1 kDa
: SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-07-757-342D-10

Query Match
Best Local Similarity 55.4%; Score 1776; DB 4; Length 674;
Matches 349; Conservative 107; Mismatches 148; Indels 26; Gaps 6;

QY 38 LTKL-----RVIPKGFAGFDLEIEISQNDVLEADVFNLSPLHRIETKANN 90
DB 26 LTRLSLAYLVKVPISQAPRLNVEIKIEISQNDVLEADVFNLSPLHRIETKANN 85
```

TELEPHONE: (617)523-3400
TELEFAX: (617)523-6440
TELEX: 200291 STRE UR
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 699 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-07-757-342D-2

Query Match 50.5%; Score 1776; DB 4; Length 699;
Best Local Similarity 55.4%; Pred. No. 5.7e-136;
Matches 349; Conservative 107; Mismatches 148; Indels 26; Gaps 6;
QY 38 LTKL-----RVIPKSPAGFDLEKIEISONDVLEIVIEADVFSLPKLHEIRIEKANN 90
DB 51 LTRLSLAYLPVKVIPSQAFGLNEVIEKIEISODSLERIEANAFDNLNLSILQNTKN 110
QY 91 LLYINPEAFONLPRLRYLLISNTGKIKHLPVHKI-OSLQKVLDDIODINIHIVARNSEM 149
DB 111 LRYIEPAGFNLPGKLSLTCNTGIRKFPDVTYVFSSESFIIEICDNLHITTPGNAFQ 170
QY 150 GLSPESVILMSKNGIEEIHNCANFGTQDLDELNSDNNLEELPNDVFGASGPVILDIS 209
DB 171 GNNESVTLKLYNGFEVQSHAFGTTLSLELKENVHLEKMHNGAFRGATGPKTLDIS 230
QY 210 RTKVHSLPNEGLENKLLRARSYRLAKLNLNOKFVTLMEASLTYPHSCCAFLNKRQIS 269
DB 231 STKLQALPSGLSIEQRIALITSSYSLKLPSTRETFVNLLEATLTPSHCCAFRLN---- 285
QY 270 ELHPICKNKSILRODIDMTQIGDORVSLIDDEPSYK--GSDMMYNEFDYDLCNEVVVDV 326
DB 286 ---PTKQNFSSHSEISNFQCESTVRKVSNTKNTLYSSMLAESELSUGWDYETGCLPXT 341
QY 327 TCSKPDAPNCPEDIMGYNLRLVIFISILAITGNTTVLVVLTTSQYKLTVPRLMCNL 386
DB 342 RCAPEAPNCPEDIMGYDGLRVLIWILINILAITGNTTVLVVLTTSQYKLTVPRLMCNL 401
QY 387 AFADLCIGYLLLTASVDIHTKSYHNYADMTQAGCDAAGFTVPFASLSVYTLTAYT 446
DB 402 SFADFCHGLYLLLTASVDSOTKGYHNYADMTQAGCDAAGFTVPFASLSVYTLTAYT 461
QY 447 LERHHTTHAMOLECKVOLRHAASVMVLGWTFAFAALFPFGISSTYKYSICLPMDIDS 506
DB 462 LERHHTTHAMOLECKVOLRHAALIMLGGWLFSSLIAMLPVGSNTKYSICPMDVET 521
QY 507 PLSQYVNALVNLVAFVYICGCTHYILTVRNPTIVSSSDTKIAKRMATLIFTDFLC 566
DB 522 TLSQVYILTLINVAFFIACACIKIYFAVRNPELMATNKDTKIAKMAILIFTDFTC 581
QY 567 MAPISFAISASLKVPILTSKAKILVLYPINSKANPELYAIFTKFRDRDPFILLSKF 626
DB 582 MAPISFAISAAFTVITNSVLLVLYPINSKANPELYAIFTKFRDRDPFILLSKF 641
QY 627 GYEMOAGIYRTTSSATHNFARKSHCSS 656
DB 642 GCCRRALRYRK-----DFSATYSNCKN 665

RESULT 10
US-07-741-453A-56
Sequence 56, Application US/07741453A
Patent No. 6228597
GENERAL INFORMATION:
APPLICANT: PARMENTIER, MARC
APPLICANT: LIBERT, FREDERIC
APPLICANT: DUMONT, JACQUES
APPLICANT: VASSART, GILBERT
TITLE OF INVENTION: POLYPEPTIDES HAVING THYROTROPIN-RECEPTOR
TITLE OF INVENTION: ACTIVITY, NUCLEIC ACID SEQUENCES CODING FOR SUCH RECEPTORS
TITLE OF INVENTION: AND POLYPEPTIDES, AND APPLICATIONS OF THESE POLYPEPTIDES

NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHMAN DARBY & CUSHMAN
STREET: 1615 L STREET, N.W.
CITY: WASHINGTON, D.C.
COUNTRY: U.S.A.
ZIP: 20036
COMPUTER READABLE FORM:
MEDIUM TYPE: Disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07741,453A
FILING DATE: 19911015
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: KOKULIS, PAUL N.
REGISTRATION NUMBER: 16773
REFERENCE/DOCKET NUMBER: 91913/1107/US/ST
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 861-3000
TELEFAX: (202) 822-0944
TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO: 56:
SEQUENCE CHARACTERISTICS:
LENGTH: 792 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-741-453A-56

Query Match 47.5%; Score 1670; DB 4; Length 792;
Best Local Similarity 50.3%; Pred. No. 2.7e-127;
Matches 368; Conservative 100; Mismatches 166; Indels 98; Gaps 21;

QY 28 PRNAIEIRFVLTCL--RVIPKSPAGFDLEKIEISONDVLE-----VIEADVFSLPK 79
DB 59 PRAGLS--RLSTYLPKIPVISOAFRGLNEVVKIEISODSLEPIGHGCKIEANAFDNLN 117
QY 80 LHEIRIEKANLLINPEAFONLPRLRYLLISNTGIRK-----LPAVHKIQSLQ-KVLL 132
DB 118 LSEILQNTNLYVIEPGATNLPRLAYLSICNTGIRKPIGCHGCLPDVTKIFSSEFNIL 177
QY 133 DIQDNIHIVARNFMSGLSFESVILMSKNGIEEIHNC-----AFNGTQDELNLSDN 186
DB 178 EICDNLHITVPAFAFOGMNNEITLKLNGFEPGPIGHGCEIQSHAFNGTLLISLEKEN 237
QY 187 NNLEELPNDVFGASGVILDISRTKVHS-----LNHGLENLKLRARSTYRLKLPN 240
DB 238 AHLKMHNDAPFRGARGPSILDISSTKLOAPIGHGCLPSYGLSIOTLIATSSYSLKLKPS 297
QY 241 LDKFETLMEASLTYPHSCCAFLN-----KRQ-----ISELHPICKNKSILRODIDD 286
DB 298 REKFTNLLDALTYPHSCCAFLNPPIGHGCTKQNFSESIKFNKSCOSTARRPNNET 357
QY 287 MTQIGDORVSLIDDEPSYKGSDDMMYNEFDY-DLCNEVVVDVTCSPKPDAPNCPEDIMGYN 345
DB 358 LYSIFAFAESELSDWDPIGHGCEYD--YGPIGHGCFSPKT--LQCAPEADPAFNPCEIDIMGYD 414
QY 346 ILRVLIWFISTLATGTNTVLVW-----LTTQYKLTVPFLMCNLAFAADLCIGYLL 399
DB 415 FLRVLIWILINILAIMGNVTVLFAPIGHGCLLTSHYKLTVPFLMCNLSFADFCMGLYLL 474
QY 400 IASVDIHTKSYHNYAIDW-----QTGAGDAAGFTVPFASLSVYTLTITLERWHIT 453
DB 475 IASVDAOTKGYYNHAIWDPIGHGCGTNGCSVAGFTVPFASLSVYTLTITLERWHIT 534
QY 454 THAMOLECKVOLRHA-----ASVNLGWTFAFAALFPFGISSTYKYSICLPMDIDSP 507
DB 535 TYAQLDQKLRHRAPIGHGCEIPIMLGGWLFSTLIAMLPVGVSSYKYSICLPMDIVETT 594

QY 508 LSOLYVALLY-----LVAFVYVCCGYHYIYVNPVTVSSSDTKIAKPMATLIP 561
DB 595 LQVILPILPICHGGLVAFVYVCCGYHYIYVNPVTVSSSDTKIAKPMATLIP 564
QY 562 TQVILPILPICHGGLVAFVYVCCGYHYIYVNPVTVSSSDTKIAKPMATLIP 564
DB 655 TDFTCMAPICHGGLVAFVYVCCGYHYIYVNPVTVSSSDTKIAKPMATLIP 714
QY 616 RRD-----FVLLSKGCGYEMQAIYRTTSSATHNPHARKSHC-----SSAP-RVTN 662
DB 715 RRDPIGCHGGLVAFVYVCCGYHYIYVNPVTVSSSDTKIAKPMATLIP 765
QY 663 SYLVPLNHSQ 674
DB 766 KUTLPIGHCQ 777

RESULT 11
US-07-741-453A-61
Sequence 61, Application US/07741453A
Patent No. 6228597
GENERAL INFORMATION:
APPLICANT: PARMENTIER, MARC
APPLICANT: LIBERT, FREDERIC
APPLICANT: DUMONT, JACQUES
TITLE OF INVENTION: POLYPEPTIDES HAVING THYROTROPIN-RECEPTOR
TITLE OF INVENTION: ACTIVITY, NUCLEIC ACID SEQUENCES CODING FOR SUCH RECEPTORS
TITLE OF INVENTION: AND POLYPEPTIDES, AND APPLICATIONS OF THESE POLYPEPTIDES
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHMAN DARBY & CUSHMAN
STREET: 1615 L STREET, N.W.
CITY: WASHINGTON, D.C.
COUNTRY: U.S.A.
ZIP: 20036
COMPUTER READABLE FORM:
MEDIUM TYPE: Disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07741453A
FILING DATE: 19911015
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: KOKULIS, PAUL N.
REGISTRATION NUMBER: 16773
REFERENCE/DOCKET NUMBER: 91913/1107/US/ST
TELEPHONE: (202) 861-3000
TELEFAX: (202) 822-0944
TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO: 61:
SEQUENCE CHARACTERISTICS:
LENGTH: 764 amino acids
TYPE: AMINO ACID
STRANDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-741-453A-61

Query Match
Best Local Similarity: 49.61, Pred. No. 3,2e-126; Matches 339; Conservative 110; Mismatches 179; Indels 55; Gaps 11;
6 CHSNC-----RVFLCQSDSVTEPTDPRNAIELEFVLKLVTPKSGFQGLEKTELS 61
29 CECHOEDPRV-CKD--IQRIPS-LPSPOTLALIEHLTIPSHAFSLNPSRIYVS 84
62 ONDVLVEADVSNLPLKHEIRIEKIANLVIINPEAPONLPSRLYLLISMTGKHPAV 121
85 IDLTLOQLSHSFNLSKVTHIEIRNRLNLTIDPDALKELPLAFLGIPNTGLKMPDL 144

QY 122 HKIOSQ-KVLLDIQDMNHHVARNFPGLSFESVILMSKNGTEIEHNCFNFGTOLDE 180
DB 145 TVTSDTDFILEITDMPHTSIPVPAVQGLCNETLTKLNGFTSVQGTAFNGTKLDA 204
QY 181 LNLSDNNLEELPNDVQGA-SGPVILDIISRTKVSUNGLKLEKLBASSTYRLKLP 239
DB 205 VYLKKNKYLTVIKDADFVYSGFSLDVSQTSYALPSGLEHLEKLIARMTWTLKLP 264
QY 240 MLDFKVTLMESALITPSSHCCAFANLAROISELHPI-CNKSIL-----RODIDMT 288
DB 265 LSLSPHLTRADLSTPSSHCCAFKOKKIRGLTESLMCNESMSQSLRQKRSVNALNSPLHQ 324
QY 289 -----QIGDORVSLID-----DEPSYKGSQM-----MYNE 314
DB 325 EYENLGDSIVGKEKSKFOOTHANNAHYVFFEDQEDIEIGFQGLKLNPOEETLQAFDSH 384
QY 315 FQDCLNEVDVTCSPKPAFNPCEDIHGYNLRVLIWFIISALITGNTVLVVLTSOY 374
DB 385 TDYTCOSQEDVCTPSPBPNCEDIHGYNLRVLIWFIISALITGNTVLVVLTSOY 444
QY 375 LNVPPFLKNAFADICIGYLLIASVDIHTKSOYHNYATDMQTCAGCQAGPTVPA 434
DB 445 KLVNPFKLNALAFADICIGYLLIASVDIHTKSOYHNYATDMQTCAGCQAGPTVPA 504
QY 435 KLVNPFKLNALAFADICIGYLLIASVDIHTKSOYHNYATDMQTCAGCQAGPTVPA 434
DB 505 SELSVTVTLTILERHVAITFAHRLDKIRLHRAAIIIVGGMVCCFLALLPLVGLISYA 564
QY 495 KYVICUPMDIDSPLSQLYNALLYLVAFVYVCCGYHYIYVNPVTVSSSDTKIAK 554
DB 565 KYVICUPMDIDSPLSQLYNALLYLVAFVYVCCGYHYIYVNPVTVSSSDTKIAK 624
QY 555 RYATLFTDFLCNATISFAISASLKVPLTVSKAKILLVLPYVINSANPELVAITKN 614
DB 625 RYATLFTDFLCNATISFAISASLKVPLTVSKAKILLVLPYVINSANPELVAITKN 684
QY 615 FREDFTLLSKGCGYEMQAIYRTTSSATHNPHARKSHC-----SSAP-RVTN 662
DB 685 FREDFTLLSKGCGYEMQAIYRTTSSATHNPHARKSHC-----SSAP-RVTN 707

RESULT 12
US-07-741-453A-54
Sequence 54, Application US/07741453A
Patent No. 6228597
GENERAL INFORMATION:
APPLICANT: PARMENTIER, MARC
APPLICANT: LIBERT, FREDERIC
APPLICANT: DUMONT, JACQUES
TITLE OF INVENTION: POLYPEPTIDES HAVING THYROTROPIN-RECEPTOR
TITLE OF INVENTION: ACTIVITY, NUCLEIC ACID SEQUENCES CODING FOR SUCH RECEPTORS
TITLE OF INVENTION: AND POLYPEPTIDES, AND APPLICATIONS OF THESE POLYPEPTIDES
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHMAN DARBY & CUSHMAN
STREET: 1615 L STREET, N.W.
CITY: WASHINGTON, D.C.
COUNTRY: U.S.A.
ZIP: 20036
COMPUTER READABLE FORM:
MEDIUM TYPE: Disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07741453A
FILING DATE: 19911015
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: KOKULIS, PAUL N.
REGISTRATION NUMBER: 16773

Db 415 GYAFRLVHLINLNLAIAGNLTVLVTRATHCGLLTSRKLTVPRFLMCLNSFADPCNGLY 474
QY 397 LLLTASVDIHTKSYHNVAIDW-----OTGAGCDAAGFTTVFASLSVYTLTATLERN 450
Db 475 LLLTASVDSOTKGYNYHAIIDWATHCGGTGGCGAGFTTVFASLSVYTLTATLERN 534
QY 451 HTITHAMOLECKVQLRAHAS-----VWVLGWTFAAALPPIFGISSTKMSVCLPMDI 504
Db 535 HTITAVOLDOKLRLHARATHCGIPMLGGMLESTLATMPLVGISTNKMVSLCLMDIV 594
QY 505 DSPLSQLYMVALV-----LNYLAFVYICGCTHYIYLVTRNPTIVSSSDTKIAKMAT 558
Db 595 ESTLSQVYTLISLIRATHCGUNVAVFYACATIRIFYAVONPELTAPNKDKTIAKQAI 654
QY 559 LIPTDFCLMA-----PISFAISASLVPLTVSKAKILLVLPFPINSCANPFLYAIT 612
Db 655 LIPTDFCLMAHATCPISFAISASLVPLTVSKAKILLVLPFPINSCANPFLYAIT 714
QY 613 KNPRED-----PILLSKRCGYEMQAIYRTSSNTHNFAKSHCSS 656
Db 715 KAFORDRATHCGFLLLSRFGCCCKRAELRYRK-----EFSAYTSCKN 758

RESULT 14
US-07-741-453A-59
: Sequence 59, Application US/07741453A
: Patent No. 6248597
: GENERAL INFORMATION:
: APPLICANT: PARMENTIER, MARC
: APPLICANT: LIBERT, FREDERIC
: APPLICANT: DOMONT, JACQUES
: APPLICANT: VASSART, GILBERT
: TITLE OF INVENTION: POLYPEPTIDES HAVING THYROTROPIN-RECEPTOR
: TITLE OF INVENTION: ACTIVITY NUCLEIC ACID SEQUENCES CODING FOR SUCH RECEPTORS
: TITLE OF INVENTION: ACTIVITY NUCLEIC ACID SEQUENCES CODING FOR SUCH RECEPTORS
: NUMBER OF SEQUENCES: 62
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: CUSHMAN DABBY & CUSHMAN
: STREET: 1615 L STREET, N.W.
: CITY: WASHINGTON, D.C.
: COUNTRY: U.S.A.
: ZIP: 20036
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent in Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/07741453A
: FILING DATE: 19911015
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: KOKULIS, PAUL N.
: REGISTRATION NUMBER: 16773
: REFERENCE/DOCKET NUMBER: 91913/1107/US/ST
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (202) 861-3000
: TELEFAX: (202) 822-0944
: TELEX: 6714627 CUSH
: INFORMATION FOR SEQ ID NO: 59:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 764 amino acids
: TYPE: AMINO ACID
: TOPOLOGY: single
: MOLECULE TYPE: protein
US-07-741-453A-59

Query Match 46.7% Score 1641.5; DB 4; Length 764;
Best Local similarity 49.3%; Pred. No. 5.3e-125;
Matches 336; Conservative 110; Mismatches 182; Indels 55; Gaps 11;
QY 6 CHCSN-----RVFLQDSKVTEIPTDLPNNALRLVTLKLRVFKSGFAGDGLEKIEIS 61

Db 29 CCEHODEFRV-TCKD--IQRPIS-LPPSTOTLAKLIEHLRTIPSHAFSMLNPSIRSIYVS 84
QY 62 QNDVLEVIDADVNSLPFLHEIRIEKANWLLYIMPFAQNPULPSLYLLISNTGKIKHLPAY 121
Db 85 IDLTLOOLESUSFVNLKSYTHIEIRNTRNLTIDPDLAKELPLAFLOIFGLKAMPOL 144
QY 122 HKIOSLO-KVLLDQDINENIHVARNSPGLSPESVILWLSKNGIEETHNCACFNCTOLDE 180
Db 145 TKVSTDTDFILEITDNPYMTSIPVNAFOGLNETLTLKLYNGFTSVQCYAFNCTKLOA 204
QY 181 LNLSDNNIEELPNDFOGA--SGPVILDIISRTKVHSLPHGLNKLKLRLARSTYRLKLLP 239
Db 205 VTLNKNKYLTVIKDAFGGVYSGPSLDVDSOTSVTALPSKLEHLKELIARNTMTLKKLP 264
QY 240 NLDKFPVTLMEASLTYPSCAFANLKRQISELHPI-CNKSTL-----RQDIDDMT----- 288
Db 265 LSLGFLHLTRADISYSPSCAFANLKRQISELHPI-CNKSTL-----RQDIDDMT----- 324
QY 289 ----QIDQORVSLID-----DEPSYCKGSDM-----MYNE 314
Db 325 EYENLQDSIVGYKSKFODTHNANYVFFEDQEDILIQELKNQOETLOAFDSH 384
QY 315 FQYDLCEVVDVTCSPKDPANPCEDIMGYNLTILNFIISILAITGNTTVLVLTTSOY 374
Db 385 XYDTICGDSDEMVCPTKSDENPCEDIMGYKFLRIYVWVSVLLALLGNVFLVLLILTSHY 444
QY 375 KLTVPRLMCLNAPADLCIGIYLLLIASVDIHTKSOVHNYAIDMQTGAGCDAAGFTTFA 434
Db 445 KLVPRFLMCLNAPADPCMGVYLLLIASVDLTHSEYVNHAIQDQTGCGTAGTFFTFA 504
QY 435 SELSVYTLTATLERHHTITHAKOLECKVQLRHAASVWYLGMTAFAPAAALPFIIGISYM 494
Db 505 SELSVYTLTATLERHHTITHAKOLECKVQLRHAASVWYLGMTAFAPAAALPFIIGISYM 564
QY 495 KVSICLPMDSPLQVLYMALLVUNLVAFVYICGCTHYIYLVTRNPTIVSSSDTKIAK 554
Db 565 KVSICLPMDSPLQVLYMALLVUNLVAFVYICGCTHYIYLVTRNPTIVSSSDTKIAK 624
QY 555 RNATLFTDPLCMAPISFAISASLVPLTVSKAKILLVLPFPINSCANPFLYAITKN 614
Db 625 RNATLFTDPLCMAPISFAISASLVPLTVSKAKILLVLPFPINSCANPFLYAITKN 684
QY 615 FRDPTLLSKFCGYEMQAIYR 637
Db 685 FORDVFTLLSKFCGCKRQAOYR 707

RESULT 15
US-07-757-342D-5
: Sequence 5, Application US/07757342D
: Patent No. 6248597
: GENERAL INFORMATION:
: APPLICANT: ICARASHI, MASAO
: APPLICANT: MINEGISHI, TAKASHI
: APPLICANT: MAKIURA, KAZUO
: TITLE OF INVENTION: PROTEIN, DNA AND USE THEREOF
: NUMBER OF SEQUENCES: 10
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &
: CUSHMAN
: STREET: 130 Water Street
: CITY: Boston
: STATE: Massachusetts
: COUNTRY: US
: ZIP: 02109
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent in Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/07757342D

Job time : 23.2326 secs

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: FILING DATE: 10-Sep-1991
: CLASSIFICATION: <Unknown>
: ATTORNEY/AGENT INFORMATION:
: NAME: BUCKLEY, Linda M.
: REGISTRATION NUMBER: 31003
: REFERENCE/DOCKET NUMBER: 41226
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (617)523-3400
: TELEFAX: (617)523-6440
: TELEX: 200291 STRE UR
: INFORMATION FOR SEQ ID NO: 5:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 764 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-07-757-342D-5

Query Match      46.7%; Score 1640.5; DB 4; Length 764;
Best Local Similarity 49.2%; Pred. No. 6.4e-125;
Matches 336; Conservative 110; Mismatches 182; Indels 55; Gaps 11;

QY 6 CHCSN-----RVFLCDSKVTEIPTDLPNAIELRVLTGLRVIPKGSFAGFDLEKIEIS 61
Db 29 CECHOEDFRV--TKCD--IQRIPL--LPPSTOTLKLIETHLRTPSHAFSLNPLNISRIYVS 84
QY 62 QNDVLEIVLEADVSNLPLKHEIRIEKANNLLYINPEAFQNLPSLRLLYSNTGKHLPAV 121
Db 85 IDVTIQQLESFYSNLSKVTHIEIRNTRNLTYYIDPAULKELPLFLKFLGIFNTGLKMFDDL 144
QY 122 HKIQSLQ--KVLIQDININIHIVARNSPMGLSFESVILWLSKNGEIEHNCFAFNCTOLDE 180
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QY 181 LNLSDNNLEELPNDVFOGA--SGPVLDISRTKVHSLPNHGLNKLKLRARSTYRLKKLP 239
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QY 240 NLDKFTVLEASLTYPSCCAFANLKRQISELHPI--CNKSL-----RQDIDDMT----- 288
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QY 375 KLTVPREFLMCLAFADLCIGIYVLLIASVDIHTKSOYHNYAIDMOTGAGCDAAGFTVFA 434
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QY 555 RMATLIFTDFLCMAPIFSFASLSKVLPLITVSKAKILLVLYFPYINSCANPLYAIFTKN 614
Db 625 RMVLIPTDFLCMAPIFSYALSAILNKPLITVSNKILLVLYFPLNSCANPLYAIFTKE 684
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Search completed: June 16, 2003, 13:37:58

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 16, 2003, 13:36:01 : Search time 165.911 Seconds
(without alignments)
434.981 Million cell updates/sec

Title: US-09-877-804-7
Perfect score: 3516
Sequence: 1 CHHMLCHSRRVFLCQDSKV.....SAPRVTNSVYLPLNHSN 675

Scoring table: BLOSUM62
Gapup 10.0, Capext 0.5

Searched: 408643 seqs, 106915682 residues
Total number of hits satisfying chosen parameters: 408643

Minimum DB seq length: 0
Maximum Match 100%

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_AA:
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3516	100.0	675	10	US-09-877-804-7 Sequence 7, Appl 1
2	3516	100.0	692	9	US-09-965-536A-11 Sequence 11, Appl 1
3	3516	100.0	692	10	US-09-877-804-6 Sequence 6, Appl 1
4	3482	99.0	688	9	US-09-965-536A-12 Sequence 12, Appl 1
5	3149.5	89.6	695	10	US-09-804-626-8 Sequence 8, Appl 1
6	3010.5	85.6	687	9	US-09-965-536A-13 Sequence 13, Appl 1
7	2577.5	73.3	693	9	US-09-965-536A-14 Sequence 14, Appl 1
8	2103.5	59.9	676	10	US-09-877-804-9 Sequence 9, Appl 1
9	1997.5	52.1	676	10	US-09-877-804-8 Sequence 8, Appl 1
10	1797	51.1	700	10	US-09-877-804-2 Sequence 2, Appl 1
11	1797	51.1	700	10	US-09-877-804-3 Sequence 3, Appl 1
12	1783.5	50.7	676	9	US-09-965-536A-15 Sequence 5, Appl 1
13	1776	50.5	699	10	US-09-804-626-6 Sequence 6, Appl 1
14	1638.5	46.6	764	9	US-10-045-624B-2 Sequence 2, Appl 1
15	1505.5	42.8	516	10	US-09-804-626-4 Sequence 4, Appl 1
16	1353	38.5	458	10	US-09-862-767A-5 Sequence 5, Appl 1
17	1191	33.9	359	10	US-09-862-767A-7 Sequence 7, Appl 1
18	910.5	23.1	861	10	US-09-804-551B-20 Sequence 20, Appl 1
19	675	19.2	341	10	US-09-877-804-4 Sequence 4, Appl 1

Sequence 2, Appl 1
Sequence 16, Appl 1
Sequence 26, Appl 1
Sequence 27, Appl 1
Sequence 28, Appl 1
Sequence 2, Appl 1
Sequence 10, Appl 1
Sequence 3, Appl 1
Sequence 5, Appl 1
Sequence 9, Appl 1
Sequence 7, Appl 1
Sequence 6, Appl 1
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Sequence 24, Appl 1
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Sequence 3, Appl 1
Sequence 6, Appl 1
Sequence 1, Appl 1
Sequence 1, Appl 1
Sequence 2, Appl 1
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Sequence 8, Appl 1
Sequence 7, Appl 1
Sequence 8, Appl 1
Sequence 4, Appl 1

ALIGNMENTS

RESULT 1
US-09-877-804-7
; Sequence 7, Application US/09877804
; Title: US-09-877-804-7
; GENERAL INFORMATION:
; APPLICANT: Nikolova, Karoly
; APPLICANT: McFarland, Keith C.
; APPLICANT: Seaburg, Peter H.
; TITLE OF INVENTION: Glycoprotein Hormone Receptor Molecules
; FILE REFERENCE: P0576P1C2
; CURRENT APPLICATION NUMBER: US/09/877-804
; CURRENT FILING DATE: 2001-09-04
; PRIOR APPLICATION NUMBER: US 08/207,814
; PRIOR FILING DATE: 1994-03-07
; PRIOR APPLICATION NUMBER: US 07/701,153
; PRIOR FILING DATE: 1991-10-31
; PRIOR APPLICATION NUMBER: US 07/347,693
; PRIOR FILING DATE: 1993-05-05
; NUMBER OF SEQ ID NOS: 22
; SEQ ID NO 7
; LENGTH: 675
; TYPE: PPT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: deduced sequence
US-09-877-804-7

Query Match 100.0%; Score 3516; DB 10; Length 675;
Best Local Similarity 100.0%; Pred. No. 1.4e-284;
Matches 675; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CHHMLCHSRRVFLCQDSKVTEPTDLPRAETLRLVPLKRVIPKGSFAGFGLKIEI 60
Db 1 CHHMLCHSRRVFLCQDSKVTEPTDLPRAETLRLVPLKRVIPKGSFAGFGLKIEI 60
Qy 61 SONDYLEVLEADVFNPLKLETRIEKANNLLYNPAFONLPSLYLLISNTGKILPA 120
Db 61 SONDYLEVLEADVFNPLKLETRIEKANNLLYNPAFONLPSLYLLISNTGKILPA 120
Qy 121 VHKIQSLQKVLDDQNTINIRHIVARNSPGLSPFSLVILMSKNGIEEIHNCAPNCTQLOB 180
Db 121 VHKIQSLQKVLDDQNTINIRHIVARNSPGLSPFSLVILMSKNGIEEIHNCAPNCTQLOB 180

Db 121 VHKIQSLQKVLDDIQDNIHIVARNFPMGLSFESVILWLSKNGIEEIHNCFAFNGTQOLDE 180
QY 181 LNLSDNNLEELPNDVFOGASGPVILDSRTKVSHPNHLNGLNKKLRARSTYRLKKLPN 240
Db 181 LNLSDNNLEELPNDVFOGASGPVILDSRTKVSHPNHLNGLNKKLRARSTYRLKKLPN 240
QY 241 LDKFVTLMASLTYSCHCAAFANLKRQISELHPICNKSILRQIDDMTOIGDQVSLIDD 300
Db 241 LDKFVTLMASLTYSCHCAAFANLKRQISELHPICNKSILRQIDDMTOIGDQVSLIDD 300
QY 301 EPSYKGSMDMYNEFDYDLCNEVVDVTCSPKPDAPNCPEDIMGYNLRVLWIFISILAIT 360
Db 301 EPSYKGSMDMYNEFDYDLCNEVVDVTCSPKPDAPNCPEDIMGYNLRVLWIFISILAIT 360
QY 361 GNTTVLVLTTSQYKLTVPFLMCNLAFAADLCIGIYLLIASVDIHTKSOYHNYAIDWQT 420
Db 361 GNTTVLVLTTSQYKLTVPFLMCNLAFAADLCIGIYLLIASVDIHTKSOYHNYAIDWQT 420
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Db 421 GAGCDAAGFTFVASELSVYTLTAITLERWHTITHAMOLECKVOLRHAASVMVLGWTFAF 480
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Db 481 AALFPFIFGISSYMKVSIICLPMDIDSPLSQLYVMALLVNLVAFVVICGCTHYIYLTVRN 540
QY 541 PTIVSSSDTKIAKRMATLIFTDFLCMAPISFPAISASLKVPLTVSKAKILLVLFYPIN 600
Db 541 PTIVSSSDTKIAKRMATLIFTDFLCMAPISFPAISASLKVPLTVSKAKILLVLFYPIN 600
QY 601 SCANPELYAIFTKFRDRDFILLSKFCGYEMOAOIYRTETSSATHNFHARKSHCSSAPRV 660
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QY 661 TNSYVLVPLNHSSQN 675
Db 661 TNSYVLVPLNHSSQN 675

RESULT 2
US-09-965-536A-11
; Sequence 11, Application US/09965536A
; Publication No. US20030027323A1
; GENERAL INFORMATION:
; APPLICANT: FEDER, J. N.
; APPLICANT: MINTIER, G.
; APPLICANT: RAMANATHAN, C. S.
; APPLICANT: HAWKEN, D. R.
; TITLE OF INVENTION: A NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGPRBMV5,
; TITLE OF INVENTION: EXPRESSED HIGHLY IN BRAIN AND OVARIAN TISSUES
; FILE REFERENCE: D0041NP
; CURRENT APPLICATION NUMBER: US/09/965,536A
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 60/235,713
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/261,781
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: 60/306,605
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 60/310,436
; PRIOR FILING DATE: 2001-08-03
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 11
; LENGTH: 692
; TYPE: PRT
; ORGANISM: RAT
US-09-965-536A-11

Query Match 100.0%; Score 3516; DB 9; Length 692;
Best Local Similarity 100.0%; Pred. No. 1.4e-284;
Matches 675; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHHNLCHCSNRVFLCQDSKVTEIPTDLPRNATELRFVLTKLRYIPKGSFAGFDLEKIEI 60
Db 18 CHHMLCHCSNRVFLCQDSKVTEIPTDLPRNATELRFVLTKLRYIPKGSFAGFDLEKIEI 77
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Db 78 SONDVLEAVEADVFNLPKLHEIRTEKANNLLYINPEAFONLPSRLYLLISNTGIKHLPA 137
QY 121 VHKIQSLQKVLDDIQDNIHIVARNFPMGLSFESVILWLSKNGIEEIHNCFAFNGTQOLDE 180
Db 138 VHKIQSLQKVLDDIQDNIHIVARNFPMGLSFESVILWLSKNGIEEIHNCFAFNGTQOLDE 197
QY 181 LNLSDNNLEELPNDVFOGASGPVILDSRTKVSHPNHLNGLNKKLRARSTYRLKKLPN 240
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Db 258 LDKFVTLMASLTYSCHCAAFANLKRQISELHPICNKSILRQIDDMTOIGDQVSLIDD 317
QY 301 EPSYKGSMDMYNEFDYDLCNEVVDVTCSPKPDAPNCPEDIMGYNLRVLWIFISILAIT 360
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QY 481 AALFPFIFGISSYMKVSIICLPMDIDSPLSQLYVMALLVNLVAFVVICGCTHYIYLTVRN 540
Db 498 AALFPFIFGISSYMKVSIICLPMDIDSPLSQLYVMALLVNLVAFVVICGCTHYIYLTVRN 557
QY 541 PTIVSSSDTKIAKRMATLIFTDFLCMAPISFPAISASLKVPLTVSKAKILLVLFYPIN 600
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QY 601 SCANPELYAIFTKFRDRDFILLSKFCGYEMOAOIYRTETSSATHNFHARKSHCSSAPRV 660
Db 618 SCANPELYAIFTKFRDRDFILLSKFCGYEMOAOIYRTETSSATHNFHARKSHCSSAPRV 677
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Db 678 TNSYVLVPLNHSSQN 692

RESULT 3
US-09-877-804-6
; Sequence 6, Application US/09877804
; Patent No. US20020061557A1
; GENERAL INFORMATION:
; APPLICANT: Nikolics, Karoly
; APPLICANT: McFarland, Keith C.
; APPLICANT: Segalo, Deborah L.
; APPLICANT: Seeburg, Peter H.
; TITLE OF INVENTION: Glycoprotein Hormone Receptor Molecules
; FILE REFERENCE: P0576PIC2
; CURRENT APPLICATION NUMBER: US/09/877,804
; CURRENT FILING DATE: 2001-09-04
; PRIOR APPLICATION NUMBER: US 08/207,814
; PRIOR FILING DATE: 1994-03-07
; PRIOR APPLICATION NUMBER: US 07/781,153
; PRIOR FILING DATE: 1991-10-31
; PRIOR APPLICATION NUMBER: US 07/347,683
; PRIOR FILING DATE: 1989-05-05
; NUMBER OF SEQ ID NOS: 22
; SEQ ID NO 6
; LENGTH: 692
; TYPE: PRT
; ORGANISM: Artificial sequence

FEATURE:
OTHER INFORMATION: deduced sequence
US-09-877-804-6

Query Match 100.0%; Score 3516; DB 10; Length 692;
Best Local Similarity 100.0%; Pred. No. 1.4e-284;
Matches 675; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 18 CHHWLCHSNNRVFLQDSKVTETPTDLPNNAIELRVLTARVLPKSGFAGGDLKLEI 77
OY 61 SONDLVLEADVSNLPLKHEIRIEKANNLLYINPEAFONPLSLRYLLISNTGKHLPA 120
DB 78 SONDLVLEADVSNLPLKHEIRIEKANNLLYINPEAFONPLSLRYLLISNTGKHLPA 137
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DB 138 VHKIOSLOKVLDDIODNINIHIVARNSPFGLSFESVILWLSKNGIEEIHNCAPNGTOLDE 197
OY 161 LNLSDNNLLELPNDVFOGASGPVILDISRTKVHSLPNHGLENLKLRARSTYRLKLLPN 240
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DB 498 AALFPIGISTMYKVSICLPHWDISPLSOLYVALLVNLVAFVYICGCTHYIYLVYRN 557
OY 541 PTIVSSSDTKIAKRMATLIPTDFLCMAPISFFAISASLKVPLITVSKAKILLVLYPIN 600
DB 558 PTIVSSSDTKIAKRMATLIPTDFLCMAPISFFAISASLKVPLITVSKAKILLVLYPIN 617
OY 601 SCANPFLYAITFNFRDFFILLSKFCGYEQHQAQIYRTETSSATHNFARKSHCSAPRV 660
DB 618 SCANPFLYAITFNFRDFFILLSKFCGYEQHQAQIYRTETSSATHNFARKSHCSAPRV 677
OY 661 TNSYVLVPLNHSN 675
DB 678 TNSYVLVPLNHSN 692

RESULT 4

US-09-965-536A-12
Sequence 12; Application US/09965536A
Patent No. US2003002733A1
GENERAL INFORMATION:
APPLICANT: FIDELITY N.
APPLICANT: MINTIER, G.
APPLICANT: RAMANATHAN, C. S.
TITLE OF INVENTION: A NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGPBWY5,
FILE REFERENCE: DOQ41NP
CURRENT APPLICATION NUMBER: US/09/965.536A
CURRENT FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: 60/235.713
PRIOR FILING DATE: 2000-09-27

US-09-804-626-8
Sequence 8; Application US/09804626
Patent No. US20020128190A1
GENERAL INFORMATION:
APPLICANT: Lobel, Leslie

RESULT 5

US-09-804-626-8
Sequence 8; Application US/09804626
Patent No. US20020128190A1
GENERAL INFORMATION:
APPLICANT: Lobel, Leslie

PRIOR APPLICATION NUMBER: 60/261.781
PRIOR FILING DATE: 2001-01-16
PUBLICATION NUMBER: 2002-07-306.605
PRIOR FILING DATE: 2000-07-306.605
PRIOR APPLICATION NUMBER: 60/310.436
PRIOR FILING DATE: 2001-08-03
NUMBER OF SEQ ID NOS: 61
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 12
LENGTH: 688
TYPE: PRT
ORGANISM: Rattus norvegicus
US-09-965-536A-12

Query Match 99.0%; Score 3482; DB 9; Length 688;
Best Local Similarity 99.3%; Pred. No. 9.7e-282;
Matches 670; Conservative 0; Mismatches 1; Indels 4; Gaps 1;

OY 1 CHHWLCHSNNRVFLQDSKVTETPTDLPNNAIELRVLTARVLPKSGFAGGDLKLEI 60
DB 18 CHHWLCHSNNRVFLQDSKVTETPTDLPNNAIELRVLTARVLPKSGFAGGDLKLEI 77
OY 61 SONDLVLEADVSNLPLKHEIRIEKANNLLYINPEAFONPLSLRYLLISNTGKHLPA 120
DB 78 SONDLVLEADVSNLPLKHEIRIEKANNLLYINPEAFONPLSLRYLLISNTGKHLPA 137
OY 121 VHKIOSLOKVLDDIODNINIHIVARNSPFGLSFESVILWLSKNGIEEIHNCAPNGTOLDE 180
DB 138 VHKIOSLOKVLDDIODNINIHIVARNSPFGLSFESVILWLSKNGIEEIHNCAPNGTOLDE 193
OY 161 LNLSDNNLLELPNDVFOGASGPVILDISRTKVHSLPNHGLENLKLRARSTYRLKLLPN 240
DB 194 LNLSDNNLLELPNDVFOGASGPVILDISRTKVHSLPNHGLENLKLRARSTYRLKLLPN 253
OY 241 LDKVPTLMEASLTYSHCACAFANKRKQISELHPICNKSILROQIDDMTOIGDQVSLIDD 300
DB 254 LDKVPTLMEASLTYSHCACAFANKRKQISELHPICNKSILROQIDDMTOIGDQVSLIDD 313
OY 301 EFSYSGSDMMYNEFDYDLCEVNDVTCSPKDPANPCEDI MGYNLRVLWLFISILAIT 360
DB 314 EFSYSGSDMMYNEFDYDLCEVNDVTCSPKDPANPCEDI MGYNLRVLWLFISILAIT 373
OY 361 GNTTVLVLTTSOYKLTVPRLMKNLAFADLCIGIYLLLIASVDIHTKSOYHNTADMT 420
DB 374 GNTTVLVLTTSOYKLTVPRLMKNLAFADLCIGIYLLLIASVDIHTKSOYHNTADMT 433
OY 421 GAGCDAAGFFTFVASELSVYTLTATILERMHTITHAMOLECKVQLRHAASVNLGWTFAF 480
DB 434 GAGCDAAGFFTFVASELSVYTLTATILERMHTITHAMOLECKVQLRHAASVNLGWTFAF 493
OY 481 AALFPIGISTMYKVSICLPHWDISPLSOLYVALLVNLVAFVYICGCTHYIYLVYRN 540
DB 494 AALFPIGISTMYKVSICLPHWDISPLSOLYVALLVNLVAFVYICGCTHYIYLVYRN 553
OY 541 PTIVSSSDTKIAKRMATLIPTDFLCMAPISFFAISASLKVPLITVSKAKILLVLYPIN 600
DB 554 PTIVSSSDTKIAKRMATLIPTDFLCMAPISFFAISASLKVPLITVSKAKILLVLYPIN 613
OY 601 SCANPFLYAITFNFRDFFILLSKFCGYEQHQAQIYRTETSSATHNFARKSHCSAPRV 660
DB 614 SCANPFLYAITFNFRDFFILLSKFCGYEQHQAQIYRTETSSATHNFARKSHCSAPRV 673
OY 661 TNSYVLVPLNHSN 675
DB 674 TNSYVLVPLNHSN 688

```

; APPLICANT: Lustbader, Joyce
; TITLE OF INVENTION: EXPRESSION OF PROPERLY FOLDED AND SOLUBLE EXTRACELLULAR DOMAIN OF
; TITLE OF INVENTION: GONADOTROPIN RECEPTOR
; FILE REFERENCE: 0575/62259/JPW/SHS
; CURRENT APPLICATION NUMBER: US/09/804,626
; CURRENT FILING DATE: 2001-03-09
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8
; LENGTH: 695
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-804-626-8

Query Match      89.6%; Score 3149.5; DB 10; Length 695;
Best Local Similarity 88.9%; Pred. No. 5.1e-254;
Matches 603; Conservative 33; Mismatches 39; Indels 3; Gaps 2;

QY 1 CHHWLCHCSNRVFLCQDSKVTEPTDLPNNAELRVLTGKLVIPKGSFAGFDLEKIEI 60
DB 18 CHHWLCHCSNRVFLCQDSKVTEPTDLPNNAELRVLTGKLVIPKGSFAGFDLEKIEI 77
QY 61 SONDVLEIADVFNSLPLKHEIRIEKANNLLYINPEAFQNLPSRLYLLISNTGKHLPA 120
DB 78 SONDVLEIADVFNSLPLKHEIRIEKANNLLYINPEAFQNLPSRLYLLISNTGKHLPA 137
QY 121 VHKSQVLLQVLLDIQDNIHIVARNFMSGLSFESVILWLSKNGIEIHNCAFNQTOLDE 180
DB 138 VHKSQVLLQVLLDIQDNIHIVARNFMSGLSFESVILWLSKNGIEIHNCAFNQTOLDE 197
QY 181 LNSDNNLEELPNDVFGASGVVLDISRTKLVHSLPNHGLENLKLRARSTYRLKLLPN 240
DB 198 LNSDNNLEELPNDVFGASGVVLDISRTKLVHSLPNHGLENLKLRARSTYRLKLLPN 257
QY 241 LDFVTLMEASLYPSHCCAFANLKRQISELHPICNKSILRQIDDMTOIGDQVSLDID 300
DB 258 LDFVTLMEASLYPSHCCAFANLKRQISELHPICNKSILRQIDDMTOIGDQVSLDID 317
QY 301 -EPSYKSGSDMYNEFDYDLCEVVDVTCSPKPDAPNCPEDIMGYNLRVLIWFISILAI 359
DB 318 NESSYSGFDMTYTEFDYDLCEVVDVTCSPKPDAPNCPEDIMGYNLRVLIWFISILAI 377
QY 360 TGNTVVLVLTTSQYKLVTPRFMLCNLAFADLCIGIYLLIASVDIHTKSOYHNYADWQ 419
DB 378 TGNTVVLVLTTSQYKLVTPRFMLCNLAFADLCIGIYLLIASVDIHTKSOYHNYADWQ 437
QY 420 TGACDAAGFTTFVASELSVYTLTAITLERWHITTHAMOLECKVQLRHAASVVMWGTF 479
DB 438 TGACDAAGFTTFVASELSVYTLTAITLERWHITTHAMOLECKVQLRHAASVVMWGTF 497
QY 480 FAALFPFIIGISSYMKVSIPLMDIDSPLSQLYMALLVNLVAFVVCIGCYTHIYLTVR 539
DB 498 FAALFPFIIGISSYMKVSIPLMDIDSPLSQLYMALLVNLVAFVVCIGCYTHIYLTVR 557
QY 540 NPTIVSSSDTKIAKRMATLIETDFLCMAPISFFAISASLKVPLITYSKAKILLVFPYI 599
DB 558 NPTIVSSSDTKIAKRMATLIETDFLCMAPISFFAISASLKVPLITYSKAKILLVFPYI 617
QY 600 NSCANPFLYAIETKFNRRDFFILLSKFCGYEMQAQIYRTETSSATHNPHARKSCHSSAPR 659
DB 618 NSCANPFLYAIETKFNRRDFFILLSKFCGYEMQAQIYRTETSSATHNPHARKSCHSSAPR 677
QY 660 VT--NSYVLPVPLNHSSQN 675
DB 678 VTSGSTYILVPLSLHAQN 695

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RESULT 6
 US-09-965-536A-13
 ; Sequence 13, Application US/09965536A
 ; Publication No. US20030027323A1
 ; GENERAL INFORMATION:
 ; APPLICANT: FEDER, J. N.

```

; APPLICANT: MINTIER, G.
; APPLICANT: RAMANATHAN, C. S.
; APPLICANT: HAWKEN, D. R.
; TITLE OF INVENTION: A NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGPRBMV5,
; TITLE OF INVENTION: EXPRESSED HIGHLY IN BRAIN AND OVARIAN TISSUES
; FILE REFERENCE: D0041NP
; CURRENT APPLICATION NUMBER: US/09/965,536A
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 60/235,713
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/261,781
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: 60/306,605
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 60/310,436
; PRIOR FILING DATE: 2001-08-03
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 687
; TYPE: PRT
; ORGANISM: Equus asinus
US-09-965-536A-13

Query Match      85.6%; Score 3010.5; DB 9; Length 687;
Best Local Similarity 86.0%; Pred. No. 1.9e-242;
Matches 582; Conservative 38; Mismatches 48; Indels 9; Gaps 3;

QY 1 CHHWLCHCSNRVFLCQDSKVTEPTDLPNNAELRVLTGKLVIPKGSFAGFDLEKIEI 60
DB 18 CHHWLCHCSNRVFLCQDSKVTEPTDLPNNAELRVLTGKLVIPKGSFAGFDLEKIEI 77
QY 61 SONDVLEIADVFNSLPLKHEIRIEKANNLLYINPEAFQNLPSRLYLLISNTGKHLPA 120
DB 78 SONDVLEIADVFNSLPLKHEIRIEKANNLLYINPEAFQNLPSRLYLLISNTGKHLPA 137
QY 121 VHKSQVLLQVLLDIQDNIHIVARNFMSGLSFESVILWLSKNGIEIHNCAFNQTOLDE 180
DB 138 VHKSQVLLQVLLDIQDNIHIVARNFMSGLSFESVILWLSKNGIEIHNCAFNQTOLDE 197
QY 181 LNSDNNLEELPNDVFGASGVVLDISRTKLVHSLPNHGLENLKLRARSTYRLKLLPN 240
DB 198 LNSDNNLEELPNDVFGASGVVLDISRTKLVHSLPNHGLENLKLRARSTYRLKLLPN 257
QY 241 LDFVTLMEASLYPSHCCAFANLKRQISELHPICNKSILRQIDDMTOIGDQVSLDID 300
DB 258 LDFVTLMEASLYPSHCCAFANLKRQISELHPICNKSILRQIDDMTOIGDQVSLDID 316
QY 301 -EPSYKSGSDMYNEFDYDLCEVVDVTCSPKPDAPNCPEDIMGYNLRVLIWFISILAI 360
DB 317 DES-----HWSEFDYDLCEVVDVTCSPKPDAPNCPEDIMGYNLRVLIWFISILAI 370
QY 361 GNTTVVLVLTTSQYKLVTPRFMLCNLAFADLCIGIYLLIASVDIHTKSOYHNYADWQ 420
DB 371 GNTTVVLVLTTSQYKLVTPRFMLCNLAFADLCIGIYLLIASVDIHTKSOYHNYADWQ 430
QY 421 GAGCDAAGFTTFVASELSVYTLTAITLERWHITTHAMOLECKVQLRHAASVVMWGTF 480
DB 431 GAGCDAAGFTTFVASELSVYTLTAITLERWHITTHAMOLECKVQLRHAASVVMWGTF 490
QY 481 AAALFPFIIGISSYMKVSIPLMDIDSPLSQLYMALLVNLVAFVVCIGCYTHIYLTVR 540
DB 491 AAALFPFIIGISSYMKVSIPLMDIDSPLSQLYMALLVNLVAFVVCIGCYTHIYLTVR 550
QY 541 PTIVSSSDTKIAKRMATLIETDFLCMAPISFFAISASLKVPLITYSKAKILLVFPYI 600
DB 551 PTIVSSSDTKIAKRMATLIETDFLCMAPISFFAISASLKVPLITYSKAKILLVFPYI 610
QY 601 NSCANPFLYAIETKFNRRDFFILLSKFCGYEMQAQIYRTETSSATHNPHARKSCHSSAPR 660
DB 611 NSCANPFLYAIETKFNRRDFFILLSKFCGYEMQAQIYRTETSSATHNPHARKSCHSSAPR 670
QY 661 TN--SYVLVPLNHSSQN 675

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RESULT 9

US-09-877-804-8
; Sequence 8, Application US/09877804
; Patent No. US20020061557A1
; GENERAL INFORMATION:
; APPLICANT: Nikolics, Karoly
; APPLICANT: McFarland, Keith C.
; APPLICANT: Segalo, Deborah L.
; APPLICANT: Seeburg, Peter H.
; TITLE OF INVENTION: Glycoprotein Hormone Receptor Molecules
; FILE REFERENCE: P0576PIC2
; CURRENT APPLICATION NUMBER: US/09/877,804
; PRIOR FILING DATE: 2001-09-04
; PRIOR APPLICATION NUMBER: US 08/207,814
; PRIOR FILING DATE: 1994-03-07
; PRIOR APPLICATION NUMBER: US 07/781,153
; PRIOR FILING DATE: 1991-10-31
; PRIOR APPLICATION NUMBER: US 07/347,683
; PRIOR FILING DATE: 1989-05-05
; NUMBER OF SEQ ID NOS: 22
; SEQ ID NO 8
; LENGTH: 348
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: deduced sequence
US-09-877-804-8

Query Match 52.1%; Score 1832; DB 10; Length 348;
Best Local Similarity 100.0%; Pred. No. 1.2e-144;
Matches 348; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHHWLCHSNRVFLCQDSKVTEIPTDLPRNAIELRVLTGLKRVIPKGSFAGFGDLEKTEI 60
DB 1 CHHWLCHSNRVFLCQDSKVTEIPTDLPRNAIELRVLTGLKRVIPKGSFAGFGDLEKTEI 60

QY 61 SONDVLEIADVNSLPLKHEIRIEKANNLLYINPEAFONLPSRLYLLISNTGKHLPA 120
DB 61 SONDVLEIADVNSLPLKHEIRIEKANNLLYINPEAFONLPSRLYLLISNTGKHLPA 120

QY 121 VHKIQSLQKVLDDIQDNIHIVARNSEFMGLSFESVILWLSKNGIEEHNCAFNQTOLDE 180
DB 121 VHKIQSLQKVLDDIQDNIHIVARNSEFMGLSFESVILWLSKNGIEEHNCAFNQTOLDE 180

QY 181 LNLSDNNLEELPNDVFOGASGPVILDSRTKVHSLPNHGLENLKLRARSTYRLKLPN 240
DB 181 LNLSDNNLEELPNDVFOGASGPVILDSRTKVHSLPNHGLENLKLRARSTYRLKLPN 240

QY 241 LDKFVTLMEASLTPSHCCAFANLAKROISELHPICNKSILRODIDDMTOIGDQVSLIDD 300
DB 241 LDKFVTLMEASLTPSHCCAFANLAKROISELHPICNKSILRODIDDMTOIGDQVSLIDD 300

QY 301 EPSYKSGSDMYNEFDYDLCEVVDVTCSPKPDFAFNPCEDIMGYNILR 348
DB 301 EPSYKSGSDMYNEFDYDLCEVVDVTCSPKPDFAFNPCEDIMGYNILR 348

RESULT 10

US-09-877-804-3
; Sequence 3, Application US/09877804
; Patent No. US20020061557A1
; GENERAL INFORMATION:
; APPLICANT: Nikolics, Karoly
; APPLICANT: McFarland, Keith C.
; APPLICANT: Segalo, Deborah L.
; APPLICANT: Seeburg, Peter H.
; TITLE OF INVENTION: Glycoprotein Hormone Receptor Molecules
; FILE REFERENCE: P0576PIC2
; CURRENT APPLICATION NUMBER: US/09/877,804
; CURRENT FILING DATE: 2001-09-04
; PRIOR APPLICATION NUMBER: US 08/207,814
; PRIOR FILING DATE: 1994-03-07
; PRIOR APPLICATION NUMBER: US 07/781,153

; PRIOR FILING DATE: 1991-10-31
; PRIOR APPLICATION NUMBER: US 07/347,683
; PRIOR FILING DATE: 1989-05-05
; NUMBER OF SEQ ID NOS: 22
; SEQ ID NO 3
; LENGTH: 674
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: deduced sequence
US-09-877-804-3

Query Match 51.1%; Score 1797; DB 10; Length 674;
Best Local Similarity 56.5%; Pred. No. 2.6e-141;
Matches 359; Conservative 105; Mismatches 149; Indels 22; Gaps 7;

QY 28 PRNAIELRVLTGL--RVIPKGSFAGFGDLEKIEISONDVLEIADVNSLPLKHEIRI 85
DB 25 PRAGL-ARLSLYLPVKVIPSQAFGLNEVVKIEISQSDSLERIEANAFDNLNLSSELLI 83

QY 86 EKANNLLYINPEAFONLPSRLYLLISNTGKIKHLPVAVHKIQSLQ-KVLDDIQDNIHIVA 144
DB 84 QNTKNLLYIEGCAFTNLPRLKYLSCNTGIRPLDPTVKISSSEFNFILLEICDNLHITTP 143

QY 145 RNSFMGLSFESVILWLSKNGIEEHNCAFNQGLDELNLSNNLEELPNDVFOGASGPV 204
DB 144 GNAFOGMNNEVTLKLYNGFEVQSHAFNGTTLISLELKENIYLEKMHSGAFQOGATGPS 203

QY 205 ILDISRTKVHSLPNHGLENLKLRARSTYRLKLRKLNLDKLVFLMEASLTPSHCCAFANL 264
DB 204 ILDISRTKVHSLPNHGLENLKLRARSTYRLKLRKLNLDKLVFLMEASLTPSHCCAFANL 263

QY 265 KRQISELHPICNKSILRODIDDMTOIGDQVSLIDDPEPSYG---KGSOMMYNEFDYDLN 321
DB 264 PKK-----EQNFSEFSEFENFSKQCESTVRKADNETLYSAIPEENELSGWDYDGFCS 315

QY 322 EVDVTCSPKPDFAFNPCEDIMGYNILRVLIWPIISILATGTNTVTLVLTSTYKLTVPFR 381
DB 316 PKT-LQCAPEPDFAFNPCEDIMGYAFRLVILINILINILAFGLNLTVFLVLTSTYKLTVPFR 374

QY 382 LMCNLAFAFADLCIGIYLLLIASVDIHTKSOYHNAYADMTGACGDAAGFTVFASELSVYT 441
DB 375 LMCNLSFADFMCGLYLLLIASVDSQTKOYVNHADMTGSCGGAAGFTVFASELSVYT 434

QY 442 LTATLWRHTTITHAMQLECKVQLRHAASVYVWLGWTFAPAAALFPIFGISSYMKYSICLP 501
DB 435 LTVITLWRHTTITYAVQLDQKLRHRAIPIMLGGWLFSTLIATMPLVGLISNTYMKYSICLP 494

QY 502 MDIDSPLSOLYVALLVNLVAFVVICGCTHYIYLTVRNPTIVSSSTSKIAKRMATLIF 561
DB 495 MDVESTLSQVYLSLILNVAFFVVICACIYIRIYFAVQNPETAPNKOTKIAKRMATLIF 554

QY 562 TDFLCMAPIPSFAISASLKVPLITYSKAKILLVLEVPINSCANPELYAFTKFNFRDPI 621
DB 555 TDFTCMAPIPSFAISAFKVPLITYVNSKILLVLPVNSCANPELYAFTKFNFRDPI 621

QY 622 LLSKFGCYEMAQIYRTETSSATHNFARKSHCSS 656
DB 615 LLSRFGCKRRAEALYRRK-----EFSAYTSNCKN 643

RESULT 11

US-09-877-804-2
; Sequence 2, Application US/09877804
; Patent No. US20020061557A1
; GENERAL INFORMATION:
; APPLICANT: Nikolics, Karoly
; APPLICANT: McFarland, Keith C.
; APPLICANT: Segalo, Deborah L.
; APPLICANT: Seeburg, Peter H.
; TITLE OF INVENTION: Glycoprotein Hormone Receptor Molecules
; FILE REFERENCE: P0576PIC2
; CURRENT APPLICATION NUMBER: US/09/877,804

? APPLICANT: HAWKEN, D. B.
 ? TITLE OF INVENTION: A NOVEL HUMAN C-PROTEIN COUPLED RECEPTOR, UG96PM5,
 ? TITLE OF INVENTION: EXPRESSED HIGHLY IN BRAIN AND OVARIAN TISSUES
 ? FILE REFERENCE: D0041P
 ? CURRENT APPLICATION NUMBER: US/09/965,536A
 ? CURRENT FILING DATE: 2001-09-26
 ? PRIOR APPLICATION NUMBER: 60/735,713
 ? PRIOR FILING DATE: 2000-09-27
 ? PRIOR APPLICATION NUMBER: 60/261,781
 ? PRIOR FILING DATE: 2001-01-16
 ? PRIOR APPLICATION NUMBER: 60/306,605
 ? PRIOR FILING DATE: 2001-07-19
 ? PRIOR APPLICATION NUMBER: 60/310,436
 ? PRIORITY DATES: 2000-08-03
 ? NUMBER OF SEQ. NOS: 61
 ? SOFTWARE: PatentIn Ver. 2.1
 ? SEQ. ID NO. 15
 ? LENGTH: 676
 ? TYPE: PRT
 ? ORGANISM: Callithrix jacchus
 ? US-09-965-536A-15
 ? US

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: SOFTWARE: Patentin Ver. 2.1
: SEQ ID NO 15
: LENGTH: 676
: TYPE: CDS
: ORGANISM: Gallitrix jacchus
: accession: U9-965-306A.15

      50.7%;   Score 1783.5;   DB 9;   Length 676;
      Best Match
      Query Loc. Similarity 55.8%;   Pred. No. 3,4e-140;
      Matches 359;   Conservative 99;   Mismatches 140;   Indels 45;   Gaps 6;

QY      38  LTKI-----RVIPSGFAGGDEKIEITISQNDVLEIVADVPSNLPKLHEIRIEKANN 90
Db      55  LTRLSUAYLPVKVPSQAFRGUNLVKIKIEISQSDSLRIEAFANPDLNLSELIOHTKN 114
QY      91  LXTINPEAFQNLPSRLYLLISNTGKHLPVAKHISIQ-KVLVDIQDNIHIVARNSEFM 149
Db      115  LHLEPGFATMLPKRLYSCTGNTGKRPFDVPIKFSSTFNPLETCONLHITIPGAFQ 174
QY      150  LSGPSVYHLHSNGEIEETHCANSTQDDELWLDNNNIBELNDVDFOGAGPVLIDIS 209
Db      175  GNNSESITLKLKNGCFEYVOSHAFNGTTVISLVAKENVHLERIHINGAFGATGPTSID 234
QY      210  RTKVSHSLPHGLENNKLKLARSTYRKLKLPLNOLKFWTLMWASLTYPSSCCAFANLKR 269
Db      235  STFKLQALPHSGLESIQTLATSSYSLKLPLSRKKFANLLQATLTYPSSCCAFRNVPVT 292
QY      270  ELHPICNKSILRODIDMTQIGDORVSLTDDEPSTGKSGDMYNEFDYDLGNEVDVTC 329
Db      293  -----DYAIPASQSGMDYDYG-FLKPTPKCA 321
QY      330  KPQDANPCEDINGNHLRVLWISLTAIGNTVTVLVVITSQKTVPRFLKMLCHLAPA 389
Db      322  PEPPDANPCEDINGNHLRVLWISLTAIGNNTVTVLVVITSQKTVPRFLKMLCHLAPA 381
QY      390  DLCIGYVLLLASVDIHTKSOYHNVAIDMQTGACDAGGFTVPASELSVYTLTAITLER 449
Db      382  DPCMGYVLLLASVDSOTKQGYNNIATDMQTGSGCNTAGGFTVPASELSVYTLTAITLER 441
QY      450  WHITTHAMQLECKVQLRRHAASVYVLGWTFAFAALFPIFGISYSYMKVSICLPMDID 509
Db      442  WHITTAHJLDOKLRHATLLMGGLPESLLIAMPLUGVSNYMYKVSICLPMHIEPTFS 501
QY      510  QLYVMALVWLAVFVYCGCTHTHYLTVRNPTIVSSSOTKIKAKRMATLIPTDFLCMA 569
Db      502  QATVFELVWLAVFYIICITICFTVPRVAPNSNPSTOTAKKMAKLIPTDFLCMA 561
QY      570  ISYFELVWLAVPLTVYSKATLLYFDPYINSCNAPPSLITAKKMAKLIPTDFLLSFG 629
Db      562  ISFSAISAAFMPLTVTNSKVLLVLYFDPINSCNAPPLYLPTKTPRDFLLLGAFGCC 621
QY      630  ENQAQVYRTETSSA-THNFHARKSICSSAPRVNYSVYVLPINH 671
Db      622  KURALEYRKDFQSAVTSY---KNQFTGSSKPSQSTLKLALH 661

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DB 562 ISFATSAAFKMLPLITYNSKVLLVLPYF INSCANPFLYALTPTKTRFFROFLLIGAFQCC 671

QY 630 ENQOQYRPTSSA-THNFHAKSCSSAPRVNNSVVLVPLNH 671

DB 622 KIRAEILTKRFOFSNTMT--KNGFTGSPQSSTLALPALH 661

RESULT 13
US-09-804-626-6

```
: Sequence 6, Application US/09804626
: Patent No. US20020128190A1
: GENERAL INFORMATION:
: APPLICANT: Lushbader, Joyce
: TITLE OF INVENTION: EXPRESSION OF PROPERLY FOLDED AND SOLUBLE EXTRACELLULAR DOMAIN OF
: FILE REFERENCE: CONADOTROPIN RECEPTOR
: CURRENT FILING DATE: 2001-03-09
: NUMBER OF SEQ ID NOS: 8
: SOFTWARE: PatentIn version 3.0
: SEQ ID NO 6
: LENGTH: 699
: TYPE: PRT
: ORGANISM: Homo Sapiens
US-09-804-626-6

Query Match      50.5%; Score 1776; DB 10; Length 699;
Best Local Similarity 55.4%; Pred. No. 1.5e-139;
Matches 349; Conservative 108; Mismatches 147; Indels 26; Gaps 6;

QY 38 LTKL-----RVTPKPSFAGFDLEKIEISQNDVLEIVIEADVPSNLPKLEIRIEKANN 90
Db 51 LTRLSLAYLPVKVIPSOAFRGLNEVIRKIEISQIDSLERIEANAPDNLNLSEILQNTKN 110
QY 91 LLYINPEAFONLPSRLYLLISNTGKIKHLPVHKI-QSLQKVLDDIODNINIHIVARNFSM 149
Db 111 LRYEPGAFNLPLKLTSLICNTGIRKFPDVTKYFSSNESFLEICDNLHTTIPGNAFO 170
QY 150 GLSFESVILMSKNGIEEIHNAFNGTQDLDELNLSDNNLELNDVFOGASGVILDIS 209
Db 171 GMNESVTLYKNGFEVQSHAFNGTTLTSLLEKENVHLEKMHNGAFRATGPKTLDIS 230
QY 210 RTVHSLPNGLNLEKLLKRLARSTYRLKLLPNLDRFVTLMEASLYPSHCCAFANLKRQIS 269
Db 231 STKLOALPSGLSIEQIRLIATSSYSLKPLSPRETFVNLEATLYPSHCCAFANL----- 285
QY 270 ELHPICKNSILRODIDMTQIGDQVSLIDDEPSYK--GSDMWYNEFDYDLCNEVDV 326
Db 286 ---PTKQNFSSHISENFSKQCESTVRKVNKNTLYSSMLAESELSGWDYEGFCLPKTP- 341
QY 327 TCSKPDAPNCPEDIMGYNILRVLIWFISILAITGNTTVLVLTTSQYKLTVPFRLMNL 386
Db 342 RCAPEPDAPNCPEDIMGYDFLRVLILNLINILAINGNMTVLVLTTSYKLTVPFRLMNL 401
QY 387 AFADLCIGYILLIASVDIHTKSOYHNAIDMTQAGCDAAGFTVPFASLSVYTLTAT 446
Db 402 SFADFNGLYLLIASVDSQTKGYNNHAIIDMTQSGCSTAGFTVPFASLSVYTLTAT 461
QY 447 LERWHTTTHAMQLECKVOLRHAASVMVGLWTEFAFAAALFPFEGISSYKYSICLPMDDIS 506
Db 462 LERWHTTTHAIHLDQKRLRHAILMLGGWLFSSLIAMFLVGSNTKYSICPMDDVET 521
QY 507 PLSQLYMALVNLVAFVVCYTHYILTVRNPTIVSSSDTKIAKRMATLIFTDFLC 566
Db 522 TLSQVYILTILNVAAFFIACACIKIYFAVRNPMLMATNKDTKIAKMAILIFTDFTC 581
QY 567 MAPISFAISASLKVPLITVSKAKILLVLPYINSCANPFLYALFTKFRDRPFILLSKF 626
Db 582 MAPISFAISAAFKVPLITVNSKVLVLPYINSCANPFLYALFTKFRDRPFILLSKF 641
QY 627 GCYEMOQAIYRTETSSATHNFAHKSCHSS 656
Db 642 GCCKRRALRYRK-----DFSAYTSNCKN 665

RESULT 14
US-10-045-624B-2
: Sequence 2, Application US/10045624B
: Publication No. US20030009778A1
: GENERAL INFORMATION:
: APPLICANT: Allen, Keith D.

: TITLE OF INVENTION: TRANSGENIC MICE CONTAINING THYROID
: FILE REFERENCE: R-666
: CURRENT APPLICATION NUMBER: US/10/045.624B
: PRIOR FILING DATE: 2002-08-19
: PRIOR APPLICATION NUMBER: US 10/045.624
: NUMBER OF SEQ ID NOS: 4
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 2
: LENGTH: 764
: TYPE: PRT
: ORGANISM: Mus musculus
US-10-045-624B-2

Query Match      46.6%; Score 1638.5; DB 9; Length 764;
Best Local Similarity 49.2%; Pred. No. 4.9e-128;
Matches 337; Conservative 105; Mismatches 184; Indels 59; Gaps 10;

QY 6 CHCNRVFLCODSKVT-----EIPDLPNNAIELRVLTUKRVIPKSGFAGFDLEKTEI 60
Db 29 CECHQE-----DDFVTCHELHRIPS-LPPSTQTLKLIETHLKTIPSLAFSSLPNISRYL 83
QY 61 SONDVLEIVIEADVPSNLPKLEIRIEKANNLLYINPEAFONLPSRLYLLISNTGKIKHLP 120
Db 84 SIDATLQRLPHEPSYNSLSKMTHEIRNTRSLTYIDPDALTLPKFLGIFNTGLRIFPD 143
QY 121 VHKIQSLQ-KVLLDIQDNINIHIVARNFSMGLSPESVILMSKNGIEEIHNAFNGTQD 179
Db 144 LTKIYSTDIFILEITDNPYMTSVPENAFQGLCNETLTKLYNNGFTSVQGHAFNGTKLD 203
QY 180 ELNLSODNNLEELPNDVFOGA-SGPVILDISRTKVSHPNHLNGLNLEKLLRARSYRLKLL 238
Db 204 AVYLNKNTLYTAIDNDAFGVYSGPTLLDVSSTVATLPSKGLHLELIAKDTWTLLKL 263
QY 239 PNLDKFVTLMEASLYPSHCCAFANLKRQISELHPI-CNKSILR----- 281
Db 264 PLSLSFLHLTRADLUSYSHCCAFKQKIRGILESMLCNESIRNLRKORSVNILRGPY 323
QY 282 ----QDIDMTQIGDQVSLIDDEPS-----YKGSOM-----MY 312
Db 324 QEVEEDPGD-NSVGYKQNSKQFQSPESHYVVFEEQEDVVGQELKNPOEETLOAFE 382
QY 313 NEDYDLCNEVDVTCSPKPDAPNCPEDIMGYNILRVLIWFISILAITGNTTVLVLTTS 372
Db 383 SHYDITVCGDNEDMVCTPKSDEFNCPEDIMGYRLVWVFWFVSLALLGNIFVLILLTS 442
QY 373 QYKLTVPFRLMNLAFADLCIGYILLIASVDIHTKSOYHNAIDMTQAGCDAAGFTVP 432
Db 443 HYKLTVPFRLMNLAFADFCGVYLLIASVDLTHSEYNNHAIIDMTQGPCNTAGFTVP 502
QY 433 FASELSVYTLTATITLERWHTTTHAMQLECKVOLRHAASVMVGLWTEFAFAAALFPFIS 492
Db 503 FASELSVYTLTITLERWYAITFAMRLDRKIRLHRAVITAGGWSVCFLLALLPMVGISS 562
QY 493 YMKVSIICLPMDDISPLSQLYMALVNLVAFVVCYTHYILTVRNPTIVSSSDTKI 552
Db 563 YAKVSIICLPMDDITDTPALAYIVLVLLNVVAFVVCYTHYITVRNPQYNPRDKDTKI 622
QY 553 AKRMATLIFTDFLCMAPISFAISASLKVPLITVSKAKILLVLPYINSCANPFLYALFT 612
Db 623 AKRMATLIFTDFLCMAPISFAISASLKVPLITVSKAKILLVLPYINSCANPFLYALFT 682
QY 613 KNFRDRPFILLSKFGCYEMOQAIYR 637
Db 683 KAFORDVFIILLSKFGICKRQAOAYQ 707

RESULT 15
US-09-804-626-4
: Sequence 4, Application US/09804626
: Patent No. US20020128190A1
: GENERAL INFORMATION:
```

APPLICANT: Lobel, Leslie
APPLICANT: Lustbader, Joyce
TITLE OF INVENTION: EXPRESSION OF PROPERLY FOLDED AND SOLUBLE EXTRACELLULAR DOMAIN OF
TITLE OF INVENTION: GONADOTROPIN RECEPTOR
FILE REFERENCE: 0575/62259/JPM/SHS
CURRENT APPLICATION NUMBER: US/09/804,626
CURRENT FILING DATE: 2001-03-09
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin version 3.0
SEQ ID NO 4
LENGTH: 516
TYPE: PRT
ORGANISM: Homo Sapiens
US-09-804-626-4

Query Match 42.8%; Score 1505.5; DB 10; Length 516;
Best Local Similarity 85.5%; Pred. No. 3.5e-17;
Matches 289; Conservative 22; Mismatches 26; Indels 1; Gaps 1;

Oy 11 RVFLQDSKVTEIPDLPRNAIELRFLVTLKLRVDPKSGFAGDLEKIEISONDVLEIE 70
Db 168 RVFLQDSKVTEIPDLPRNAIELRFLVTLKLRVDPKSGFAGDLEKIEISONDVLEIE 227

Oy 71 ADVFENLPKLHEIRIEKANNLLYINPEAFONLPRLYLLISNTGKHLPAVHKIQSLQKV 130
Db 228 ADVFENLPKLHEIRIEKANNLLYINPEAFONLPRLYLLISNTGKHLPAVHKIQSLQKV 287

Oy 131 LLDIOINIHIVARNFVGLSPESVILWLSKNGIEEIHNCAPNGTOLDDELNLSDNNLE 190
Db 288 LLDIOINIHIVARNFVGLSPESVILWLSKNGIEEIHNCAPNGTOLDDELNLSDNNLE 347

Oy 191 ELPNDVFOGASCPVLDISRTKVSILPHNGLENLKLRRSTYBLKLPNLDKFTYLMXA 250
Db 348 ELPNDVFOGASCPVLDISRTKVSILPHNGLENLKLRRSTYBLKLPNLDKFTYLMXA 407

Oy 251 SLTYPSHCCAFANLKRQISELHPICNKSILRODIDDMTOIGDQVSLIDD-EPYKQSD 309
Db 408 SLTYPSHCCAFANLKRQISELHPICNKSILRODIDDMTOIGDQVSLIDD-EPYKQSD 467

Oy 310 MMTNEFDYDLCEVVDVTCSPKPDAPNCPEDIMGYNIL 347
Db 468 MMTNEFDYDLCEVVDVTCSPKPDAPNCPEDIMGYNIL 505

Search completed: June 16, 2003, 13:52:48
Job time : 166.511 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 16, 2003, 13:26:01 ; Search time 26.1704 Seconds
(without alignments)
2479.543 Million cell updates/sec

Title: US-09-877-804-7
Perfect score: 3516
Sequence: 1 CHNWLCNHNRYFLQDSKV.....SAPRVTNYSVLVPLNHSQSN 675

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues
Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR73:
1: PIR1:
2: PIR2:
3: PIR3:
4: PIR4:

Prod. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	DB ID	Description
1	3516	100.0	692	2	A34548
2	3164.5	90.0	695	1	ORHUT
3	3160.3	89.9	695	1	JN0898
4	3140.3	89.3	695	2	IC3686
5	3140.3	89.3	695	2	IC3686
6	3107.4	87.4	694	2	IC2337
7	3070.5	87.3	694	2	IC2337
8	2475	70.4	696	2	IC7161
9	1807	51.4	696	2	A41344
10	1799	51.2	700	2	A42395
11	1797	51.1	700	2	177463
12	1797	51.1	700	2	A49744
13	1776	50.5	699	1	ORHUT
14	1655	47.1	764	2	A40077
15	1642.5	46.7	764	1	ORHURH
16	1638.5	46.6	764	2	148882
17	1628	46.3	764	2	IC5643
18	1624	46.1	793	2	IC7390
19	1624	46.1	793	2	IC7386
20	1594	45.3	814	2	IC7386
21	861.5	24.3	925	2	IC2033
22	805.5	22.9	889	2	J20123
23	628.5	17.9	907	2	J20123
24	628	17.9	907	2	J20123
25	587	16.7	329	2	B41344
26	587	16.7	329	2	D41344
27	587	16.7	331	2	C41344
28	578	16.4	342	2	177461
29	521.5	14.8	1115	2	S40741

ALIGNMENTS

RESULT 1
A34548
folliotropin receptor precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C>Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 13-Aug-1999
C:Accession: A34548; A41729
R:Sprengel, R.; Braun, T.; Nikolic, K.; Segaloff, D.L.; Seeburg, P.H.
Mol. Endocrinol. 4, 525-530, 1990
A>Title: The testicular receptor for follicle stimulating hormone: structure and func
A:Reference number: A34548; MUID:91123558; PMID:2126341
A:Accession: A34548
A:Molecule type: mRNA
A:Residues: 1-692 <SP>
A:CROSS-references: GB:102842; NID:9204183; PID:AAA1175.1; PID:9204184
M:Hecker, L.L.; Day, J.; Griswold, M.D.
Mol. Endocrinol. 9, 159-170, 1995
A>Title: Structural organization of the follicle-stimulating hormone receptor gene.
A:Reference number: A41729; MUID:92149579; PMID:1738373
A:Accession: A41729
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-692 <HEC>
A:CROSS-references: GB:S81198; NID:9245344; PID:AA21415.1; PID:9245345
A>Note: sequence inconsistent with the nucleotide translation
A:Note: sequence extracted from NCBI backbone (NCBI:81117, NCBI:81119, NCBI:81121,
R:Davis, D.; Liu, X.; Segaloff, D.L.
Mol. Endocrinol. 9, 159-170, 1995
A>Title: Identification of the sites of N-linked glycosylation on the follicle-stimul
A:Reference number: A57562; MUID:95295729; PMID:776966
A:Accession: A57562
A:Contents: annotation: glycosylation sites
A:Description: receptor that mediates the biochemical effects of follitropin
C:Superfamily: glycoprotein hormone receptor; leucine-rich alpha-2-glycoprotein repoa
C:Keywords: alternative splicing; G protein-coupled receptor; glycoprotein, hormone r
F.1-15/Domain: signal sequence #status predicted <SIG>
F.16-692/Product: follitropin receptor #status predicted <MAT>
F.16-366/Domain: extracellular hormone binding #status predicted <EHB>
F.71-95/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR1>
F.71-95/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR2>
F.96-120/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>
F.121-145/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR4>
F.146-169/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR5>
F.172-193/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR6>
F.167-189/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR7>
F.398-421/Domain: transmembrane status predicted <TM1>
F.437-465/Domain: transmembrane status predicted <TM2>
F.443-465/Domain: transmembrane status predicted <TM3>
F.486-508/Domain: transmembrane status predicted <TM4>
F.529-550/Domain: transmembrane status predicted <TM5>
F.574-597/Domain: transmembrane status predicted <TM6>
F.609-630/Domain: transmembrane status predicted <TM7>
F.191.199.293/Binding site: carbohydrate (Asn) #status predicted

lutropin receptor
lutalinizing hormon
thyrotropin recept
thyrotropin recept
neuropeptide Y/pep
angiotensin II rec
MEGF5 protein - ra
allatostatin recep
somatostatin recep
elit-1 protein hom
angiotensin II rec
somatostatin recep
dopamine D1 recept
somatostatin recep

F:554/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted
F:595/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted

Query Match 100.0%; Score 3516; DB 2; Length 692;
Best Local Similarity 100.0%; Pred. No. 9.3e-237;
Matches 675; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CHHWLCHSNNRVFCQDSKVTETPTDLPRAIAELRFLVTLKRLVTPKGSFAGFGLKIEI 60
Db 18 CHHWLCHSNNRVFCQDSKVTETPTDLPRAIAELRFLVTLKRLVTPKGSFAGFGLKIEI 77
Qy 61 SONDVLEIVADVSNLPKLEIRKANNLLYINPEAFONLPSRLYLLISNTGKHLPA 120
Db 78 SONDVLEIVADVSNLPKLEIRKANNLLYINPEAFONLPSRLYLLISNTGKHLPA 137
Qy 121 VHKTSLOKVLDDTDQNNINTHIVARNFGLSPESVILWLSKNGIEIHNCFAFNGTOLDE 180
Db 138 VHKTSLOKVLDDTDQNNINTHIVARNFGLSPESVILWLSKNGIEIHNCFAFNGTOLDE 197
Qy 181 LNLSDNNLELPLNDVFGQSGPVILDSRTKVHSLPNHGLENLKLRARSTYRLKLLPN 240
Db 198 LNLSDNNLELPLNDVFGQSGPVILDSRTKVHSLPNHGLENLKLRARSTYRLKLLPN 257
Qy 241 LDKFVTLMEASLTYPSCCAFANLKRQISELHPICNKSILRQIDDDMTQIGDQVSLIDD 300
Db 258 LDKFVTLMEASLTYPSCCAFANLKRQISELHPICNKSILRQIDDDMTQIGDQVSLIDD 317
Qy 301 EPSYKGSDDMYNEFDYDLNCEVVDVTCSPKDFAFNCEIDMGYNILRVLIWFISILAIT 360
Db 318 EPSYKGSDDMYNEFDYDLNCEVVDVTCSPKDFAFNCEIDMGYNILRVLIWFISILAIT 377
Qy 361 GNTTLVVLVTSQYKLVTPRELMLNLAFLADLCIGIYLLIASVDIHTKSOYHNAIDWQT 420
Db 378 GNTTLVVLVTSQYKLVTPRELMLNLAFLADLCIGIYLLIASVDIHTKSOYHNAIDWQT 437
Qy 421 GAGDAAGFTVFASLSVYTLTATILRWHITTHAMOLECKVOLRAHASVYVLGWTFAF 480
Db 438 GAGDAAGFTVFASLSVYTLTATILRWHITTHAMOLECKVOLRAHASVYVLGWTFAF 497
Qy 481 AAALFPFIFGSIYKWKVSCILPMDIDSPLSOLYVALLVNLVAFVFCGCTHYLYLVNRN 540
Db 498 AAALFPFIFGSIYKWKVSCILPMDIDSPLSOLYVALLVNLVAFVFCGCTHYLYLVNRN 557
Qy 541 PTIVSSSDTTRIAKRMATLIFTDFLCMAPISFFAISASLKVPLITVSKAKILLVLYFPIN 600
Db 558 PTIVSSSDTTRIAKRMATLIFTDFLCMAPISFFAISASLKVPLITVSKAKILLVLYFPIN 617
Qy 601 SCANPFLYAIPTKFRNDRDFILLSKFGCYENQAOIYRTETSSATHNFHARKSHCSSAPRV 660
Db 618 SCANPFLYAIPTKFRNDRDFILLSKFGCYENQAOIYRTETSSATHNFHARKSHCSSAPRV 677
Qy 661 TNSYLVPLNHSN 675
Db 678 TNSYLVPLNHSN 692

RESULT 2

ORHUFT

N:Altitropin receptor precursor - human

N:Contains: follicle stimulating hormone receptor (FSHR)

N:Contains: follitropin receptor precursor long splice form; follitropin receptor precursor

C:Species: Homo sapiens (man)

C:Date: 30-Sep-1991 #sequence revision 06-Sep-1996 #text change 22-Jun-1999

C:Accession: 157661; 156448; PC1147; S30560; 157672; JN0122

R:Gromoll, J.; Dankbar, B.; Gudermann, T.

Mol. Cell. Endocrinol. 102, 93-102, 1994

A:Title: Characterization of the 5' flanking region of the human follicle-stimulating hormone

A:Reference number: 157661; MUID:95011044; PMID:7926278

A:Accession: 157661

A:Status: translated from GB/EMBL/DBD

A:Molecule type: DNA

A:Residues: 1-51 <GRO>

A:Cross-references: GB:S73199; NID:9685036; PIDN:AAB32071.1; PID:9685037

R:Gromoll, J.; Ried, T.; Holtgreve-Grez, H.; Nieschlag, E.; Gudermann, T.
J. Mol. Endocrinol. 12, 265-271, 1994
A:Title: Localization of the human FSH receptor to chromosome 2 p21 using a genomic f
A:Reference number: 156448; MUID:9500244; PMID:7916967

A:Status: preliminary; translated from GB/EMBL/DBD

A:Molecule type: DNA

A:Residues: 286-695 <GR>

A:Cross-references: GB:S73526; NID:9688069; PIDN:AAB32225.1; PID:9688070

R:Gromoll, J.; Gudermann, T.; Nieschlag, E.

Biochem. Biophys. Res. Commun. 188, 1077-1083, 1992

A:Title: Molecular cloning of a truncated isoform of the human follicle stimulating h

A:Reference number: PC1147; MUID:93075197; PMID:1359889

A:Accession: PC1147

A:Status: nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-223,286-294,'P',296-342 <GR3>

A:Cross-references: EMBL:X68044; NID:g31473; PIDN:CAA48179.1; PID:g31474

A:Experimental source: Testis

R:Gromoll, J.

Submitted to the EMBL Data Library, August 1992

A:Reference number: S30560

A:Accession: S30560

A:Molecule type: mRNA

A:Residues: 1-12,'R',14-223,286-294,'P',296-342 <GR4>

A:Cross-references: EMBL:X68044; NID:g31473; PIDN:CAA48179.1; PID:g31474

R:Kelton, C.A.; Cheng, S.V.; Nugent, N.P.; Schweickhardt, R.L.; Rosenthal, J.L.; Over

Mol. Cell. Endocrinol. 89, 141-151, 1992

A:Title: The cloning of the human follicle stimulating hormone receptor and its expe

A:Reference number: 157672; MUID:93246012; PMID:1301382

A:Accession: 157672

A:Status: preliminary; translated from GB/EMBL/DBD

A:Molecule type: mRNA

A:Residues: 1-679, N, 681-695 <KEL>

A:Cross-references: GB:S59900; NID:g300072; PIDN:AAB26480.1; PID:g300073

R:Minegishi, T.; Nakamura, K.; Takakura, Y.; Ibuki, Y.; Igarashi, M.

Biochem. Biophys. Res. Commun. 175, 1125-1130, 1991

A:Title: Cloning and sequencing of human FSH receptor cDNA.

A:Reference number: JN0122; MUID:91222171; PMID:1709010

A:Accession: JN0122

A:Molecule type: mRNA

A:Residues: 1-111,'T',113-196,'AV',199-306,'A',308-695 <MIN>

A:Cross-references: EMBL:M65085; NID:g182770; PIDN:AAA52477.1; PID:g182771

C:Genetics:

A:Gene: GDB:FSHR

A:Cross-references: GDB:127510; OMIM:136435

A:Map position: 2p21-2p16

A:Introns: 223/3

A:Note: the exact position of the intron cannot be determined from the experimental c

C:Function:

A:Description: receptor that mediates the biochemical effects of follitropin

C:Superfamily: glycoprotein hormone receptor; leucine-rich alpha-2-glycoprotein repee

C:Keywords: alternative splicing; G protein-coupled receptor; glycoprotein; hormone

F:1-695/Product: follitropin receptor precursor, long splice form #status predicted

F:1-223,286-695/Product: follitropin receptor precursor, short splice form #status pr

F:1-15/Domain: signal sequence #status predicted <SIG>

F:16-695/Domain: extracellular hormone binding #status predicted <NAT>

F:16-366/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR1>

F:56-70/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR2>

F:71-95/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>

F:96-120/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR4>

F:121-145/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR5>

F:146-169/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR6>

F:173-193/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR7>

F:194-218/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR8>

F:367-387/Domain: transmembrane #status predicted <TM1>

F:398-421/Domain: transmembrane #status predicted <TM2>

F:444-465/Domain: transmembrane #status predicted <TM3>

F:486-508/Domain: transmembrane #status predicted <TM4>

F:529-550/Domain: transmembrane #status predicted <TM5>

F:574-597/Domain: transmembrane #status predicted <TM6>

F:609-630/Domain: transmembrane #status predicted <TM7>

F:191,199,293,318/Binding site: carbohydrate (Asn) (covalent) #status predicted

F:555/Binding site: phosphate (Thr) (covalent) (by protein kinase C) status predicted
F:556/Binding site: phosphate (Ser) (covalent) (by protein kinase C) status predicted

Query Match 90.4%; Score 3160.5; DB 1; Length 695;
Best Local Similarity 89.4%; Pred. No. 5.1e-212;
Matches 606; Conservative 30; Mismatches 39; Indels 3; Gaps 2;
OY 1 CHHMLCHSNNRVFLQDSKVTEIPTDLPNRIELRVLTCLRVIPKGSFAGFGDLEKIEI 60
DB 18 CHHMLCHSNNRVFLQDSKVTEIPTDLPNRIELRVLTCLRVIPKGSFAGFGDLEKIEI 77
OY 61 SONDLVLEADVFNSKLPKLEIRIEKANNLLYINPEAFONLPSRLYLLISNTGKILHPA 120
DB 78 SONDLVLEADVFNSKLPKLEIRIEKANNLLYINPEAFONLPSRLYLLISNTGKILHPA 137
OY 121 VHKIOSLOKVLIDODNIHIVARNSPGLSSVILMLSKNGIEIHNCAFNQTOLDE 180
DB 138 VHKIHSQKVLIDODNIHIVARNSPGLSSVILMLSKNGIEIHNCAFNQTOLDE 197
OY 181 LNLSDNNLEELPNDVFGASGVILDISRTKVSHPNGLNKLKLRARSTYRLKLPN 240
DB 198 LNLSDNNLEELPNDVFGASGVILDISRTKVSHPNGLNKLKLRARSTYRLKLPN 257
OY 241 LDKFVTLMEASLTYPSCAFANKRQISELHPICNKSILRODIDMTQIGDORVSLIDD 300
DB 258 LEKULVAMEASLTYPSCAFANKRQISELHPICNKSILRODIDMTQIGDORVSLIDD 317
OY 301 -EPYKGSQDMNTNEFDYDLCHNEVDVTCSPKDPNCPEDINGYNILRVLIWIFISILAI 359
DB 318 NESSTRGDMHTAFEDYDLCHNEVDVTCSPKDPNCPEDINGYNILRVLIWIFISILAI 377
OY 360 TGNITVLVLTTSOYKLVTPRELACNLAFADLCIGYLLLIASVDIHTKSOYHVAIDMQ 419
DB 378 TGNITVLVLTTSOYKLVTPRELACNLAFADLCIGYLLLIASVDIHTKSOYHVAIDMQ 437
OY 420 TGACDCAAGFTTFVASELSVYTLTAITLERHHTITHAMOLECKVOLRHAASVYVLCWTF 479
DB 438 TGACDCAAGFTTFVASELSVYTLTAITLERHHTITHAMOLECKVOLRHAASVYVLCWTF 497
OY 480 FAALPPIFGISSYKVSICLPMIDPSLSQLYMALLVNLVLPVWICGCTHYLTIVR 539
DB 498 FAALPPIFGISSYKVSICLPMIDPSLSQLYMALLVNLVLPVWICGCTHYLTIVR 557
OY 540 NPTIVSSSDTKIAKRNATLIFTDPLCHAPISFFAISASLKVPLITVSKAKILLVLPYPI 599
DB 558 NPTIVSSSDTKIAKRNATLIFTDPLCHAPISFFAISASLKVPLITVSKAKILLVLPYPI 617
OY 600 NSCANPFLYALPTKFRPDPFTLLSKFCGYEMQAOIYRTETSSATHPHARKSCSSAPR 659
DB 618 NSCANPFLYALPTKFRPDPFTLLSKFCGYEMQAOIYRTETSSATHPHARKSCSSAPR 677
OY 660 VT--NSTVLVPLHSSQN 675
DB 678 VTGSGSYTLVPLSLAQN 695

RESULT 3

JN0898
foliitropin receptor precursor - crab-eating macaque
C:Alternate names: follicle-stimulating hormone receptor (FSHR)
C:Date:10-Sep-1999
C:Accession: JN0898; 876457
R:Gromoll, J.; Donker, B.; Sharma, R.S.; Nieschlag, E.
Biochem. Biophys. Res. Commun. 196, 1056-1072, 1993
A:Title: Molecular cloning of the testicular follicle stimulating hormone receptor of th
A:Reference number: JN0898; MUID:94071854; PMID:7504463
A:Accession: JN0898
A:Molecule type: mRNA
A:Residues: 1-695 <GRO>
A:Cross-references: EMBL:X74454; MID:g396801; PIDN:CAA52463.1; PID:g396802
A:Note: the authors translated the codon AGT for residue 488 as Arg
C:Function:

A:Description: receptor that mediates the biochemical effects of follitropin
C:Superfamily: glycoprotein hormone receptor; leucine-rich alpha-2-glycoprotein. repea
C:Repeat: 6 repeat; repeat: glycoprotein hormone receptor; phosphoprotein
F:1-17/Domain: 17
F:18-695/Product: follitropin receptor status predicted <PPH>
F:71-95/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR2>
F:96-120/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>
F:121-145/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR4>
F:146-169/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR5>
F:172-193/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR6>
F:194-218/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR7>
F:367-387/Domain: transmembrane status predicted <TM1>
F:399-421/Domain: transmembrane status predicted <TM2>
F:444-465/Domain: transmembrane status predicted <TM3>
F:486-508/Domain: transmembrane status predicted <TM4>
F:529-550/Domain: transmembrane status predicted <TM5>
F:569-630/Domain: transmembrane status predicted <TM6>
F:631-695/Domain: transmembrane status predicted <TM7>
F:131-189-202-318-367-421-486-508-529-550-569-630-695 (Asp) protein kinase C) status predicted
F:555/Binding site: phosphate (Thr) (covalent) (by protein kinase C) status predicted
F:556/Binding site: phosphate (Ser) (covalent) (by protein kinase C) status predicted

Query Match 89.9%; Score 3160.5; DB 1; Length 695;

Best Local Similarity 89.4%; Pred. No. 5.1e-212;

Matches 606; Conservative 30; Mismatches 39; Indels 3; Gaps 2;

OY 1 CHHMLCHSNNRVFLQDSKVTEIPTDLPNRIELRVLTCLRVIPKGSFAGFGDLEKIEI 60
DB 18 CHHMLCHSNNRVFLQDSKVTEIPTDLPNRIELRVLTCLRVIPKGSFAGFGDLEKIEI 77
OY 61 SONDLVLEADVFNSKLPKLEIRIEKANNLLYINPEAFONLPSRLYLLISNTGKILHPA 120
DB 78 SONDLVLEADVFNSKLPKLEIRIEKANNLLYINPEAFONLPSRLYLLISNTGKILHPA 137
OY 121 VHKIOSLOKVLIDODNIHIVARNSPGLSSVILMLSKNGIEIHNCAFNQTOLDE 180
DB 138 VHKIHSQKVLIDODNIHIVARNSPGLSSVILMLSKNGIEIHNCAFNQTOLDE 197
OY 181 LNLSDNNLEELPNDVFGASGVILDISRTKVSHPNGLNKLKLRARSTYRLKLPN 240
DB 198 LNLSDNNLEELPNDVFGASGVILDISRTKVSHPNGLNKLKLRARSTYRLKLPN 257
OY 241 LDKFVTLMEASLTYPSCAFANKRQISELHPICNKSILRODIDMTQIGDORVSLIDD 300
DB 258 LEKULVAMEASLTYPSCAFANKRQISELHPICNKSILRODIDMTQIGDORVSLIDD 317
OY 301 -EPYKGSQDMNTNEFDYDLCHNEVDVTCSPKDPNCPEDINGYNILRVLIWIFISILAI 359
DB 318 NESSTRGDMHTAFEDYDLCHNEVDVTCSPKDPNCPEDINGYNILRVLIWIFISILAI 377
OY 360 TGNITVLVLTTSOYKLVTPRELACNLAFADLCIGYLLLIASVDIHTKSOYHVAIDMQ 419
DB 378 TGNITVLVLTTSOYKLVTPRELACNLAFADLCIGYLLLIASVDIHTKSOYHVAIDMQ 437
OY 420 TGACDCAAGFTTFVASELSVYTLTAITLERHHTITHAMOLECKVOLRHAASVYVLCWTF 479
DB 438 TGACDCAAGFTTFVASELSVYTLTAITLERHHTITHAMOLECKVOLRHAASVYVLCWTF 497
OY 480 FAALPPIFGISSYKVSICLPMIDPSLSQLYMALLVNLVLPVWICGCTHYLTIVR 539
DB 498 FAALPPIFGISSYKVSICLPMIDPSLSQLYMALLVNLVLPVWICGCTHYLTIVR 557
OY 540 NPTIVSSSDTKIAKRNATLIFTDPLCHAPISFFAISASLKVPLITVSKAKILLVLPYPI 599
DB 558 NPTIVSSSDTKIAKRNATLIFTDPLCHAPISFFAISASLKVPLITVSKAKILLVLPYPI 617
OY 600 NSCANPFLYALPTKFRPDPFTLLSKFCGYEMQAOIYRTETSSATHPHARKSCSSAPR 659
DB 618 NSCANPFLYALPTKFRPDPFTLLSKFCGYEMQAOIYRTETSSATHPHARKSCSSAPR 677
OY 660 VT--SYVLVPLHSSQN 675
DB 678 VTGSGSYTLVPLSLAQN 695

RESULT 4

145896
follicle stimulating hormone receptor - bovine
C:Species: Bos primigenius taurus (cattle)
C:Date: 15-Oct-1996 #sequence_revision 15-Oct-1996 #text_change 21-Jan-2000
C:Accession: 145896
R:Houde, A.; Lambert, A.; Saumande, J.; Silversides, D.W.; Lussier, J.G.
Mol. Reprod. Dev. 39, 127-135, 1994
A:Title: Structure of the bovine follicle-stimulating hormone receptor complementary DNA
A:Reference number: 145896; MUID:95127199; PMID:7826612
A:Accession: 145896
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-695 <HOU>
A:Cross-references: GB:L22319; NID:g404671; PIDN:AAC37324.1; PID:g404672
C:Gene: FSHR
C:Superfamily: glycoprotein hormone receptor; leucine-rich alpha-2-glycoprotein repeat
F:71-95/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR>

Query Match 89.5%; Score 3145.5; DB 2; Length 695;
Best Local Similarity 87.9%; Pred. No. 5.6e-211;
Matches 596; Conservative 45; Mismatches 34; Indels 3; Gaps 2;

Qy 1 CHHWLCHSNRVFLCQDSKVTEIPTDLPRAIEFLVTLKRVIPKGSFAGFGDLEKIEI 60
Dy 18 CHHRLCHCSNGVFLCQDSKVTEIPTDLPRAIEFLVTLKRVIPKGSFAGFGDLEKIEI 77

Qy 61 SONDVLEIADVFSNLPKLEIRKANNLLYNPEAFONLPSRLYLLISNTGKHLPA 120
Dy 78 SONDVLEIVANVFSNLPKLEIRKANNLLYIDPAFONLPLNRLYLLISNTGKHLPA 137

Qy 121 VHKLQSLQKVLDDIQDNINIHIVARNFPMGLSFESVILWLSKNGIEETHNCAFNQTOLDE 180
Dy 138 VHKLQSLQKVLDDIQDNINIHIVARNFPMGLSFESVILWLSKNGIEETHNCAFNQTOLDE 197

Qy 181 LNLSDNNLELPNDVFGASGPVILDSRTKRVHSLPNHGLNKKLRARSTYRLKLLPN 240
Dy 198 LNLSDNSNLELPNDVFGASGPVILDSRTKRVHSLPNHGLNKKLRARSTYRLKLLPS 257

Qy 241 LDKFVTLMEASLTYPSCCAFANLKRQISELHPICNKSILRODIDDMTOIGDQVSLI-D 299
Dy 258 LEKFTVLEASLTYPSCCAFANRRQTSDLHPICNKSILRQEVDDMTQARGQVSLAI 317

Qy 300 DEPSYKSGDMYNEFDYDLCEVVDVTCSPKPAFNPCEIDMGYNILRVLWIFISILAI 359
Dy 318 DEPSYKGFDMYSEFDYDLCEVVDVTCSPKPAFNPCEIDMGYNILRVLWIFISILAI 377

Qy 360 TGNITVLVLTTSQYKLTVPFLMCLNLAFAADLCIGIYLLIASVDVHTKSOYHNYADWQ 419
Dy 378 TGNITVLVLTTSQYKLTVPFLMCLNLAFAADLCIGIYLLIASVDVHTKSOYHNYADWQ 437

Qy 420 TGACDAAAGFTTFVASELSVYTLTAITLERWHTITHAMOLECKVQLRHAASVVLWGTFA 479
Dy 438 TGACDAAAGFTTFVASELSVYTLTAITLERWHTITHAMOLECKVQLRHAASVVLWGTFA 497

Qy 480 FAALFPFTFGISSYMKVSIKLPMDIDSPLSOLYVNLVNLVAFVVICGCTHYLTVR 539
Dy 498 FAVALFPFTFGISSYMKVSIKLPMDIDSPLSOLYVNLVNLVAFVVICGCTHYLTVR 557

Qy 540 NPTIVSSSDTKIAKRMATLFTDFLCNAPISFAISASLKVPLITVSKAKILLVLPFI 599
Dy 558 NPTIVSSSDTKIAKRMATLFTDFLCNAPISFAISASLKVPLITVSKAKILLVLPFI 617

Qy 600 NSCANPFLYIAFTNFRDRFDILLSKFCYEQMQAIVRTSTSSATHNPHARKSHCSAPR 659
Dy 618 NSCANPFLYIAFTNFRDRFDILLSKFCYEQMQAIVRTSTSSATHNPHARKSHCSAPR 677

Qy 660 VTN--SYVLVPLNHSSON 675
Dy 678 VTNGSNYTLIPLRLAKN 695

RESULT 5

JC1493
follicotropin receptor - sheep
N:Alternate names: follicle stimulating hormone receptor
C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 21-Jan-2000
C:Accession: JC1493; I47080
R:Khan, H.; Yarney, T.A.; Sairam, M.R.
Biochem. Biophys. Res. Commun. 190, 888-894, 1993
A:Title: Cloning of alternatively spliced mRNA transcripts coding for variants of ovine
A:Reference number: JC1493; MUID:93176195; PMID:8439338
A:Accession: JC1493
A:Molecule type: mRNA
A:Residues: 1-695 <KHA>
A:Experimental source: testis
R:Yarney, T.A.; Sairam, M.R.; Khan, H.; Ravindranath, N.; Payne, S.; Seidah, N.G.
Mol. Cell. Endocrinol. 93, 219-226, 1993
A:Title: Molecular cloning and expression of the ovine testicular follicle stimulating
A:Reference number: I47080; MUID:93351750; PMID:8394255
A:Accession: I47080
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-695 <YAR>
A:Cross-references: GB:L07302; NID:g165884; PIDN:AAA31525.1; PID:g165885
C:Gene: FSH-R
C:Superfamily: glycoprotein hormone receptor; leucine-rich alpha-2-glycoprotein repe
C:Keywords: G protein-coupled receptor; glycoprotein; transmembrane protein
F:71-95/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR>
F:191/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 89.3%; Score 3140.5; DB 2; Length 695;
Best Local Similarity 87.5%; Pred. No. 1.2e-210;
Matches 593; Conservative 47; Mismatches 35; Indels 3; Gaps 2;

Qy 1 CHHWLCHSNRVFLCQDSKVTEIPTDLPRAIEFLVTLKRVIPKGSFAGFGDLEKIEI 60
Dy 18 CHHRLCHCSNGVFLCQDSKVTEIPTDLPRAIEFLVTLKRVIPKGSFAGFGDLEKIEI 77

Qy 61 SONDVLEIADVFSNLPKLEIRKANNLLYNPEAFONLPSRLYLLISNTGKHLPA 120
Dy 78 SONDVLEIVANVFSNLPKLEIRKANNLLYIDPAFONLPLNRLYLLISNTGKHLPA 137

Qy 121 VHKLQSLQKVLDDIQDNINIHIVARNFPMGLSFESVILWLSKNGIEETHNCAFNQTOLDE 180
Dy 138 VHKLQSLQKVLDDIQDNINIHIVARNFPMGLSFESVILWLSKNGIEETHNCAFNQTOLDE 197

Qy 181 LNLSDNNLELPNDVFGASGPVILDSRTKRVHSLPNHGLNKKLRARSTYRLKLLPN 240
Dy 198 LNLSDNSNLELPNDVFGASGPVILDSRTKRVHSLPNHGLNKKLRARSTYRLKLLPS 257

Qy 241 LDKFVTLMEASLTYPSCCAFANLKRQISELHPICNKSILRODIDDMTOIGDQVSLI-D 299
Dy 258 LEKFTVLEASLTYPSCCAFANRRQTSDLHPICNKSILRQEVDDMTQARGQVSLAI 317

Qy 300 DEPSYKSGDMYNEFDYDLCEVVDVTCSPKPAFNPCEIDMGYNILRVLWIFISILAI 359
Dy 318 DEPSYKGFDMYSEFDYDLCEVVDVTCSPKPAFNPCEIDMGYNILRVLWIFISILAI 377

Qy 360 TGNITVLVLTTSQYKLTVPFLMCLNLAFAADLCIGIYLLIASVDVHTKSOYHNYADWQ 419
Dy 378 TGNITVLVLTTSQYKLTVPFLMCLNLAFAADLCIGIYLLIASVDVHTKSOYHNYADWQ 437

Qy 420 TGACDAAAGFTTFVASELSVYTLTAITLERWHTITHAMOLECKVQLRHAASVVLWGTFA 479
Dy 438 TGACDAAAGFTTFVASELSVYTLTAITLERWHTITHAMOLECKVQLRHAASVVLWGTFA 497

Qy 480 FAALFPFTFGISSYMKVSIKLPMDIDSPLSOLYVNLVNLVAFVVICGCTHYLTVR 539
Dy 498 FAVALFPFTFGISSYMKVSIKLPMDIDSPLSOLYVNLVNLVAFVVICGCTHYLTVR 557

OY 540 NPTIVSSSDTKIAKMAITLFTDFLCMAPISTFAISASLKVLTIVSKAKILLVLPYPI 599
DB 558 NPTIVSSSDTKIAKMAITLFTDFLCMAPISTFAISASLKVLTIVSKAKILLVLPYPI 617
OY 600 NSCANPFLVIAITKFNPRDFPILLSKGCGYEMQAIYRTETSSATHNPHARKSCSSAPR 659
DB 618 NSCANPFLVIAITKFNPRDFPILLSKGCGYEMQAIYRTETSSATHNPHARKSCSSAPR 677
OY 660 VTN--SYVLVPLNHSN 675
DB 678 VTN--SYVLVPLNHSN 695
RESULT 6
JC2237
foliitropin receptor, testis - horse
N:Alternate names: eFSHR
C:Species: Equus caballus (domestic horse)
C:Date: 28-Aug-1985 #sequence_revision 07-Oct-1994 #text_change 13-Aug-1999
C:Accession: JC2237; JC2370
R:Robert, P.; Ansell, S.; Christophe, S.; Benfija, J.L.; Bellet, D.; Koman, A.; Bidart
Biochem. Biophys. Res. Commun. 201, 201-207, 1994
A:Title: Cloning and sequencing of the equine testicular foliitropin receptor.
A:Reference number: JC2237; MUID:94256980; PMID:8198575
A:Accession: JC2237
A:Molecule type: mRNA
A:Residues: 1-694 <ROB>
A:Cross-references: GB:S70150; MUID:9546896; PIDN:AAB30854.1; PID:9546897
A:Experimental source: testis
C:Superfamily: glycoprotein hormone receptor; leucine-rich alpha-2-glycoprotein repeat
F:57-70/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR>
F:71-95/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR>
F:96-120/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR>
F:121-145/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR>
F:146-169/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR>
F:172-193/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR>
F:194-218/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR>
F:366-386/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR>
F:398-420/Domain: transmembrane #status predicted <TM1>
F:443-464/Domain: transmembrane #status predicted <TM2>
F:485-507/Domain: transmembrane #status predicted <TM3>
F:528-549/Domain: transmembrane #status predicted <TM4>
F:573-596/Domain: transmembrane #status predicted <TM5>
F:608-629/Domain: transmembrane #status predicted <TM6>
F:131,195,406,429/Binding site: carbohydrate (Asn) (covalent), #status predicted
Query Match 87.4%; Score 3074; DB 2; Length 694;
Best Local Similarity 87.6%; Pred. No. 5,3e-206;
Matches 594; Conservative 35; Mismatches 45; Indels 4; Gaps 3;
OY 1 CHHMLCHSNNRVFLQDSKVTETPTDLPNRAELRVLTIVKLVIPKSGFAGDLEKIEI 60
DB 18 CHHVRVCHSNNRVFLQDSKVTETPTDLPNRAELRVLTIVKLVIPKSGFAGDLEKIEI 77
OY 61 SONVLEVEADVPSMLPKLHEIRIEKANNLLYINPEAPQNLPSLYLLISNTGKHLPA 120
DB 78 SONVLEVEADVPSMLPKLHEIRIEKANNLLYIDHDAFQNLPLQYLLISNTGKHLPA 137
OY 121 VHKIOSLQVLLDQDNIHIVANSFNGLSFESVILWLSKNGIEEHNCAFNCTOLDE 180
DB 138 VHKIOSLQVLLDQDNIHIVANSFNGLSFESVILWLSKNGIEEHNCAFNCTOLDE 197
OY 181 LNLSDNNLEELPNDFVOCAGSPVTLDSITKVLSPNGLNLEKLRASVYKLLPN 240
DB 198 LNLSTNNLEELPNDFVOCAGSPVTLDSITKVLSPNGLNLEKLRASVYKLLPN 257
OY 241 LQKPVYLMKASLYPSHCAPANLAKQISELPHCTCNKSLTRQDIDMTQIGQVSLT-D 299
DB 258 LKFPVLMKASLYPSHCAPANLAKQISELPHCTCNKSLTRQV-DMTQIGVSLD 316
OY 300 DEFSYKSGSDNNEFDYDLQNEVDVTCSPKPDAPNCPEDIMGYDILRVLIWFISLAI 359
DB 317 DESSYKSGSDNNEFDYDLQNEVDVTCSPKPDAPNCPEDIMGYDILRVLIWFISLAI 376
OY 360 TQNTVVLVYLTQSYKLVLPREFLCMAPISTFAISASLKVLTIVSKAKILLVLPYPI 419
DB 377 TQNTVVLVYLTQSYKLVLPREFLCMAPISTFAISASLKVLTIVSKAKILLVLPYPI 436
OY 420 TCAGCDAAGPFTVFASLSVYLTATITLERNHTITHANOLECKVQLRHAASVYLVGKTEA 479
DB 437 TCAGCDAAGPFTVFASLSVYLTATITLERNHTITHANOLECKVQLRHAASVYLVGKTEA 496
OY 480 FAALAPFIFIGISSYKVSICLPMQIDSPISOLYVNLVNLVLPVVGCGYTHIYLTVR 539
DB 497 FAVALPFIIGISTYKVSICLPMQIDSPISOLYVNLVNLVLPVVGCGYTHIYLTVR 556
OY 540 NPTIVSSSDTKIAKMAITLFTDFLCMAPISTFAISASLKVLTIVSKAKILLVLPYPI 599
DB 557 NPTIVSSSDTKIAKMAITLFTDFLCMAPISTFAISASLKVLTIVSKAKILLVLPYPI 616
OY 600 NSCANPFLVIAITKFNPRDFPILLSKGCGYEMQAIYRTETSSATHNPHARKSCSSAPR 659
DB 617 NSCANPFLVIAITKFNPRDFPILLSKGCGYEMQAIYRTETSSATHNPHARKSCSSAPR 676
OY 660 VTN--SYVLVPLNHSN 675
DB 677 VINGANTLVPLSHLAQN 694
RESULT 7
JC4301
foliitropin receptor - pig
N:Alternate names: follicle-stimulating hormone receptor
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 16-Nov-1995 #sequence_revision 08-Feb-1996 #text_change 21-Jan-2000
C:Accession: JC4301
R:Kemp, J.; Ishibashi-Mansals, Y.; Yerle, M.; Boson, V.; Couture, L.; Pajot, E.; Grebe
Gen. 163, 237-261, 1995
A:Title: The porcine foliitropin receptor: cDNA cloning, functional expression and chr-
A:Reference number: JC4301; MUID:9601644; PMID:7590277
A:Accession: JC4301
A:Molecule type: mRNA
A:Residues: 1-694 <REM>
A:Cross-references: GB:L31966
A:Experimental source: ovarian granulosa cells
C:Comment: This receptor belongs to the family of the G-protein coupled receptors. It
ermatogenesis in male and oogenesis in female.
C:Genetics:
A:Gene: fshr
A:Map position: 3 q2.2-q2.3
C:Superfamily: glycoprotein hormone receptor; leucine-rich alpha-2-glycoprotein repea
F:11-365/Domain: leucine-rich alpha-2-glycoprotein repeat homology <ROB>
F:70-94/Domain: leucine-rich alpha-2-glycoprotein repeat homology <TM1>
F:366-388/Domain: transmembrane #status predicted <TM2>
F:398-420/Domain: transmembrane #status predicted <TM3>
F:443-464/Domain: transmembrane #status predicted <TM4>
F:485-507/Domain: transmembrane #status predicted <TM5>
F:528-549/Domain: transmembrane #status predicted <TM6>
F:573-596/Domain: transmembrane #status predicted <TM7>
F:608-629/Domain: transmembrane #status predicted <TM7>
Query Match 87.3%; Score 3070.5; DB 2; Length 694;
Best Local Similarity 86.1%; Pred. No. 9.2e-206;
Matches 584; Conservative 40; Mismatches 51; Indels 3; Gaps 2;
OY 1 CHHMLCHSNNRVFLQDSKVTETPTDLPNRAELRVLTIVKLVIPKSGFAGDLEKIEI 60
DB 17 CHHVRVCHSNNRVFLQDSKVTETPTDLPNRAELRVLTIVKLVIPKSGFAGDLEKIEI 76
OY 61 SONVLEVEADVPSMLPKLHEIRIEKANNLLYINPEAPQNLPSLYLLISNTGKHLPA 120
DB 77 SONVLEVEADVPSMLPKLHEIRIEKANNLLYIDHDAFQNLPLQYLLISNTGKHLPA 136
OY 121 VHKIOSLQVLLDQDNIHIVANSFNGLSFESVILWLSKNGIEEHNCAFNCTOLDE 180

Db 137 VHKIQSLQKVLDDIQDNIHIVERNFSGMLSPSMLWLSKNGIRHNCFAFGTQDLE 196
Qy 181 LNLSDNNLELPNDVFOGASGPVILDSRTKVSLSLPHNGLNKKLRARSTYRLKKLPN 240
Db 197 LNLSDNNLELPNDVFOGASGPVILDSRTKVSLSLPHNGLNKKLRARSTYRLKKLPN 256
Qy 241 LDKFVTLMEASLTYPSPHCCAFANLKRQISLHLPICNKSILRQDIDDDTQICDQSVSLDD 300
Db 257 LEKFTVTLMEASLTYPSPHCCAFANLKRQISLHLPICNKSILRQDIDDDTQICDQSVSLDD 316
Qy 301 -EPYSGKSGDMYNEFDYDLCNEVVDVTCSPKDAFNPCEIDIMGYNLRLVILWFISILAI 359
Db 317 GESSLAKEFDFTMYSEFNVDLCNEVVDVTCSPKDAFNPCEIDIMGYNLRLVILWFISILAI 376
Qy 360 TGNITVTLVLTTSQYKLTVPRLMCLNLAFLDLCIGIYLLIASVDIHTKSOYHNYAIDWQ 419
Db 377 TGNITVTLVLTTSQYKLTVPRLMCLNLAFLDLCIGIYLLIASVDIHTKSOYHNYAINWQ 436
Qy 420 TGACDAAGFTVPASELSVYTLTAITLERWHITTHAMOLECKVOLRAHASVYLVGTFEA 479
Db 437 TGACDAAGFTVPASELSVYTLTAITLERWHITTHAMOLECKVOLRAHASVYLVGTFEA 496
Qy 480 FTAALPFIPIGSISSYMKVSIICLPMDIDSPLSQYVYVLLVNLVAFVVICGCIYIYLTVR 539
Db 497 FTAALPFIPIGSISSYMKVSIICLPMDIDSPLSQYVYVLLVNLVAFVVICGCIYIYLTVR 556
Qy 540 NPTIVSSSDTKIAKRMATLIFTDFLCMAPISEFAISASLKVPITVYSKAKILLVLPYPI 599
Db 557 NPTIVSSSDTKIAKRMATLIFTDFLCMAPISEFAISASLKVPITVYSKAKILLVLPYPI 616
Qy 600 NSCANPLYAIFTKNFRDRFVILLKFCGCEYEMOQAIYRTETSSATHNFHARKSHCSAPR 659
Db 617 NSCANPLYAIFTKNFRDRFVILLKFCGCEYEMOQAIYRTETSSATHNFHARKSHCSAPR 676
Qy 660 VTN--SYLVPLNHSQON 675
Db 677 ITNSSSYTLPLSLAQN 694

RESULT 8

foliitropin receptor precursor - newt
N;Alternate names: follicle-stimulating hormone receptor
C;Species: Cynops pyrrhogaster (newt)
C;Date: 17-Nov-2000 #sequence_revision 17-Nov-2000 #text_change 31-Dec-2000
R;Nakayama, Y.; Yamamoto, T.; Oba, Y.; Nagahama, Y.; Abe, S.
Biochem. Biophys. Res. Commun. 275, 121-128, 2000
A;Title: Molecular cloning, functional characterization, and gene expression of a follicle-stimulating hormone receptor, and gene expression of a follicle-stimulating hormone receptor
A;Contents: Testis
A;Accession: JC7361
A;Molecule type: mRNA
A;Residues: 1-696 <NAK>
A;Cross-references: DDBJ:AB005587
C;Comment: This protein, containing seven transmembrane domains and a large glycosylated in and thyroid stimulating hormone. This receptor has a common signal transduction pathway in and thyroid stimulating hormone.
A;Gene: fsh-r
C;Superfamily: glycoprotein hormone receptor; leucine-rich alpha-2-glycoprotein repeat
C;Keywords: disulfide bond; glycolysis; glycoprotein; hormone receptor; testis; transmembrane
F;1-17/Domain: signal sequence #status predicted <SIG>
F;18-696/Product: follicle-stimulating hormone receptor #status predicted <MAT>
F;18-359/Domain: extracellular #status predicted <EXT>
F;370-389/Domain: transmembrane #status predicted <TM1>
F;402-424/Domain: transmembrane #status predicted <TM2>
F;447-468/Domain: transmembrane #status predicted <TM3>
F;489-511/Domain: transmembrane #status predicted <TM4>
F;532-553/Domain: transmembrane #status predicted <TM5>
F;577-600/Domain: transmembrane #status predicted <TM6>
F;612-633/Domain: transmembrane #status predicted <TM7>
F;46,190,198,267,292/Binding site: carbohydrate (Asn) (covalent) #status predicted

F;445-520/Disulfide bonds: #status predicted

Query Match 70.4%; Score 2475; DB 2: Length 696;

Best Local Similarity 71.1%; Pred. No. 2.5e-164;

Matches 482; Conservative 81; Mismatches 107; Indels 8; Gaps 5;

Qy 1 CHHWLCHSNNRVFLCQDSKVTETDLPNNAIEFLVTLKRVIPKSGFAGDLEKIEI 60
Db 18 CHP-VCRLARVETCOESHVVQIPDRIPRNSITELFVLTQVTPKAASFQFEDVENIEI 76
Qy 61 SONDVLVIEADVFENLPLKHEIRKANNLLYNDEAFONLPSRLYLLISNTGKHLPA 120
Db 77 SONDVLVIEADVFENLPLKHEIRKANNLLYNDEAFONLPSRLYLLISNTGKHLPA 136
Qy 121 VHKIQSLQKVLDDIQDNIHIVERNFSGMLSPSMLWLSKNGIRHNCFAFGTQDLE 180
Db 137 VHKIQSLQKVLDDIQDNIHIVERNFSGMLSPSMLWLSKNGIRHNCFAFGTQDLE 196
Qy 181 LNLSDNNLELPNDVFOGASGPVILDSRTKVSLSLPHNGLNKKLRARSTYRLKKLPN 240
Db 197 LNLSDNNLELPNDVFOGASGPVILDSRTKVSLSLPHNGLNKKLRARSTYRLKKLPN 256
Qy 241 LDKFVTLMEASLTYPSPHCCAFANLKRQISLHLPICNKSILRQDIDDDTQICDQSVSLDD 299
Db 257 LEKFTVTLMEASLTYPSPHCCAFANLKRQISLHLPICNKSILRQDIDDDTQICDQSVSLDD 316
Qy 300 DEPSYSGKSGDMYNEFDYDLCNEVVDVTCSPKDAFNPCEIDIMGYNLRLVILWFIS 355
Db 317 DEPSYSGKSGDMYNEFDYDLCNEVVDVTCSPKDAFNPCEIDIMGYNLRLVILWFIS 376
Qy 356 ILAITGNTVTLVLTTSQYKLTVPRLMCLNLAFLDLCIGIYLLIASVDIHTKSOYHNYA 415
Db 377 ILAITGNTVTLVLTTSQYKLTVPRLMCLNLAFLDLCIGIYLLIASVDIHTKSOYHNYA 436
Qy 416 IDMQTAGCDAAGFTVPASELSVYTLTAITLERWHITTHAMOLECKVOLRAHASVYLVG 475
Db 437 IDMQTAGCDAAGFTVPASELSVYTLTAITLERWHITTHAMOLECKVOLRAHASVYLVG 496
Qy 476 WTEFAAALPFIPIGSISSYMKVSIICLPMDIDSPLSQYVYVLLVNLVAFVVICGCIYIY 535
Db 497 WTEFAAALPFIPIGSISSYMKVSIICLPMDIDSPLSQYVYVLLVNLVAFVVICGCIYIY 556
Qy 536 LTVNPTIVSSSDTKIAKRMATLIFTDFLCMAPISEFAISASLKVPITVYSKAKILLV 595
Db 557 LTVNPTIVSSSDTKIAKRMATLIFTDFLCMAPISEFAISASLKVPITVYSKAKILLV 616
Qy 596 FYPIINSCANPLYAIFTKNFRDRFVILLKFCGCEYEMOQAIYRTETSSATHNFHARKSHCS 655
Db 617 FYPIINSCANPLYAIFTKNFRDRFVILLKFCGCEYEMOQAIYRTETSSATHNFHARKSHCS 676
Qy 656 SAPR--VTNSYLVPLNHSQON 671
Db 677 PAPKYSAASTHTLVPLNN 694

RESULT 9

A41344
lutropin-choriogonadotropin receptor precursor (splice form A) - pig
N;Alternate names: lutinizing hormone-choriogonadotropin receptor
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 21-Jan-2000
C;Accession: A41344
R;Loosfelt, H.; Misrahi, M.; Atger, M.; Salesse, R.; Vu Hai-Luu Thi, M.T.; Jolivet, A.
Science 245, 525-528, 1989
A;Title: Cloning and sequencing of porcine LH-RG receptor cDNA: variants lacking tra
A;Reference number: A41344; MUID:89332517; PMID:2502844
A;Accession: A41344
A;Molecule type: mRNA
A;Residues: 1-696 <LOO>
A;Cross-references: GB:M29525; NID:g164528; PIDN:AAA31062.1; PID:g164529
C;Superfamily: glycoprotein hormone receptor; leucine-rich alpha-2-glycoprotein repeat
C;Keywords: alternative splicing; G protein-coupled receptor; glycoprotein; membrane
F;1-27/Domain: signal sequence #status predicted <SIG>

F:28-696/Product: lutropin-choriogonadotropic hormone receptor #status predicted <MAT>
F:99-123/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR>
Query Match 51.4% Score 1807; DB 2; Length 696;
Best Local Similarity 57.6% Pred No. 7 4e-118; Indels 26; Gaps 8;
Matches 361; Conservative 98; Mismatches 142;

QY 28 PRNAELRLVLTILK--RVIPKSFAGDGLKIEISQNDVLEADVFNSNLPKLHRI 85
DB 46 PRAGLS--RLSLTYLPKVPISQAFNGVNEWKIEISQSDSLERIANAFONLLNLSILL 105

QY 86 EXANLLYINPEAFONLPSRLYSILNTSGIKHLPVAKIQLQ--KVLLDQONINIHVA 144
DB 106 QNRLNLYTEPGAPTLPRKLYSLICNTGRTLPDVSKEISSEFNLEICDNLHTTVP 165

QY 145 RNSPGLSSESVILMLSKNGIEIHNCAPNGTOLDNLSONNNLEELPNDVFGASGPV 204
DB 166 ANAFQGNESITLALYNGFEVSHAFNGTLLSLEKENAKHAKHNDAPFRGSPS 225

QY 205 ILDISRTKVSILPHNGLENKILKARSTYELKLPNLDKFTVLEASITYPSCCAPNL 264
DB 226 ILDISSTKLQALPSGLSIOQLTATSYSLATPSREKFTNLLDNLATLTPSHCCAFNL 285

QY 265 --KRO-----ISELPICTNKSILRODIDDMTOIGDQVSLIDDEPSYSGSDMMYNEDP 316
DB 286 PTKQNFSEFSIFKNSKQCESTARPNNETL-----YSAFAE-----SELSDDWDYD 332

QY 317 YDLQNEVDVTCSPKDPNCPEDINGNIRLVNLFISILAITGNTVTLVLTYSOKL 376
DB 333 YGCSPT--LQCAPEPDNCPEDINGDFLRVILINILAIINGNTVTLVLTSHYKL 391

QY 377 TVPRLNCLAPADLCIGYLLIASVDIHTSQYHNYAIDMOTGACDAGFFVPVASE 436
DB 392 TVPRLNCLSPADPCGILLLIASVDIHTSQYHNYAIDMOTGACDAGFFVPVASE 451

QY 437 LSVTLTALTLERHHTTHAMOLECKVOLHRAASVWLGTFPAALPFIIGISYKVKY 496
DB 452 LSVTLTALTLERHHTTAYALQDLKLRHAIPLMGLMFLSTLMLPLVGVSYMYK 511

QY 497 SICLPMIDPSLSQVYVWALLVNLVAFVVGCGYTHIYLVTRNPTIVSSSDTKIAKRM 556
DB 512 SICLPMIDVETLSQVTLILILNVAFIICACYIKIYFAVQNPMLATNKDTIAKRM 571

QY 557 ATLIFDTLCHAPISFSAISLKVPLITVSKAKILLVLPINSCANPFLYAIPTKNER 616
DB 572 AVLIPTDTPOMPISFSAISLKVPLITVSKAKILLVLPINSCANPFLYAIPTKNER 631

QY 617 RDPFTLLSKFCYEMAOIYRTETSA 643
DB 632 RDPFTLLSKGCKHQAELYRKFDSA 658

RESULT 10
A42395

N:lutropin receptor - mouse
N:Alternate names: lutelinizing hormone-choriogonadotropin receptor

C:Species: Mus musculus (house mouse)
C:Date: 04-Mar-1993 #sequence,revision 18-Nov-1994 #text_change 13-Aug-1999

C:Accession: A42395
R:Gudermaun, T.; Birnbaumer, M.; Birnbaumer, L.

A:Title: Evidence for dual coupling of the murine lutelinizing hormone receptor to adenylyl cyclase and phospholipase C

A:Reference number: A42395; PMID:92165799; PMID:1311310

A:Status: preliminary
A:Molecule type: mRNA

A:Residues: 1-700 <GUD>
A:Cross-references: GB:M81310; GB:M81318; NID:g198811; PID:AAA9432.1; PID:g198812

A:Note: sequence extracted from NCBI backbone (NCBI:84064, NCBI:P84066)

C:Superfamily: glycoprotein hormone receptor; leucine-rich alpha-2-glycoprotein repeat

C:Keywords: G protein-coupled receptor; transmembrane protein

F:54-77/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR>

F:78-102/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR>
F:103-127/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR>
F:128-152/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR>
F:153-177/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR>
F:180-201/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR>
F:202-226/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR>

Query Match 51.2% Score 1799; DB 2; Length 700;
Best Local Similarity 55.1% Pred No. 2 7e-117; Indels 34; Gaps 9;
Matches 362; Conservative 108; Mismatches 153;

QY 28 PRNAELRLVLTILK--RVIPKSFAGDGLKIEISQNDVLEADVFNSNLPKLHRI 85
DB 51 PRAGL--ARLSLTLPKVPISQAFNGVNEWKIEISQSDSLERIANAFONLLNLSILL 109

QY 86 EXANLLYINPEAFONLPSRLYSILNTSGIKHLPVAKIQLQ--KVLLDQONINIHVA 144
DB 110 QNRLNLYTEPGAPTLPRKLYSLICNTGRTLPDVSKEISSEFNLEICDNLHTTVP 169

QY 145 RNSPGLSSESVILMLSKNGIEIHNCAPNGTOLDNLSONNNLEELPNDVFGASGPV 204
DB 170 GNAFQGNESITLALYNGFEVSHAFNGTLLSLEKENAKHAKHNDAPFRGSPS 229

QY 205 ILDISRTKVSILPHNGLENKILKARSTYELKLPNLDKFTVLEASITYPSCCAPNL 264
DB 230 ILDISSTKLQALPSGLSIOQLTATSYSLATPSREKFTNLLDNLATLTPSHCCAFNL 289

QY 265 KROISELHPICNKSILRODIDDMTOIGDQVSLIDDEPSY--KGSDDMMYNEDPDLN 321
DB 290 PKK-----EQNFSEFSIFKNSKQCESTARPNNETL--YSAFAE-----SELSDDWDYD 341

QY 322 EYVDVTCSPKDPNCPEDINGNIRLVNLFISILAITGNTVTLVLTYSOKLTPRPF 381
DB 342 PRT--LQCTPEPDNCPEDINGVAFRLVILINILAIINGNTVTLVLTSHYKLTPRPF 400

QY 382 LKCNLAPADLCIGYLLIASVDIHTSQYHNYAIDMOTGACDAGFFVPVASELSVYT 441
DB 401 LKCNLAPADPCGILLLIASVDIHTSQYHNYAIDMOTGACDAGFFVPVASELSVYT 460

QY 442 LTAITLERHHTTHAMOLECKVOLHRAASVWLGTFPAALPFIIGISYKVKYICLP 501
DB 461 LTVITLERHHTTAYALQDLKLRHAIPLMGLMFLSTLMLPLVGVSYMYKICLP 520

QY 502 MOIDPSLSQVYVWALLVNLVAFVVGCGYTHIYLVTRNPTIVSSSDTKIAKRMATLIP 561
DB 521 MOVETLSQVYVWALLVNLVAFVVGCGYTHIYLVTRNPTIVSSSDTKIAKRMATLIP 580

QY 562 TPTLCHAPISFSAISLKVPLITVSKAKILLVLPINSCANPFLYAIPTKNERDFFI 621
DB 581 TPTLCHAPISFSAISLKVPLITVSKAKILLVLPINSCANPFLYAIPTKNERDFFI 640

QY 622 LLSKFCYEMAOIYRTETSA-----TUNFHAKS-----HCS--SAPRV 660
DB 641 LLSRFGCKHQAELYRKFDSACTPNSKNGPPRSPKSPQAKLSIVHCOQPTTPRV 697

RESULT 11
I77463

N:lutelinizing hormone/chorionic gonadotropin receptor - rat

C:Species: Rattus sp. (rat)

C:Date: 02-Aug-1996 #sequence,revision 02-Aug-1996 #text_change 21-Jan-2000

C:Accession: I77463
R:Aatsinki, J.T.; Pietila, E.M.; Lakkakorpi, J.T.; Rajaniemi, H.J.

A:Title: Expression of the LH/CG receptor gene in rat ovarian tissue is regulated by gonadotropin-releasing hormone

A:Reference number: I57668; PMID:92347604; PMID:1353463

A:Status: preliminary
A:Molecule type: DNA

A:Residues: 1-700 <RES>
A:Cross-references: GB:S40803; NID:g252163; PIDN:AMB22680.1; PID:g252164

C:Genetics:
A:Introns: 58/2; 82/2; 107/2; 132/2; 183/2; 206/2; 231/2; 293/2; 320/2

C:Superfamily: glycoprotein hormone receptor; leucine-rich alpha-2-glycoprotein repeat
F:153-177/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR>

Query Match 51.18; Score 1797; DB 2; Length 700;
Best Local Similarity 56.5%; Pred. No. 3.7e-117;
Matches 359; Conservative 105; Mismatches 149; Indels 22; Gaps 7;

Qy 28 PRNAIELRVLTKL--RVIPKSGFAGDGLKIEISQNDVLEVEADVFNPLKHEIRI 85
Db 51 PRAGL-ARLSITLVPKVPISQAPRGLNEVVKIEISQSDSLERIEANAFDNLNLSLLI 109

Qy 86 EKANNLLYINPEAFONLPSRLYLISNTGKIKHLPVAVHKIOSLQ-KVLLDIOQDNIHIVA 144
Db 110 QNTKLLYIEGAFNLPRLKLSICNTGIRTPDVTKISSSEFNFILEICDNLHITIP 169

Qy 145 RNSPGLSFESVILWLSKNGIEEHNCAFNQTDLDELNSDNNLEELPNDVFOGASGPV 204
Db 170 GNAFOGMNNEVTLKLYGNGFEVQSHAFNGTTLISLEKNIYLEKMHSGAFQATGPS 229

Qy 205 ILDIRTKVHSLPNHGLENLKLRARSTYRLKLPNLDKFTVLMASLTYPSSHCAFANL 264
Db 230 ILDISSTKLQALPHSGLESIOTLALSSYSLKTLPSKEFTSLVAILTYPSHCAFRNL 289

Qy 265 KRQISELHPICNKSILRQIDDMTQIGDQVSLIDDEPSYG---KGSDDMYNEFDYDLN 321
Db 290 PKK-----EQNFSFISFENFSKQCESTYRKADNETLYSAIFEENELSGWDYDYGCS 341

Qy 322 EVDVTCSPKPDANPCEDINGNMLRVLWIFISILAITGNTVVLVLTTSQYKLTVPFR 381
Db 342 PKT-LOCAPEPDANPCEDINGYAFRLVILWILINLAIFGLNLTFLVLLTSRYKLTVPF 400

Qy 382 LMCNLAFADICIGIYLLIASVDIHTKSOYHNYALDQGTAGCDAAAGFTVFASLSVYT 441
Db 401 LMCNLSPADFCMGLYLLIASVDSQTKQYIHNADMTGSGCGAAGFTVFASLSVYT 460

Qy 442 LTATLERTHWTTHAMOLECKVQLRHAASVMVLGNTFAFAALPFIPIGSIYMKVSI 501
Db 461 LTVITLERHWTITAVDQKRLRHAIPMLGGNLFSTLIATWPLVIGISNMYKVSICLP 520

Qy 502 MDIOSPLSOLVMALLVNLAVFVVICGCTHYIITVNPNTIVSSSDTKAKRMATLIF 561
Db 521 MDVESTLSQVLTSLILNVAFFVVICACIRYIFAVQNPBELTAPNKNKTKAKRMATLIF 580

Qy 562 TDFLCMAIPSFASISAKVLPIITVSKAKILLVLPINSCANPLFYAIFTKNRRDPFI 621
Db 581 TDFTCMAIPSFASIAKFPVLIITVNSKILLVLPYNSCANPLFYAIFTKAQRDPL 640

Qy 622 ILSKFCGYEQIAQYIYRTTSATHNFHARKSHCS 656
Db 641 LLSRFGCKRRAELRYRK-----EFSATYSCKN 669

RESULT 12

A49744

lutropin-choriogonadotropin receptor precursor - rat

N:Alternate names: luteinizing hormone-choriogonadotropin receptor

C:Species: Rattus norvegicus (Norway rat)

C:Date: 03-May-1994 #sequence_revision 13-Sep-1998 #text_change 13-Aug-1999

C:Accession: A49744; A40545; A41343; A61453; A32460

R:KOO, Y.B.; JI, I.; Slaughter, R.G.; JI, T.H.

Endocrinology 128, 2297-2308, 1991

A:Title: Structure of the luteinizing hormone receptor gene and multiple exons of the co

A:Reference number: A49744; MUID:91209270; PMID:2010252

A:Accession: A49744

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-700 <KOO>

A:Cross-references: GB:M68917

A:Note: authors translated the codon CAA for residue 307 as Glu, AAC for residue 355 as

R:Tsai-Morris, C.H.; Buczko, E.; Wang, W.; Xie, X.Z.; Dufau, M.L.

J. Biol. Chem. 266, 11355-11359, 1991

A:Title: Structural organization of the rat luteinizing hormone (LH) receptor gene.

A:Reference number: A40545; MUID:91250455; PMID:2040640

A:Accession: A40545
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-320 <TSA>
A:Cross-references: GB:M63918; GB:M63919; GB:M63920; GB:M63921; GB:M63922; GB:M63923;
R:McFarland, K.C.; Sprengel, R.; Phillips, H.S.; Koehler, M.; Rosemblyt, N.; Nikolic
Science 245, 494-499, 1989
A:Title: Lutropin-choriogonadotropin receptor: an unusual member of the G protein-cou
A:Reference number: A41343; MUID:89332512; PMID:2502842

A:Accession: A41343
A:Molecule type: mRNA
A:Residues: 1-700 <MCF>
A:Cross-references: GB:M26199; NID:g205178; PIDN:AAA41528.1; PID:g205179
R:Dufau, M.L.; Minegishi, T.; Buczko, E.S.; Delgado, C.J.; Zhang, R.
J. Steroid Biochem. 33, 715-720, 1989
A:Title: Characterization and structure of ovarian and testicular LH/hCG receptors.

A:Reference number: A61453; MUID:90097014; PMID:2601325
A:Accession: A61453
A>Status: preliminary
A:Molecule type: protein
A:Residues: 27-33, 'X', 35-37, 'X', 39, 'X', 41-44 <DUF>
R:Roche, P.C.; Ryan, R.J.
J. Biol. Chem. 264, 4636-4641, 1989
A:Title: Purification, characterization, and amino-terminal sequence of rat ovarian
A:Reference number: A32460; MUID:89174723; PMID:2925659

A:Accession: A32460
A:Molecule type: protein
A:Residues: 27-32, 'LX', 35-37 <ROC>
C:Genetics:

A:Introns: 58/2; 107/2; 132/2; 157/2; 183/2; 206/2; 231/2; 293/2; 320/2
C:Superfamily: glycoprotein hormone receptor; leucine-rich alpha-2-glycoprotein repeat
C:Keywords: alternative splicing; G protein-coupled receptor; glycoprotein; hormone
F:54-77/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR1>
F:78-102/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR2>
F:103-127/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>
F:128-152/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR4>
F:153-177/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR5>
F:180-201/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR6>
F:202-226/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR7>
F:368-389/Domain: transmembrane #status predicted <TM1>
F:400-422/Domain: transmembrane #status predicted <TM2>
F:444-466/Domain: transmembrane #status predicted <TM3>
F:489-511/Domain: transmembrane #status predicted <TM4>
F:530-551/Domain: transmembrane #status predicted <TM5>
F:575-598/Domain: transmembrane #status predicted <TM6>
F:610-631/Domain: transmembrane #status predicted <TM7>
F:103, 178, 199, 295, 303, 317/Binding site: carbohydrate (Asn) (covalent) #status predict
F:647, 648/Binding site: palmitate (Cys) (covalent) #status predicted
F:681/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predict

Query Match 51.18; Score 1797; DB 2; Length 700;

Best Local Similarity 56.5%; Pred. No. 3.7e-117;

Matches 359; Conservative 105; Mismatches 149; Indels 22; Gaps 7;

Qy 28 PRNAIELRVLTKL--RVIPKSGFAGDGLKIEISQNDVLEVEADVFNPLKHEIRI 85
Db 51 PRAGL-ARLSITLVPKVPISQAPRGLNEVVKIEISQSDSLERIEANAFDNLNLSLLI 109

Qy 86 EKANNLLYINPEAFONLPSRLYLISNTGKIKHLPVAVHKIOSLQ-KVLLDIOQDNIHIVA 144
Db 110 QNTKLLYIEGAFNLPRLKLSICNTGIRTPDVTKISSSEFNFILEICDNLHITIP 169

Qy 145 RNSPGLSFESVILWLSKNGIEEHNCAFNQTDLDELNSDNNLEELPNDVFOGASGPV 204
Db 170 GNAFOGMNNEVTLKLYGNGFEVQSHAFNGTTLISLEKNIYLEKMHSGAFQATGPS 229

Qy 205 ILDIRTKVHSLPNHGLENLKLRARSTYRLKLPNLDKFTVLMASLTYPSSHCAFANL 264
Db 230 ILDISSTKLQALPHSGLESIOTLALSSYSLKTLPSKEFTSLVAILTYPSHCAFRNL 289

Qy 265 KRQISELHPICNKSILRQIDDMTQIGDQVSLIDDEPSYG---KGSDDMYNEFDYDLN 321
Db 290 PKK-----EQNFSFISFENFSKQCESTYRKADNETLYSAIFEENELSGWDYDYGCS 341

A:Reference number: S38280; MUID:94019814; PMID:8413627
A:Accession: S38280
A:Molecule type: DNA
A:Residues: 615-642 <PAR>
A:Experimental source: Thyroid adenomas
A:Note: mutations to Cys-619 or to Ile-623 in hyperfunctioning thyroid adenomas cause co
C:Comment: See PIR:JC1319 for a splice form of thyrotropin receptor which lacks the sev
C:Genetics:
A:Gene: GDB:TSHR
A:Cross-references: GDB:125313; OMIM:275200
A:Map position: 14q31-14q31
A:Introns: 231/2
A:Note: the list of introns is incomplete; the eighth of eight introns is shown
C:Function:
A:Description: receptor that mediates the biochemical effects of thyrotropin
C:Keywords: glycoprotein hormone receptor; leucine-rich alpha-2-glycoprotein repeat
C:Keywords: signal peptide; protein-coupled receptor; glycoprotein; hormone rece
F:1-21/Domain: signal peptide predicted <M1>
F:22-76/Domain: thyrotropin receptor status predicted <M2>
F:53-76/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR1>
F:77-101/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR2>
F:102-126/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>
F:127-151/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR4>
F:152-176/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR5>
F:179-200/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR6>
F:201-226/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR7>
F:419-440/Domain: transmembrane #status predicted <TM1>
F:451-473/Domain: transmembrane #status predicted <TM2>
F:496-517/Domain: transmembrane #status predicted <TM3>
F:538-560/Domain: transmembrane #status predicted <TM4>
F:560-602/Domain: transmembrane #status predicted <TM5>
F:563-682/Domain: transmembrane #status predicted <TM6>
F:683-692/Domain: transmembrane #status predicted <TM7>
F:77-99,113,177,198,302/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 46.7% Score 1642.5; DB 1: Length 764;
Best Local Similarity 49.2%; Pred. No. 2, 3e-106;
Matches 336; Conservative 110; Mismatches 182; Indels 55; Gaps 11;

Oy	6	CHCSN----	RVFLQDSKVTETPDLPNRLVLTLLKLVIPKSGFAGDLEKIEIS	61
Db	20	CECHQEDFRV-TCKD--	IORIPS-LPPSTOTLKLIETHLRTIPSHAPSNLPNIRVVS	84
Oy	62	QNDVLEIVADVFNPKLHEIRTEKANNLYINPEAFORLPSRLYLLISMTGKHLPAV	121	
Db	85	IDVTYLOQLESFYNLSKVTHEIRNRLTYIDPOLKELPLKFLGIFNTGLKMFPLD	144	
Oy	122	HKIOSLO-KVLLDIOQDNIHIVARNSPGLSPESVILMLSKNGIEEHNCAFNQDLDE	180	
Db	145	TVYTDIPFLIEIDTPWTSIPVWNGICNETHLKLTYNGFTSVGCTAFNGTKLDA	204	
Oy	181	LMLSDNNHLELPNDVPGA-SGPVLDISRTVUSLPNGLKLEKLBASTYRLKLP	239	
Db	205	VLLNNKYLTVIDKDFGVSGLDVSQTSVYALPSKGLHLEHLEIARNTWTLKLP	264	
Oy	240	NLQKFTVLMESLSTPSHCAPANLAKROISELHPN-CNKSIL-----RODIDDMT-----	288	
Db	265	LSLSFLHLTRADLSTPSHCAPNKKIRKINGTLESIMCNESHQSLRQKSVNLSPLHQ	324	
Oy	289	-----QIGQVRVSLID-----DEPSYKGSMD-----WYNE	314	
Db	325	EYENLGDGSIYGVKEKSKFODTHNHHYVFEDEDEIIGFGOLKNPQETLQAFOSH	384	
Oy	315	FYDOLCNEVDVTCSPKPDAPNCPEDIMGYNILRVLIWFTISLITGNTTVLVVLTQY	374	
Db	385	YDTYTCGSDADVTPKSDPFPNCPEDIMGYNILRVLIWFTISLITGNTTVLVVLTQY	444	
Oy	375	KLVTPPEPLKCNLPADLCIGYLLALLASVDITKSYHNYAIDHOTGACGACAGETVFA	434	
Db	445	KLAVPRELKNLAPADPCNGMTLLIASVDLTTHSEYTHAIDMQTCPCGCTAGPTVFA	504	
Oy	435	SELSVYTLTATLENTTITHAMQCKVQLRHAASVYVLGWTFAFAALPFIPIGJSYIM	494	

Db	505	SELSVYTLTATLENTTITHAMQCKVQLRHAASVYVLGWTFAFAALPFIPIGJSYIM	564
Oy	495	KVSIQCLPMDISPSLSQLYVNALVVLWLAFLVVICGCTTHIYTVRNPTIVSSSDTKIAK	554
Db	565	KVSIQCLPMDISPSLSQLYVNALVVLWLAFLVVICGCTTHIYTVRNPTIVSSSDTKIAK	624
Oy	555	RMATLIPTDFLCMAPISFPAISLASLAVPLITVSKAKILLVLFYPINSCANPFLYALPTKN	614
Db	625	RMATLIPTDFLCMAPISFPAISLASLAVPLITVSKAKILLVLFYPINSCANPFLYALPTKN	684
Oy	615	FRDFFILLSKFGCYVEMOAOIYR	637
Db	685	FORDVFIILLSKFGCKCKROAOYR	707

Search completed: June 16, 2003, 13:37:01
Job time : 28.1704 secs

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OK protein - protein search, using sw model

Run on: June 16, 2003, 11:39:51 ; Search time 19,7513 Seconds
(without alignments)
1417.454 Million cell updates/sec

Title: US-09-877-804-7

Perfect score: 3516

Sequence: 1 CHHMLCHSRNRYFLQDSKV.....SAPRVTNLYVLPHISSON 675

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3516	100.0	692	1 FSHR-RAT	P20395 ratnus norv
2	3346	95.2	692	1 FSHR-MOUSE	P35378 mus musculus
3	3169.5	90.1	695	1 FSHR-HUMAN	P33945 homo sapien
4	3160.5	89.9	695	1 FSHR-MACFA	P32122 macaca fasc
5	3145.5	89.5	695	1 FSHR-BOVIN	P35376 bos taurus
6	3140.5	89.3	695	1 FSHR-SHEEP	P35379 ovis aries
7	3092.5	88.0	695	1 FSHR-PIG	P49059 sus scrofa
8	3074	87.4	694	1 FSHR-MORSE	P47799 equus caball
9	3057.5	86.7	694	1 FSHR-EQUUS	Q95179 equus asinu
10	2977.5	83.9	687	1 FSHR-CHICK	P38763 gallus gall
11	1807.5	51.4	701	1 LSHR-CHICK	P36582 bos taurus
12	1807	51.4	696	1 LSHR-PIG	P36582 bos taurus
13	1799	51.2	700	1 LSHR-MOUSE	P30730 mus musculus
14	1797	51.1	700	1 LSHR-RAT	P16235 ratnus norv
15	1776	50.5	699	1 LSHR-HUMAN	P22888 homo sapien
16	1766.5	50.2	676	1 LSHR-CALJA	O02721 callithrix
17	1655	47.1	764	1 TSHR-CANFA	P14763 canis famil
18	1638.5	46.6	764	1 TSHR-MOUSE	P47750 mus musculus
19	1637.5	46.6	764	1 TSHR-HUMAN	P16473 homo sapien
20	1632.5	46.4	763	1 TSHR-BOVIN	Q27987 bos taurus
21	1628	46.3	764	1 TSHR-SHEEP	P36495 ovis aries
22	1619	46.0	764	1 TSHR-RAT	P21463 ratnus norv
23	1589.5	45.2	538	1 LSHR-SHEEP	Q28585 ovis aries
24	1286.5	35.2	956	1 LSHR-CHICK	Q90674 gallus gall
25	1286.5	35.2	956	1 LSHR-CHICK	Q90674 gallus gall
26	638.5	17.9	907	1 LSHR-HUMAN	P35479 anthopleura
27	638	17.9	907	1 LSHR-MOUSE	Q92104 homo sapien
28	596.5	16.2	951	1 LSHR-HUMAN	Q92104 homo sapien
29	571	16.2	951	1 LSHR-RAT	Q92104 homo sapien
30	531.5	14.8	1115	1 GPCR-LYMT	P46023 lymnaea sta
31	517.5	14.7	828	1 LGR6-HUMAN	Q9hbx8 homo sapien
32	483.5	13.8	757	1 LGR7-HUMAN	Q9hbx9 homo sapien
33	472.5	13.4	737	1 LGR8-MOUSE	Q91225 mus musculus

ALIGNMENTS

RESULT 1	FSHR-RAT	FSHR-RAT	STANDARD:	PRT:	692 AA.
ID	FSHR-RAT	FSHR-RAT	STANDARD:	PRT:	692 AA.
AC	01-FEB-1991 (Rel. 17, Created)	01-FEB-1991 (Rel. 17, Last sequence update)			
DT	01-FEB-1991 (Rel. 17, Last sequence update)	01-FEB-1991 (Rel. 17, Last sequence update)			
DT	16-OCT-2001 (Rel. 40, Last annotation update)	16-OCT-2001 (Rel. 40, Last annotation update)			
DE	Follicle stimulating hormone receptor precursor (FSH-R) (Follicotropin receptor).	Follicle stimulating hormone receptor precursor (FSH-R) (Follicotropin receptor).			
DE	FSHR.	FSHR.			
GN	Rattus norvegicus (Rat).	Rattus norvegicus (Rat).			
OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.			
OX	NCBI_TaxID=10116;	NCBI_TaxID=10116;			
RN	[1]	[1]			
RP	SEQUENCE FROM N.A.	SEQUENCE FROM N.A.			
RC	TISSUE: Sertoli cells.	TISSUE: Sertoli cells.			
RA	MEDLINE=91125358; PubMed=2126341;	MEDLINE=91125358; PubMed=2126341;			
RA	Angelier R., Braun T., Nikolic N., Segaloff D.L., Seeburg P.H.;	Angelier R., Braun T., Nikolic N., Segaloff D.L., Seeburg P.H.;			
RT	Functional receptor for follicle stimulating hormone: structure and functional characterization of cloned cDNA.	Functional receptor for follicle stimulating hormone: structure and functional characterization of cloned cDNA.			
RL	Mol. Endocrinol. 4:525-530(1990).	Mol. Endocrinol. 4:525-530(1990).			
RN	[2]	[2]			
RP	SEQUENCE FROM N.A.	SEQUENCE FROM N.A.			
RA	MEDLINE=92149579; PubMed=1738373;	MEDLINE=92149579; PubMed=1738373;			
RA	Heckert L.L., Daley I.J., Griswold M.D.;	Heckert L.L., Daley I.J., Griswold M.D.;			
RT	Structural organization of the follicle-stimulating hormone receptor gene.	Structural organization of the follicle-stimulating hormone receptor gene.			
RL	Mol. Endocrinol. 6:70-80(1992).	Mol. Endocrinol. 6:70-80(1992).			
CC	FUNCTION: RECEPTOR FOR FOLLICLE STIMULATING HORMONE. THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE ADENYLATE CYCLASE.	FUNCTION: RECEPTOR FOR FOLLICLE STIMULATING HORMONE. THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE ADENYLATE CYCLASE.			
CC	CELLULAR LOCATION: Integral membrane protein.	CELLULAR LOCATION: Integral membrane protein.			
CC	TISSUE SPECIFICITY: SERTOLI CELLS AND OVARIAN GRANULOSA CELLS.	TISSUE SPECIFICITY: SERTOLI CELLS AND OVARIAN GRANULOSA CELLS.			
CC	FUNCTION: RECEPTOR FOR FOLLICLE STIMULATING HORMONE.	FUNCTION: RECEPTOR FOR FOLLICLE STIMULATING HORMONE.			
CC	FSH/LSH/TFH SUPPAMIL 6 LEUCINE-RICH REPEATS (LRR).	FSH/LSH/TFH SUPPAMIL 6 LEUCINE-RICH REPEATS (LRR).			
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CC	EMBL: L02842; AAA41175.1;	EMBL: L02842; AAA41175.1;			
CC	PIR: A34548; A34548.	PIR: A34548; A34548.			
CC	PIR: A17295; A17295.	PIR: A17295; A17295.			
CC	InterPro: IPR000276; GPCR_Rhodopsin.	InterPro: IPR000276; GPCR_Rhodopsin.			
CC	InterPro: IPR001611; LRR.	InterPro: IPR001611; LRR.			
CC	InterPro: IPR00372; LRR_Nterm.	InterPro: IPR00372; LRR_Nterm.			
CC	Pfam: PF00001; 7tm.1.1.	Pfam: PF00001; 7tm.1.1.			
CC	Pfam: PF00560; LRR.3.	Pfam: PF00560; LRR.3.			
CC	Pfam: PF01462; LRRNT.1.	Pfam: PF01462; LRRNT.1.			

SMART: SM00013; LRRNT: 1.
 DR PROSITE; PS00237; G-PROTEIN RECP_FL1; 1.
 DR PROSITE; PS00262; G-PROTEIN RECP_FL2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein; Signal;
 KW Phosphorylation; Repeat; Leucine-rich repeat.
 FT SIGNAL 1 17
 FT CHAIN 18 692
 FT DOMAIN 18 365
 FT TRANSMEM 366 386
 FT DOMAIN 387 397
 FT TRANSMEM 398 420
 FT DOMAIN 421 442
 FT TRANSMEM 443 464
 FT DOMAIN 465 484
 FT TRANSMEM 485 507
 FT DOMAIN 508 527
 FT TRANSMEM 528 549
 FT DOMAIN 550 572
 FT TRANSMEM 573 596
 FT DOMAIN 597 607
 FT TRANSMEM 608 629
 FT DOMAIN 630 692
 FT REPEAT 44 68
 FT REPEAT 69 93
 FT REPEAT 119 143
 FT REPEAT 170 192
 FT REPEAT 193 216
 FT REPEAT 218 240
 FT DISULFID 441 516
 FT CARBOHYD 191 191
 FT CARBOHYD 199 199
 FT CARBOHYD 293 293
 SQ SEQUENCE 692 AA; 77681 MW; 267EA78C7CFD8EC6 CRC64;
 Query Match 100.0%; Score 3516; DB 1; Length 692;
 Best Local Similarity 100.0%; Pred. No. 6.6e-219;
 Matches 675; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CHHWLCHSNNRVFLQDSKVTETPTDLPRAIELRFLVTKLRVPIKGSFAGFGDLEKIEI 60
 DB 18 CHHWLCHSNNRVFLQDSKVTETPTDLPRAIELRFLVTKLRVPIKGSFAGFGDLEKIEI 77
 QY 61 SONDVLEIADVFSLPKLHEIRIEKANNLLINPEAFONLPSRLYLLISNTGKHLPA 120
 DB 78 SONDVLEIADVFSLPKLHEIRIEKANNLLINPEAFONLPSRLYLLISNTGKHLPA 137
 QY 121 VHKIQSLQKVLDDIQDNNINIHIVARNFSGLSFESVILMSKNGIEIEHNCAPNGTOLDE 180
 DB 138 VHKIQSLQKVLDDIQDNNINIHIVARNFSGLSFESVILMSKNGIEIEHNCAPNGTOLDE 197
 QY 181 LNLSDNNLEELPNDVFGAGSGVILDISRTKVSHPNGLNKLKLRARSTYRLKLPN 240
 DB 198 LNLSDNNLEELPNDVFGAGSGVILDISRTKVSHPNGLNKLKLRARSTYRLKLPN 257
 QY 241 LDKFVTLEASLTVPSCCAFANLKROISELHPICNKSILRQDIDDMTQIGDQVSLIDD 300
 DB 258 LDKFVTLEASLTVPSCCAFANLKROISELHPICNKSILRQDIDDMTQIGDQVSLIDD 317
 QY 301 EPSYKSGSDMMYNEFDYDLNCEVVDVTCSPKPAFNPCEIDMGYNILRVLIWFISILAIT 360
 DB 318 EPSYKSGSDMMYNEFDYDLNCEVVDVTCSPKPAFNPCEIDMGYNILRVLIWFISILAIT 377
 QY 361 GNTTVLVLTTSQYKLVTPRLMCLNAPADLCIGYLLLIASVDIHTKQSHVNAIDWQT 420
 DB 378 GNTTVLVLTTSQYKLVTPRLMCLNAPADLCIGYLLLIASVDIHTKQSHVNAIDWQT 437
 QY 421 GAGCDAAGFTVFASLSVYTLTATLERWHTITHAMOLECKVOLRHAASVWVLGWTFAF 480
 DB 438 GAGCDAAGFTVFASLSVYTLTATLERWHTITHAMOLECKVOLRHAASVWVLGWTFAF 497
 QY 481 AAALFPFIFGSIYMKVSIICLPMDIDSPLSQLYVNVALLVNLVAFVWICGCTHYLYTVRN 540
 DB 498 AAALFPFIFGSIYMKVSIICLPMDIDSPLSQLYVNVALLVNLVAFVWICGCTHYLYTVRN 557

RESULT 2

FSHR_MOUSE STANDARD; PRT; 692 AA.
 AC P35378; Q9QW8; Q9D4C2;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Follicle stimulating hormone receptor precursor (FSH-R) (Follitropin receptor).
 DE FSHR.
 GN Mus musculus (Mouse).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 RN [1]
 RC STRAIN=129/Sv; TISSUE=Testis;
 RA Tena-Sempere M., Manna P.R., Huhtaniemi I.T.;
 RT "Molecular cloning of the mouse follicle stimulating hormone receptor complementary deoxyribonucleic acid: functional expression of alternatively spliced variants and receptor inactivation by a C566T transition in exon 7 of the coding sequence."
 RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RC SEQUENCE FROM N.A.
 RP STRAIN=C57BL/6J; TISSUE=Testis;
 RX MEDLINE=21085660; PubMed=11217851;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Alzava K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaoka I., Saito T., Okazaki Y., Gotohori T., Bono H., Kasukawa T., Saito R., Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H., Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T., Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L., Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohsaki S., Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection."
 RL Nature 409:685-690(2001).
 RN [3]
 RC SEQUENCE OF 1-51 FROM N.A.
 RX MEDLINE=93093308; PubMed=1459341;
 RA Huhtaniemi I.T., Eskola V., Pakarinen P., Matikainen T., Sprengel R.;
 RT "The murine lutinizing hormone and follicle-stimulating hormone receptor genes: transcription initiation sites, putative promoter sequences and promoter activity."
 RL Mol. Cell. Endocrinol. 88:55-66(1992).
 CC -1- FUNCTION: RECEPTOR FOR FOLLICLE STIMULATING HORMONE. THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE ADENYLATE CYCLASE.

Db	138	PHKTSIQKLVLDIDODNIHIIHIIARISPMGLSPESVYLWLNKNGIQEIHCAFNGTQDLE	139	
Oy	181	LNLSDDNNLZELPNVDFOGASGPVILDISRTKVHSLPHGLNLUKKARSTYRLKKLPN	240	
Db	198	LNLSDDNNLZELPNVDFOGASGPVILDISRTKVHSLPHGLNLUKKARSTYRLKKLPN	257	
Oy	241	LQKFTVLPAESLTPSHCCAFANLKRQISELHPICNKSILRODIDMTOIGDQPSLEDD	300	
Db	258	LQKFTVLPAESLTPSHCCAFANRROTSELHPICNKSISRODIDMTOIGDQPSLVDD	317	
Oy	301	EPSTGKSDMMYNFEDYDLCNEVDVDTCSPPKPAFNPCEDIIMYNIURLVLIWFISLAI	360	
Db	318	EPSTGKSDMLYSEFDYDLCNEFDVDTCSPPKPAFNPCEDIIMYNIURLVLIWFISLAI	377	
Oy	361	GNTTVLVLTTSQYKLVTPRFUMCNLAFADLCIGIYLLLIASVDIHTKSOYHNHTADMOT	420	
Db	378	GNTTVLVLTTSQYKLVTPRFUMCNLAFADLCIGIYLLLIASVDIHTKSOYHNHTADMOT	437	
Oy	421	GAGCDAAGPFTVFASLSVYTLATILTERPHHTITHAMOLECKVOLHAAVWLGWTFAP	480	
Db	438	GAGCDAAGPFTVFASLSVYTLAAITLERPHHTITHAMOLECKVOLCHAAISIMVGNAPF	497	
Oy	481	AAALPFIPIGSISSMYKVSICLUPMDIDPSQLYVNALVNLVAPFVTCGCTHYIYTVRN	540	
Db	498	AAALPFIPIGSISSMYKVSICLUPMDIDPSQLYVNALVNLVAPFVTCGCTHYIYTVRN	557	
Oy	541	PTVYSSSDTKIARKRMATLIPTDFLCHMAPISFPAISAKLVPIITVSKAKILLVLYPIN	600	
Db	558	PTVYSSSDTKIARKRMATLIPTDFLCHMAPISFPAISAKLVPIITVSKAKILLVLYPIN	617	
Oy	601	SCANPELYAIFTNFRDPTFLLSKFCQYEQAOIKYPTTSNTSNTHARKSHCCSAPRV	660	
Db	618	SCANPELYAIFTNFRDPTFLLSKFCQYEQAOIKYPTTSNTSNTHFSRKNPCSSAPRV	677	
Oy	661	TSNSVLVPLNHSSQN	675	
Db	678	TSNSVLVPLNHSSQN	692	
RESULT 3				
FSHR_HUMAN				
IC	FSHR_HUMAN	STANDARD;	PRT: 695 AA.	
DT	P23943; 1992 (Rel. 21, Created)			
DT	01-JUN-1994 (Rel. 20, sequence update)			
DT	16-OCT-2001 (Rel. 40, Last annotation update)			
DE	Follicle stimulating hormone receptor precursor (FSH-R) (Follitropin receptor).			
DE	FSHR.			
GN	GN Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_Taxid:9606;			
RC	[1]			
RC	SEQUENCE FROM N.A.			
RC	TSISSUE-Testis.			
RC	MDLINE-9122171; PubMed-1709010;			
RC	MDLINE-9122171; PubMed-1709010;			
RT	Mineshish T., Nakamura K., Takakura Y., Ibuki Y., Igarashi M.,			
RT	"Cloning and sequencing of human FSH receptor cDNA";			
RL	Biochem. Biophys. Res. Commun. 175:1125-1130(1991).			
RL	[2]			
RC	SEQUENCE FROM N.A.			
RC	TSISSUE-Testis.			
RC	MDLINE-93346012; PubMed-1301382;			
RC	Kalton C.A., Cheng S.V., Nugent N.P., Schweickhardt R.L.,			
RA	Rosenthal J.C., Overton S.A., Wands G.D., Kuzaja J.B., Luchette C.A.,			
RA	Chappel S.L.,			
RT	"Effect of the human follicle stimulating hormone receptor and			
RT	its expression in COS-7 CHO cells";			
RL	Mol. Cell. Endocrinol. 89:141-151(1992).			
RL	[3]			
RC	SEQUENCE FROM N.A.			
RC	TSISSUE-Testis.			
RC	MDLINE-93346012; PubMed-1301382;			
RC	Kalton C.A., Cheng S.V., Nugent N.P., Schweickhardt R.L.,			
RA	Rosenthal J.C., Overton S.A., Wands G.D., Kuzaja J.B., Luchette C.A.,			
RA	Chappel S.L.,			
RT	"Effect of the human follicle stimulating hormone receptor and			
RT	its expression in COS-7 CHO cells";			
RL	Mol. Cell. Endocrinol. 89:141-151(1992).			
RL	[3]			
RC	SEQUENCE FROM N.A.			
RC	TSISSUE-Testis.			
RC	MDLINE-93346012; PubMed-1301382;			
RC	Kalton C.A., Cheng S.V., Nugent N.P., Schweickhardt R.L.,			
RA	Rosenthal J.C., Overton S.A., Wands G.D., Kuzaja J.B., Luchette C.A.,			
RA	Chappel S.L.,			
RT	"Effect of the human follicle stimulating hormone receptor and			
RT	its expression in COS-7 CHO cells";			
RL	Mol. Cell. Endocrinol. 89:141-151(1992).			
RL	[3]			
RC	SEQUENCE FROM N.A.			
RC	TSISSUE-Testis.			
RC	MDLINE-93346012; PubMed-1301382;			
RC	Kalton C.A., Cheng S.V., Nugent N.P., Schweickhardt R.L.,			
RA	Rosenthal J.C., Overton S.A., Wands G.D., Kuzaja J.B., Luchette C.A.,			
RA	Chappel S.L.,			
RT	"Effect of the human follicle stimulating hormone receptor and			
RT	its expression in COS-7 CHO cells";			
RL	Mol. Cell. Endocrinol. 89:141-151(1992).			
RL	[3]			
RC	SEQUENCE FROM N.A.			
RC	TSISSUE-Testis.			
RC	MDLINE-93346012; PubMed-1301382;			
RC	Kalton C.A., Cheng S.V., Nugent N.P., Schweickhardt R.L.,			
RA	Rosenthal J.C., Overton S.A., Wands G.D., Kuzaja J.B., Luchette C.A.,			
RA	Chappel S.L.,			
RT	"Effect of the human follicle stimulating hormone receptor and			
RT	its expression in COS-7 CHO cells";			
RL	Mol. Cell. Endocrinol. 89:141-151(1992).			
RL	[3]			

RA Tilly L.T., Aihara T., Nishimori K., Jai X.-C., Billig H.,
 RA Kowalski K.I., Perles E.A., Hsueh A.J.;
 RL Submitted (xxx-1992) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE OF 1-342 FROM N.A.
 RC TISSUE-testis;
 RX MEDLINE-93075197; PubMed-1359889;
 RA Gromoll J., Gudermann T., Nieschlag E.;
 RT "Molecular cloning of a truncated isoform of the human follicle
 RT stimulating hormone receptor";
 RL Biochem. Biophys. Res. Commun. 188:1077-1083(1992).
 RN [5]
 RP SEQUENCE OF 1-51 FROM N.A.
 RX MEDLINE-95011044; PubMed-7926278;
 RA Gromoll J., Dankbar B., Gudermann T.;
 RT "Characterization of the 5' flanking region of the human follicle-
 RT stimulating hormone receptor gene";
 RL Mol. Cell. Endocrinol. 102:93-102(1994).
 RN [6]
 RP 3D-STRUCTURE MODELING OF 49-228.
 RX MEDLINE-96363672; PubMed-8747461;
 RA Jiang X., Dreano M., Buckler D.R., Cheng S., Ythier A., Wu H.,
 RA Hendrickson W.A., el Tayar N.;
 RT "Structural predictions for the ligand-binding region of glycoprotein
 RT hormone receptors and the nature of hormone-receptor interactions";
 RL Structure 3:1341-1353(1995).
 CC 1- FUNCTION: RECEPTOR FOR FOLLICLE STIMULATING HORMONE. THE ACTIVITY
 CC OF THIS RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE
 CC ADENYLATE CYCLASE.
 CC 1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC 1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM (SHOWN HERE) AND A
 CC SHORT FORM; ARE PRODUCED BY ALTERNATIVE SPLICING.
 CC 1- TISSUE SPECIFICITY: SERTOLI CELLS AND OVARIAN GRANULOSA CELLS.
 CC 1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 CC FSH/LSH/TSH SUBFAMILY.
 CC 1- SIMILARITY: CONTAINS 5 LEUCINE-RICH REPEATS (LRR).
 CC -----
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 CC -----
 DR EMBL; M65085; AAA52477.1;
 DR EMBL; S59900; AAB26480.1;
 DR EMBL; M55489; AAA52478.1;
 DR EMBL; X68044; CAA48179.1;
 DR EMBL; S73199; AAB32071.1;
 DR PIR; JN0122; JN0122.
 DR PDB; 1XUN; 15-MAY-97.
 DR Genew; HGNC:3969; FSHR.
 DR MIM; 136435.
 DR InterPro; IPR000276; GPCR_Rhodpsn.
 DR InterPro; IPR001611; LRR.
 DR InterPro; IPR000372; LRR_Nterm.
 DR Pfam; PF00001; 7tm.1; 1.
 DR Pfam; PF00560; LRR; 3.
 DR Pfam; PF01482; LRRNT; 1.
 DR SMART; SH00013; LRRNT; 1.
 DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1;
 DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein; Signal;
 KW phosphorylation; Repeat; Leucine-rich repeat; Alternative splicing;
 KW 3D-structure.
 FT SIGNAL 1 17 POTENTIAL.
 FT CHAIN 18 695 FOLLICLE STIMULATING HORMONE RECEPTOR.
 FT DOMAIN 18 366 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 367 387 1 (POTENTIAL).
 FT DOMAIN 388 398 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 399 421 2 (POTENTIAL).
 FT DOMAIN 422 443 EXTRACELLULAR (POTENTIAL).

FT	TRANSMEM	444	465	3 (POTENTIAL).
FT	DOMAIN	466	485	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	486	508	4 (POTENTIAL).
FT	DOMAIN	509	528	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	529	550	5 (POTENTIAL).
FT	DOMAIN	551	573	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	574	597	6 (POTENTIAL).
FT	DOMAIN	598	608	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	609	630	7 (POTENTIAL).
FT	DOMAIN	631	695	CYTOPLASMIC (POTENTIAL).
FT	REPEAT	69	93	LRR 1.
FT	REPEAT	119	143	LRR 2.
FT	REPEAT	170	192	LRR 3.
FT	REPEAT	193	216	LRR 4.
FT	REPEAT	218	240	LRR 5.
FT	DISULFID	442	517	BY SIMILARITY.
FT	CARBOHYD	191	191	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	199	199	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	293	293	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	318	318	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	224	285	MISSING (IN SHORT ISOFORM).
FT	VARSPIC	342	695	MISSING (IN SHORT ISOFORM).
FT	CONFLICT	13	13	S -> R (IN REF. 4).
FT	CONFLICT	112	112	N -> T (IN REF. 1).
FT	CONFLICT	197	198	EL -> AV (IN REF. 1).
FT	CONFLICT	295	295	S -> P (IN REF. 4).
FT	CONFLICT	307	307	T -> A (IN REF. 1).
FT	CONFLICT	680	680	N -> S (IN REF. 1).
FT	CONFLICT	680	680	N -> S (IN REF. 1).
SQ	SEQUENCE	695 AA; 78294 MW; 723B8E71F76D2CD5 CRC64;		

Query Match 90.1%; Score 3169.5; DB 1; Length 695;
 Best Local Similarity 89.5%; Pred. No. 1.3e-196;
 Matches 607; Conservative 31; Mismatches 37; Indels 3; Gaps 2;

QY	1	CHHWLCHSNRVFLCQDSKVTEIPTDLPRNATELRLVTLKRVIPKSGPAGDLEKIEI	60
DB	18	CHHRICHSNRVFLCQESKVTEIPSDLPNATELRLVTLKRVIPKSGPAGDLEKIEI	77
QY	61	SONDVLIEADVFSNPKLHEIRIEKANLNYINPEAFONLPSRLYLSINTGKHLPA	120
DB	78	SONDVLIEADVFSNPKLHEIRIEKANLNYINPEAFONLPSRLYLSINTGKHLPD	137
QY	121	VHKIQSLQKVLIDQDNIHIVARNFGLSFESVILWLSKNGIEIINCAFNPGTQDLE	180
DB	138	VHKIHSQKVLIDQDNIHIVARNFGLSFESVILWLSKNGIEIINCAFNPGTQDLE	197
QY	181	LNLSDDNNLEELPNDVFOGASGVILDISRTKVHSLPNHGLENLKRLARSTYRLKKLPN	240
DB	198	LNLSDDNNLEELPNDVFOGASGVILDISRTKVHSLPNHGLENLKRLARSTYRLKKLPN	257
QY	241	LKQFVTLMEASLTYPSSHCAFAANLKRQISELHPICNKSILRQDIDMTQIGDQVSLIDD	300
DB	258	LEKLVALMEASLTYPSSHCAFAANLKRQISELHPICNKSILRQVVDYMTQIGDQVSLIDD	317
QY	301	-EPSYCKGSDMYNEEDYDLCEVVDVTCSPKDAFNPCEDIMGYNLRLVLIWFISILAI	359
DB	318	NESSYRGEDMTYTFEDYDLCEVVDVTCSPKDAFNPCEDIMGYNLRLVLIWFISILAI	377
QY	360	TGNTTVLWLTTSQYKLTVPFLMCMNLAFADLCIGIYLLLIASVDIHTKSOYHNYAIDWQ	419
DB	378	TGNTTVLWLTTSQYKLTVPFLMCMNLAFADLCIGIYLLLIASVDIHTKSOYHNYAIDWQ	437
QY	420	TGACDAAAGFTVFASLSVYTLTATLERWHTITHAMQLECKVQLRHAASVAVLGTWFA	479
DB	438	TGACDAAAGFTVFASLSVYTLTATLERWHTITHAMQLECKVQLRHAASVAVLGTWFA	497
QY	480	FAAALPIFGISYMKVSIICLPMDDISPLSOLVMSLVNLVAFVVICCYTHIYLTVR	539
DB	498	FAAALPIFGISYMKVSIICLPMDDISPLSOLVMSLVNLVAFVVICCYTHIYLTVR	557
QY	540	NPTIVSSSDTKIAKRAMATLIFTDFLCMAPISEFAISAKVPLITYSKAKILLVLPYPI	599
DB	558	NPTIVSSSDTKIAKRAMATLIFTDFLCMAPISEFAISAKVPLITYSKAKILLVLPYPI	617

OY 600 NSCANPFLYALPTKPRDFILLKSCGYEMOQIYRTSTSAHFNHAKSHCSAPR 659
 DB 618 NSCANPFLYALPTKPRDFILLKSCGYEMOQIYRTSTSAHFNHAKSHCSAPR 677
 OY 660 VTN--SYVLVPLNHSN 675
 DB 678 VTNGSYILVPLNLSLAQN 695

RESULT 4
 FSHR_MACPA STANDARD; PRT: 695 AA.
 AC FSHR_MACPA
 DT 01-OCT-1993 (rel. 27, Created)
 DT 01-OCT-1993 (rel. 27, Last sequence update)
 DT 16-OCT-2001 (rel. 40, Last citation update)
 DE Follicle stimulating hormone receptor precursor (FSH-R) (Follitropin receptor).
 DE FSHR.
 GN
 OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea; Macaca.
 OC Cercopithecoidea; Macaca.
 OX NCBI_TaxID=9541;
 RN
 RP SEQUENCE FROM R.A.
 RC TISSUE=Testis;
 RA MEDLINE=94071854; PubMed=7504463;
 RA Gromoll J., Dankbar B., Sharma R.S., Nieschlag E.;
 RT Molecular cloning of the testicular follicle stimulating hormone receptor of the non human primate Macaca fascicularis and identification of multiple transcripts in the testis.;
 RT Biol. Reprod. 66:214-29 (2002).
 CC -1- FUNCTION: RECEPTOR FOR FOLLICLE STIMULATING HORMONE. THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE ADENYLATE CYCLASE.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 CC FSH/LSH SUBFAMILY.
 CC -1- SIMILARITY: CONTAINS 6 LEUCINE-RICH REPEATS (LRR).
 CC
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 CC ENBL; X74454; CA52463.1;
 DR PIR; S36452; S36452.
 DR PIR; JN0898; JN0898.
 DR HSP; P23945; IXUN.
 DR InterPro: IPR000276; GPCR_Rhodpsn.
 DR InterPro: IPR001611; LRR.
 DR InterPro: IPR000372; LRR_Nterm.
 DR Pfam: PF00001; 7tm_1; 1.
 DR Pfam: PF00560; LRR; 3.
 DR Pfam: PF01462; LRRNT; 1.
 DR Pfam: PF01463; LRRNT; 1.
 DR PROSITE; PS00237; G-PROTEIN_RECEP_F1_1.
 DR PROSITE; PS0263; G-PROTEIN_RECEP_F1_1.
 DR G-protein coupled receptor; Transmembrane; Glycoprotein; Signal; Phosphorylation; Repeat; Leucine-rich repeat.
 KW SIGNAL 1 17
 FT CHAIN 18 695 FOLLICLE STIMULATING HORMONE RECEPTOR.
 FT DOMAIN 18 366 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 367 387 1 (POTENTIAL).
 FT DOMAIN 388 398 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 399 421 2 (POTENTIAL).
 FT DOMAIN 422 443 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 444 465 3 (POTENTIAL).

FT DOMAIN 466 485 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 486 508 4 (POTENTIAL).
 FT DOMAIN 509 529 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 530 550 5 (POTENTIAL).
 FT DOMAIN 551 573 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 574 597 6 (POTENTIAL).
 FT DOMAIN 598 608 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 609 630 7 (POTENTIAL).
 FT DOMAIN 631 695 CYTOPLASMIC (POTENTIAL).
 FT REPEAT 44 68 LRR 1.
 FT REPEAT 69 93 LRR 2.
 FT REPEAT 119 143 LRR 3.
 FT REPEAT 170 192 LRR 4.
 FT REPEAT 193 216 LRR 5.
 FT REPEAT 218 240 LRR 6.
 FT DISULFID 442 517 BY SIMILARITY.
 FT CARBOHYD 191 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD 192 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD 293 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD 318 N-LINKED (GLCNAC...) (POTENTIAL).
 SQ SEQUENCE 695 AA: 78343 MH: 0060A233729B5250 CRC64;
 Query Match 89.9%; Score 3160.5; DB 1; Length 695;
 Best Local Similarity 89.4%; Pred. No. 4.9e-196;
 Matches 606; Conservative 30; Mismatches 39; Indels 3; Gaps 2;
 OY 1 CHHWLCHCSNRVFLCQDSKVTEIPDLPNNAIELRFLVTKLRVPGKSPAGFGDLEKIEI 60
 DB 18 CHHWLCHCSNRVFLCQDSKVTEIPDLPNNAIELRFLVTKLRVPGKSPAGFGDLEKIEI 77
 OY 61 SONDVLEIADVFNLPKLEIRIKERKANLLYINPEAFONLPSLYLLISNTGIAKHPA 120
 DB 78 SONDVLEIADVFNLPKLEIRIKERKANLLYINPEAFONLPSLYLLISNTGIAKHPD 137
 OY 121 VHKIQSLQKVLQIDQINHIHIVARNSPGLSFESVILMSKNGIEEIHNCAPNGQDLE 180
 DB 138 VHKIHSFORVLQIDQINHIHIVARNSPGLSFESVILMSKNGIEEIHNCAPNGQDLE 197
 OY 181 LKLSNDNNLEELPNDVPGAGCPVLTDSRTKYVSLNGLKLEKLRARSTYKLLKPN 240
 DB 198 LKLSNDNNLEELPNDVPGAGCPVLTDSRTKYVSLNGLKLEKLRARSTYKLLKLP 257
 OY 241 LKLSNDNNLEELPNDVPGAGCPVLTDSRTKYVSLNGLKLEKLRARSTYKLLKLP 300
 DB 258 LKLSNDNNLEELPNDVPGAGCPVLTDSRTKYVSLNGLKLEKLRARSTYKLLKLP 317
 OY 301 EPSTYKSGSDMTNEFDYDLCHREYVDVTCSPKDPANPCEDIMGYNILRVLINFISLAI 359
 DB 318 EPSTYKSGSDMTNEFDYDLCHREYVDVTCSPKDPANPCEDIMGYNILRVLINFISLAI 377
 OY 360 TGMVTYVLYLTTSQYKLTVPFLMCLNAPADZIGIYLLIASVDIHTSYHNYAIDMQ 419
 DB 378 TGMVTYVLYLTTSQYKLTVPFLMCLNAPADZIGIYLLIASVDIHTSYHNYAIDMQ 437
 OY 420 TGACDCAAGFTVFASELSVYTLTAITLERHHTITHAMOLECKVOLRHAASVYVLCMTFA 479
 DB 438 TGACDCAAGFTVFASELSVYTLTAITLERHHTITHAMOLECKVOLRHAASVYVLCMTFA 497
 OY 480 FAALPFIPIGISTYKVSICLPMIDISPLSQYVLLVNLVNLVNLVNLVNLVNLVNLV 539
 DB 498 FAALPFIPIGISTYKVSICLPMIDISPLSQYVLLVNLVNLVNLVNLVNLVNLVNLV 557
 OY 540 NPTIVSSSOTKIAKRWATLPTDFLCHAPISFPFASISKVKPLTVSKAKILLVLPYPI 599
 DB 558 NPTIVSSSOTKIAKRWATLPTDFLCHAPISFPFASISKVKPLTVSKAKILLVLPYPI 617
 OY 600 NSCANPFLYALPTKPRDFILLKSCGYEMOQIYRTSTSAHFNHAKSHCSAPR 659
 DB 618 NSCANPFLYALPTKPRDFILLKSCGYEMOQIYRTSTSAHFNHAKSHCSAPR 677
 OY 660 VTN--SYVLVPLNHSN 675
 DB 678 VTNGSYILVPLNLSLAQN 695

```

RESULT 5
FSHR_BOVIN
ID FSHR_BOVIN STANDARD: PRT; 695 AA.
AC P35376;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Follicle stimulating hormone receptor precursor (FSH-R) (Follitropin
DE receptor).
DE FSHR.
GN Bos taurus (Bovine).
OS Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Holstein; TISSUE=Ovary, and Testis;
RX MEDLINE=95127199; PubMed=7826612;
RA Houde A., Lambert A., Saumande J., Silversides D.W., Lussier J.G.;
RT "Structure of the bovine follicle-stimulating hormone receptor
RT complementary DNA and expression in bovine tissues.";
RL Mol. Reprod. Dev. 39:127-135(1994).
CC -!- FUNCTION: RECEPTOR FOR FOLLICLE STIMULATING HORMONE. THE ACTIVITY
CC OF THIS RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE
CC ADENYLATE CYCLASE.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC FSH/LSH/TSH SUBFAMILY.
CC -!- SIMILARITY: CONTAINS 6 LEUCINE-RICH REPEATS (LRR).
CC -----
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CC -----
DR EMBL; L22319; AAC37324.1;
DR HSPG; P23945; IUXN.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR InterPro; IPR001611; LRR.
DR InterPro; IPR000372; LRR_Nterm.
DR Pfam; PF00001; 7tm_1; 1.
DR Pfam; PF00560; LRR; 4.
DR Pfam; PF01462; LRRNT; 1.
DR SMART; SM00013; LRRNT; 1.
DR PROSITE; PS00237; G_PROTEIN_RECF_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECF_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Signal;
KW Phosphorylation; Repeat; Leucine-rich repeat.
FT SIGNAL 1
FT CHAIN 17
FT DOMAIN 18 695
FT DOMAIN 18 366
FT TRANSMEM 367 387
FT DOMAIN 388 398
FT TRANSMEM 399 421
FT DOMAIN 422 443
FT TRANSMEM 444 465
FT DOMAIN 466 485
FT TRANSMEM 486 508
FT DOMAIN 509 528
FT TRANSMEM 529 550
FT DOMAIN 551 573
FT TRANSMEM 574 597
FT DOMAIN 598 608
FT TRANSMEM 609 630
FT DOMAIN 631 695
FT REPEAT 44 68
FT REPEAT 69 93

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FT REPEAT 119 143
FT REPEAT 170 192
FT REPEAT 193 216
FT REPEAT 218 240
FT DISULFID 442 517
FT CARBOHYD 191 191
FT CARBOHYD 199 199
FT CARBOHYD 293 293
SQ SEQUENCE 695 AA; 78084 MW; 18F9DFEC046380D CRC64;

Query Match 89.5%; Score 3145.5; DB 1; Length 695;
Best Local Similarity 87.9%; Pred. No. 4.5e-195;
Matches 596; Conservative 45; Mismatches 34; Indels 3; Gaps 2;

Qy 1 CHHWLCHSNNRVFLCQDSKVTETDLPNRAIELRVLTKLRIPIPKSPAGFGDLEKIEI 60
Db 18 CHHRLCHCSNGVFLCQESKVTETPSDLPDRAVELRVLTKLRIPIPKSPAGFGDLEKIEI 77
Qy 61 SQNDVLEIVADVFESNLPKLEIRIEKANNLLYINPEAFQNLPSRLYLLISNTGKILPA 120
Db 78 SQNDVLEIVANVFESNLPKLEIRIEKANNLLYIDPAFQNLPLNRYLLISNTGKILPA 137
Qy 121 VHKTSQKQVLLDQDNIHINIVARNSPFGLSPFESVILMLSKNGIEIHNCAFNQTOIDE 180
Db 138 VHKTSQKQVLLDQDNIHINIVARNSPFGLSPFESVILMLSKNGIEIHNCAFNQTOIDE 197
Qy 181 LNLSDNNLELNDVFGGASGPVILDSRTKVSLSLPHNGLNKLKLRSTYRLKLPN 240
Db 198 LNLSDNNLELNDVFGGASGPVILDSRTKVSLSLPHNGLNKLKLRSTYRLKLPN 257
Qy 241 LDKFVTLMEASLTYPSPHCCFANLKRQISELHPICNKSILRQDIDDDMTQIGDQSVLT-D 299
Db 258 LDKFVTLMEASLTYPSPHCCFANLKRQISELHPICNKSILRQDIDDDMTQIGDQSVLT-D 317
Qy 300 DEPSYKSGSDMMYNEFDYDLCNEVVDVTCSPKPAFNPCEPDIMGYNLRLVILFISILAI 359
Db 318 DEPSYKSGSDMMYNEFDYDLCNEVVDVTCSPKPAFNPCEPDIMGYNLRLVILFISILAI 377
Qy 360 TGNVTVLVLTTSYKLTVPRLMCLNLAFLDCLGIYLLIASVDIHTKSOYHNVAIDMQ 419
Db 378 TGNVLVLVLTTSYKLTVPRLMCLNLAFLDCLGIYLLIASVDIHTKSOYHNVAIDMQ 437
Qy 420 TGACGDAAGFETVFASELSVYTLTAITLERWHTITHAMOLECKVQLRHAASVMVLGWTFA 479
Db 438 TGACGDAAGFETVFASELSVYTLTAITLERWHTITHAMOLECKVQLRHAASVMVLGWTFA 497
Qy 480 FFAALPFIPIGSISSYMKVSIICLPMDIDSPLSOLYVWALLVNLVAFVVICGCTHYIYLV 539
Db 498 FFAALPFIPIGSISSYMKVSIICLPMDIDSPLSOLYVWALLVNLVAFVVICGCTHYIYLV 557
Qy 540 NPTIVSSSDTKIAKRWATLFTDFLCMAPISFFAISASLKVPLITVSKAKILLVLFYPI 599
Db 558 NPTIVSSSDTKIAKRWATLFTDFLCMAPISFFAISASLKVPLITVSKAKILLVLFYPI 617
Qy 600 NSCANPELYAIFTNFRDFFILLSKFCGYEQMAQIYRTSSATHNPHARKSHCSSAPR 659
Db 618 NSCANPELYAIFTNFRDFFILLSKFCGYEQMAQIYRTSSATHNPHARKSHCSSAPR 677
Qy 660 VTN--SYVLVPLNHSQN 675
Db 678 VTNGSNVTLPLRLHAKN 695

RESULT 6
FSHR_SHEEP
ID FSHR_SHEEP STANDARD: PRT; 695 AA.
AC P35379; Q28573; Q28574; Q9TS19;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Follicle stimulating hormone receptor precursor (FSH-R) (Follitropin
DE receptor).
DE FSHR.
GN

```

OS Ovis aries (Sheep).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Caprinae; Ovis.
 OX NCBI_TaxID=9940;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM FSH-R1).
 RC TISSUE-Testis;
 RX MEDLINE=93351750; PubMed=8394255;
 RA Yarney T.A., Sairam M.R., Khan H., Ravindranath N., Payne S.,
 RA Seidah N.G.;
 RT "Molecular cloning and expression of the ovine testicular follicle
 RT stimulating hormone receptor";
 RL Mol. Cell. Endocrinol. 93:219-226(1993).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM FSH-R2 AND FSH-R3).
 RC STRAIN=Dorset-Leicester; Tissue=Testis;
 RX MEDLINE=93176195; PubMed=8439338;
 RA Klon H., Yarney T.A., Sairam M.R.;
 RT "Cloning of alternatively spliced mRNA transcripts coding for variants
 RT of ovine testicular follicle receptor lacking the G protein
 RT coupling domains";
 RL Biochem. Biophys. Res. Commun. 190:888-894(1993).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORM FSH-R2), AND CHARACTERIZATION.
 RC STRAIN=Dorset-Leicester-Suffolk 1; TISSUE-Testis;
 RX MEDLINE=98031015; PubMed=9364440;
 RA Yarney T.A., Jiang L., Khan H., MacDonald E.A., Laird D.W.,
 RA Sairam M.R.;
 RT "Molecular cloning, structure, and expression of a testicular
 RT follicle receptor with selective alteration in the carboxy terminus
 RT that affects signaling function";
 RL J. Reprod. Dev. 48:436-470(1997).
 RN [4]
 RP SEQUENCE FROM N.A. (ISOFORM FSH-R3), AND CHARACTERIZATION.
 RC STRAIN=Dorset-Leicester-Suffolk 1; TISSUE-Ovary;
 RX MEDLINE=20391225; PubMed=10527886;
 RA Babu P.S., Jiang L., Sairam A.M., Touyz R.M., Sairam M.R.;
 RT "Structural features and expression of an alternatively spliced growth
 RT factor type I receptor for follicle signaling in the developing
 RT ovary";
 RL Mol. Cell Biol. Res. Commun. 2:21-27(1999).
 RN [5]
 RP SEQUENCE OF 1-51 FROM N.A.
 RX MEDLINE=98031017; PubMed=9364442;
 RA Sairam M.R., Subbarayan V.S.R.;
 RT "Cloning of the human follicle stimulating hormone receptor and potential control
 RT element of the human follicle stimulating hormone receptor gene";
 RL Mol. Reprod. Dev. 48:480-487(1997).
 CC -1- FUNCTION: Receptor for follicle stimulating hormone. The activity
 CC of isoform FSH-R1 is mediated by G proteins which activate
 CC adenylyl cyclase. Isoforms FSH-R2 and FSH-R3 also bind FSH, but
 CC this does not result in activation of calcium signaling.
 CC FSH-R3 may be involved in calcium signaling.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Plasma membrane
 CC (isoforms FSH-R1 and FSH-R2); Cell surface (isoform FSH-R3).
 CC -1- ALTERNATIVE PRODUCTS: 4 isoforms; FSH-R1 (shown here), FSH-R2,
 CC FSH-R3 and FSH-R4; are produced by alternative splicing.
 CC -1- TISSUE SPECIFICITY: Isoform FSH-R3 is expressed in ovary and
 CC testis, but not in kidney.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 CC -1- SIMILARITY: CONTAINS 6 LEUCINE-RICH REPEATS (LRR).
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 CC or send an email to license@isb-sib.ch).
 CC EMBL: L07307; AAA31525.1;

DR EMBL: L12766; AAA31523.1;
 DR EMBL: L12767; AAA31524.1;
 DR EMBL: A33175; CA61749.1;
 DR EMBL: A33176; CA61750.1;
 DR EMBL: AF090438; AAC61749.1;
 DR PIR: JCI493; JCI493;
 DR HSP: P23945; 1XUN;
 DR InterPro: IPR000276; GPCR_Rhodopsin.
 DR InterPro: IPR001611; LRR_Nterm.
 DR InterPro: IPR000372; LRR_Nterm.
 DR Pfam: PF00001; 7tm_1.1;
 DR Pfam: PF00560; LRR.4;
 DR Pfam: PF01462; LRRNT.1;
 DR SMART: SM0013; LRRNT.1;
 DR PROSITE: PS00237; G-PROTEIN_RECEP_FL_1.1;
 DR PROSITE: PS0262; G-PROTEIN_RECEP_FL_2.1;
 KW G-protein coupled receptor; Transmembrane; Glycoprotein; Signal;
 KW Phosphorylation; Repeat; Leucine-rich repeat; Alternative splicing.
 FT SIGNAL 1 67
 FT EXTRACELLULAR 68 100
 FT CYTOPLASMIC (POTENTIAL) 101 110
 FT DOMAIN 111 367
 FT TRANSMEM 368 398
 FT DOMAIN 399 421
 FT TRANSMEM 422 443
 FT DOMAIN 444 465
 FT TRANSMEM 466 485
 FT DOMAIN 486 508
 FT TRANSMEM 509 528
 FT DOMAIN 529 550
 FT TRANSMEM 551 573
 FT TRANSMEM 574 597
 FT DOMAIN 598 608
 FT TRANSMEM 609 630
 FT DOMAIN 631 695
 FT REPEAT 696 98
 FT REPEAT 99 143
 FT REPEAT 144 191
 FT REPEAT 192 216
 FT REPEAT 217 240
 FT REPEAT 241 517
 FT DISULFID 442 517
 FT CARBOHYD 191 191
 FT CARBOHYD 199 199
 FT CARBOHYD 293 293
 FT VARSPLIC 126 133
 FT VARSPLIC 135 695
 FT VARSPLIC 224 259
 FT VARSPLIC 260 695
 FT VARSPLIC 643 670
 FT VARSPLIC 671 695
 SQ SEQUENCE 695 AA; 78237 MW; PBF75D8D8C0D4B CRC64;
 Query Match 89.3%; Score 3140.5; DB 1; Length 695;
 Best Local Similarity 87.5%; Pred. No. 9.4e-195;
 Matches 593; Conservative 47; Mismatches 35; Indels 3; Gaps 2;
 OY 1 CHHMLCHSNRVFLQDSKVTETPTDUPRNATLRLVTLKRVIPKGSFAGGDEKIEI 60
 DB 18 CHHRLCHSNRVFLQDSKVTETPTDUPRNATLRLVTLKRVIPKGSFAGGDEKIEI 77
 OY 61 SONDVLEVDYFNSLKPHEIRERIANLLYINPEAPQLPSRLYLLISWTGKHLPA 120
 DB 78 SONDVLEVDYFNSLKPHEIRERIANLLYINPEAPQLPSRLYLLISWTGKHLPA 137
 OY 121 VHKIOTSLQVLLDQDNINHTVARNFSGLSFESVILWLSKNGIEETHNCAPNCTOLDE 180
 DB 138 VHKIOTSLQVLLDQDNINHTVARNFSGLSFESVILWLSKNGIEETHNCAPNCTOLDE 197

Qy 181 LNLSDNNLELPNDVFGASGPVILDSRTKVLHSLPNHGLEKLLKRASTYRLKKLPN 240
D 198 LNLSDNNLELPNDVFGASGPVILDSRTKVLHSLPNHGLEKLLKRASTYRLKKLPN 257
Qy 241 LDKFVTLWEASLTYPSCCHCAFAKROISELHPICNKSLIQDIDDMTQIGDQVSLI-D 299
D 258 LEKFTVLEASLTYPSCCHCAFAKRRRQTSOLHPICNKSLIQEVDMMTQARGORISLAED 317
Qy 300 DEPSYGRGSDMYNEFDYDLCLNEVDVTCSPKPAFNPCEIDMAGYNILRLVLIWIFISILAI 359
D 318 DEPSYGRGSDMYNEFDYDLCLNEVDVTCSPKPAFNPCEIDMAGYNILRLVLIWIFISILAI 377
Qy 360 TGNITVLLVLTTSYKLTVPRLMCLNLAFAADLCIGIYLLIASVDIHTKSOYHNYAIDWQ 419
D 378 TGNITVLLVLTTSYKLTVPRLMCLNLAFAADLCIGIYLLIASVDIHTKSOYHNYAIDWQ 437
Qy 420 TGACDAAAGFTVFASLSVYTLTAITLERWHTTTHAMQLECKVOLRHAASVMVLGWTFA 479
D 438 TGACDAAAGFTVFASLSVYTLTAITLERWHTTTHAMQLECKVOLRHAASVMVLGWTFA 497
Qy 480 FAALFPIEGISSYMKVSYICLPMDIDPSLYVWALLVNLVAFVVICGTYHIYLTVR 539
D 498 FAALFPIEGISSYMKVSYICLPMDIDPSLYVWALLVNLVAFVVICGTYHIYLTVR 557
Qy 540 NPTIVSSSDTKIAKRNATLIFTDFLCMAPISFAISASLKVPITVSKAKILLVLFYPI 599
D 558 NPTIVSSSDTKIAKRNATLIFTDFLCMAPISFAISASLKVPITVSKAKILLVLFYPI 617
Qy 600 NSCANPELYAIFTNFRDRDFILLSKFCYEMQAQIYRTSSATHNFHARKSCSSAPR 659
D 618 NSCANPELYAIFTNFRDRDFILLSKFCYEMQAQIYRTSSATHNFHARKSCSSAPR 677
Qy 660 VTN--SYVLVPLNISSON 675
D 678 VTNGSNYTLPLRLHAKN 695

RESULT 7

FSHR_PIG STANDARD: PRT: 695 AA.
AC P49059; 077514;
DT 01-FEB-1996 (Rel. 33, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Follicle stimulating hormone receptor precursor (FSH-R) (Follitropin receptor).
GN FSHR.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_Taxid:9823;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-Ovary;
RX MEDLINE=96011644; PubMed=7590277;
RA Remy J.J., Labib-Mansais Y., Verle M., Bozon V., Couture L.,
RA Pajot E., Grebert D., Salese R.;
RT The porcine follitropin receptor: cDNA cloning, functional
expression and chromosomal localization of the gene.;
RL Gene 163:257-261(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE-Ovary;
RA Wang Y.F., Meyer K.B., Schmidt K., Wan S.J., Degen S.J.F.,
RA la Barbera A.R.;
RT Porcine follicle-stimulating hormone receptor.;
RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: RECEPTOR FOR FOLLICLE STIMULATING HORMONE. THE ACTIVITY
OF THIS RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE
ADENYLATE CYCLASE.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
FSH/LSH/TSH SUBFAMILY.

CC -1- SIMILARITY: CONTAINS 6 LEUCINE-RICH REPEATS (LRR).
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entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
or send an email to license@isb-sib.ch).
CC EMBL; L31966; AAA86933.1; -
DR EMBL; AF025377; AAC24981.1; -
DR HSP; P23945; 1XUN.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR InterPro; IPR001611; LRR.
DR InterPro; IPR000372; LRR_Nterm.
DR Pfam; PF00001; 7tm_1; 1.
DR Pfam; PF00560; LRR; 2.
DR Pfam; PF01462; LRRNT; 1.
DR SMART; SM00013; LRRNT; 1.
DR PROSITE; PS00237; G_PROTEIN_RECP_FL_1; 1.
DR PROSITE; PS00262; G_PROTEIN_RECP_FL_2; 1.
DR G-protein coupled receptor; Transmembrane; Glycoprotein; Signal;
KW Phosphorylation; Repeat; Leucine-rich repeat.
FT SIGNAL 1 17 POTENTIAL
FT CHAIN 18 695 FOLLICLE STIMULATING HORMONE RECEPTOR.
FT DOMAIN 18 366 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 367 387 1 (POTENTIAL).
FT DOMAIN 388 398 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 399 421 2 (POTENTIAL).
FT DOMAIN 422 443 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 444 465 3 (POTENTIAL).
FT DOMAIN 466 485 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 486 508 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 509 528 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 529 550 5 (POTENTIAL).
FT DOMAIN 551 573 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 574 597 6 (POTENTIAL).
FT DOMAIN 598 608 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 609 630 7 (POTENTIAL).
FT DOMAIN 631 695 CYTOPLASMIC (POTENTIAL).
FT REPEAT 44 68 LRR 1.
FT REPEAT 69 93 LRR 2.
FT REPEAT 119 143 LRR 3.
FT REPEAT 170 192 LRR 4.
FT REPEAT 193 216 LRR 5.
FT REPEAT 218 240 LRR 6.
FT DISULFID 442 517 BY SIMILARITY.
FT CARBOHYD 191 191 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 199 199 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 293 293 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 2 2 S -> A (IN REF. 1).
FT CONFLICT 13 13 T -> S (IN REF. 1).
FT CONFLICT 60 60 V -> A (IN REF. 1).
FT CONFLICT 166 166 V -> M (IN REF. 1).
FT CONFLICT 215 215 Q -> H (IN REF. 1).
FT CONFLICT 247 247 K -> R (IN REF. 1).
FT CONFLICT 257 257 S -> T (IN REF. 1).
FT CONFLICT 334 334 D -> N (IN REF. 1).
FT CONFLICT 349 349 E -> K (IN REF. 1).
FT CONFLICT 352 352 T -> A (IN REF. 1).
FT CONFLICT 383 383 V -> E (IN REF. 1).
FT CONFLICT 407 407 A -> T (IN REF. 1).
FT CONFLICT 421 421 V -> I (IN REF. 1).
FT CONFLICT 427 427 T -> S (IN REF. 1).
FT CONFLICT 435 435 D -> N (IN REF. 1).
FT CONFLICT 483 483 L -> V (IN REF. 1).
FT CONFLICT 550 550 T -> I (IN REF. 1).
FT CONFLICT 586 586 A -> V (IN REF. 1).
FT CONFLICT 607 607 S -> L (IN REF. 1).
FT CONFLICT 691 691 R -> H (IN REF. 1).
SQ SEQUENCE 695 AA; 78172 MW; E9EBEDB29C79C450 CRC64;

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Query Match      88.0%; Score 3092.5; DB 1; Length 695;
Best Local Similarity 86.7%; Prod No 1,2e-191;
Matches 568; Conservative 43; Mismatches 44; Indels 3; Gaps 2;

Oy 1 CHHILCHSRRVFLCQDSKVTEIPDLPNRALEFLVTLKRVIPKGSFGDLEKTEI 60
Db 18 CHHILCHSRRVFLCQDSKVTEIPDLPNRALEFLVTLKRVIPKGSFGDLEKTEI 77
Oy 61 SONDVLEIVADVFSNPLKHEIRIEKANALLYINPEAFONPLSLRYLLISMTGKHLPA 120
Db 78 SONDVLEIVADVFSNPLKHEIRIEKANALLYIDPAFONPLSLRYLLISMTGKHLPA 137
Oy 121 VRIKOSLOKVLIDQNIHIIHIVANSFGLSPFESVILWLSKNGIEEIHNCANFTQLODE 180
Db 138 VRIKOSLOKVLIDQNIHIIHIVANSFGLSPFESVILWLSKNGIEEIHNCANFTQLODE 197
Oy 181 LNLSDNNLEELNDVFCAGSPVILDSRTKVSHPNGLNKLKARSTYKLLKLPN 240
Db 198 LNLSDNNLEELNDVFCAGSPVILDSRTKVSHPNGLNKLKARSTYKLLKLPN 257
Oy 241 LDKFVTLKASLTTPSHCCAFANLKRTOISELHPICNKSILRODIDDMTOIGDORVSLDD 300
Db 258 LDKFVTLKASLTTPSHCCAFANLKRTOISELHPICNKSILRODIDDMTOIGDORVSLDD 317
Oy 301 -EPSTGKSDMYHEFDYDLCNEVDVTCSPKDPANPCEDIMGYNLRVLWIFSLAI 359
Db 318 GESSLAKFVTMTSEFDYDLCNEVDVTCSPKDPANPCEDIMGHDIRVLWIFSLAI 377
Oy 360 TGMVTLVILTSOYKLVLPFLMCHLAFADICIGIYLLIASVDIHTKSOYHNIAIMQ 419
Db 378 TGMVTLVILTSOYKLVLPFLMCHLAFADICIGIYLLIASVDIHTKSOYHNIAIMQ 437
Oy 420 TGAGCDAAGFTVFASELSVYTLTATLIERWHITTHAMOLECKVLRHAASVYLVGTFEA 479
Db 438 TGAGCDAAGFTVFASELSVYTLTATLIERWHITTHAMOLECKVLRHAASVYLVGTFEA 497
Oy 480 FFAALFPFIQISSTMYKVSICLPMDIDSPQLSVYLLVYLAFLVYICGCTHYILTVR 539
Db 498 FFAALFPFIQISSTMYKVSICLPMDIDSPQLSVYLLVYLAFLVYICGCTHYILTVR 557
Oy 540 NPTVSSSDTKIARMAITLFTDFCNAPISFPAISASLKVPILTVSKAKILLVLPFI 599
Db 558 NPTVSSSDTKIARMAITLFTDFCNAPISFPAISASLKVPILTVSKAKILLVLPFI 617
Oy 600 NSCANPELYAETKAFERDFPILLSFCYHQAOQIVTETSATHNEARKSHCSSAPR 659
Db 618 NSCANPELYAETKAFERDFPILLSFCYHQAOQIVTETSATHNEARKSHCSSAPR 677
Oy 660 VTN--STVLVPLNRSSON 675
Db 678 ITNSSVYTLPLSLAON 695

RESULT 8
FSHR_HORSE STANDARD; PRY: 694 AA.
AC P47799; 1996 (Rel. 33, Created)
BT 01-FEB-1996 (Rel. 43, Last sequence update)
DT 16-OCT-2003 (Rel. 46, Last annotation update)
DE Pollicle stimulating hormone receptor precursor (FSH-R) (Follitropin receptor).
GN FSHR
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RX MEDLINE=9425690; PubMed=8198575;
RA Robert P., Anselme S., Christophe S., Benifla J.L., Bellet D.,
  Roman A., Bizard J.M.;

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*Cloning and sequencing of the equine testicular follitropin
receptor. Biochem. Res. Commun. 201:201-207(1994).
-1- FUNCTION: RECEPTOR FOR FOLLICLE STIMULATING HORMONE. THE ACTIVITY
OF THIS RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE
ADENYLATE CYCLASE AMONG ALL MAMMALIAN FSH RECEPTORS ON THE HORSE
RECEPTOR DOES NOT BIND LH/CHORIONIC GONADOTROPHIN (CG).
-1- SUBCELLULAR LOCATION: Integral membrane protein.
-1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
-1- SIMILARITY: CONTAINS 6 LEUCINE-RICH REPEATS (LRR).
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activities without the express consent of the EMBL is prohibited. (See
http://www.isb-sib.ch/announce/ or send an email to
licensing@sib.ch)
EMBL: S70150; AAB10854.1;
DB HSPB: P23945; LXUN.
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR InterPro: IPR001611; LRR.
DR InterPro: IPR000372; LRR_Nterm.
DR Pfam: PF00001; 7tm.1.1.
DR Pfam: PF00560; LRR_3.
DR Pfam: PF01462; LRRNT_1.
DR PRINTS: PR00237; GPCRHOOPS.
DR SMART: SM0013; LRRNT_1.
DR PROSITE: PS00237; G-PROTEIN_RECEP_F1_1; 1.
DR PROSITE: PS00264; G-PROTEIN_RECEP_F2_1; 1.
KW Chromatin coupled receptor; Transmembrane; Glycoprotein; Signal;
KW Polypeptide; Polarity; Repeat; Leucine rich repeat.
FT SIGNAL 1 17
FT CHAIN 18 694 FOLLICLE STIMULATING HORMONE RECEPTOR.
FT DOMAIN 18 365 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 366 386 1 (POTENTIAL).
FT DOMAIN 387 397 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 398 420 2 (POTENTIAL).
FT DOMAIN 421 442 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 443 464 3 (POTENTIAL).
FT DOMAIN 465 484 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 485 507 4 (POTENTIAL).
FT DOMAIN 508 527 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 528 549 5 (POTENTIAL).
FT DOMAIN 550 572 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 573 595 6 (POTENTIAL).
FT DOMAIN 596 629 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 630 694 7 (POTENTIAL).
FT REPEAT 44 68 LRR 1.
FT REPEAT 69 93 LRR 2.
FT REPEAT 119 143 LRR 3.
FT REPEAT 168 192 LRR 4.
FT REPEAT 193 216 LRR 5.
FT REPEAT 218 240 LRR 6.
FT DISULFID 441 516 BY SIMILARITY.
FT CARBOHYD 191 191 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 199 199 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 288 288 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 293 293 N-LINKED (GLCNAC...) (POTENTIAL).
FT SEQUENCE 694 AA; 78004 MW; E2F077C5E8CBA34 CRC64;
Query Match 87.4%; Score 3074; DB 1; Length 694;
Best Local Similarity 87.6%; Prod No 1,8e-190;
Matches 594; Conservative 35; Mismatches 45; Indels 4; Gaps 3;
Oy 1 CHHILCHSRRVFLCQDSKVTEIPDLPNRALEFLVTLKRVIPKGSFGDLEKTEI 60
Db 18 CHHILCHSRRVFLCQDSKVTEIPDLPNRALEFLVTLKRVIPKGSFGDLEKTEI 77
Oy 61 SONDVLEIVADVFSNPLKHEIRIEKANALLYINPEAFONPLSLRYLLISMTGKHLPA 120

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Db 78 QY 121 Db 138 QY 181 Db 198 QY 241 Db 258 QY 300 Db 317 QY 360 Db 377 QY 420 Db 437 QY 480 Db 497 QY 540 Db 557 QY 600 Db 617 QY 660 Db 677

SONDVLVEIANVSNPKLHEIRIEKANNLLYIDHDAFONLPNLOYLLISNTGKHLPA 137
 VKHQSLQKVLDDIODNINIHIVARNFPMGLSPESVILWLSKNGIEEIHNCAPNGTOLDE 180
 VKHQSLQKVLDDIODNINIHIVARNFPMGLSPESVILWLSKNGIEEIHNCAPNGTOLDE 197
 LNLSDNNLEELPNDVFGAGSGPVILDISRTKQVHSLPNHGLNKKLRSYRKLKLPN 240
 LNLSDNNLEELPNDVFGAGSGPVILDISRTKQVHSLPNHGLNKKLRSYRKLKLPN 257
 LDKFVTLMEASLYPSHCCAFANLKRQISELHPICNKSILRQDIDDMTOIGDORVSLI-D 299
 LERFVAMEANLYPSHCCAFANWRQTSLOQTCKNSILRQEV-DMTQARGERSVLAED 316
 DEPSYKSGSDMYNEFDYDLCNEVDVDTCSKPDFAFNPCEIDMGYNILRVLIWFSILAI 359
 DESSYPKGFDMYSEFYDLCNEVDVDTCSKPDFAFNPCEIDMGYNILRVLIWFSILAI 376
 TGNTVTLVLTTSQYKLTVPFRLMCNLAFAADLCIGIYLLIASVDHTSKQYHNYAIDWQ 419
 TGNILVILITTSQYKLTVPFRLMCNLAFAADLCIGIYLLIASVDHTSKQYHNYAIDWQ 436
 TGAGCDAAGFTVFASLSVYTTAITLERWHHTITHAMQLECKVQLRHAASVVLGWTFA 479
 TGAGCDAAGFTVFASLSVYTTAITLERWHHTITHAMQLECKVQLRHAASVVLGWTFA 496
 FAALPFIPIGSISSYKMYICPLMDIDSPLSQLYMALLVNLVAFVVCYTHIYLTVR 539
 FAVALLPIGSISSYKMYICPLMDIDSPLSQLYMALLVNLVAFVVCYTHIYLTVR 556
 NPTIVSSSDTKAKRATLITFDLCMAPISEFAISASLKVPPLITVSKAKILLVLFYPI 599
 NPNTIVSSSDTKAKRATLITFDLCMAPISEFAISASLKVPPLITVSKAKILLVLFYPI 616
 NSCANPLYAIFTNFRDRDFILLSKFCYEMOAOIYRTTSSATHNFHARKSHCSAPR 659
 NSCANPLYAIFTNFRDRDFILLSKFCYEMOAOIYRTTSSATHNFHARKSHCSAPR 676
 VTN--SYVLVPLNHSN 675
 VINGANCTVPLSLHAQN 694

RESULT 9

FSHR_EQUAS STANDARD: PRT: 687 AA.
 AC Q95179;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Follicle stimulating hormone receptor precursor (FSH-R) (Follitropin receptor).
 DE FSHR.
 OS Equus asinus (Donkey).
 GN Equus.
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
 OX NCBI_TaxID=9793;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-Testis;
 RX MEDLINE=97338913; PubMed=9195473;
 RA Richard F., Martinat N., Remy J.-J., Salesse R., Combarnous Y.;
 RT "Cloning, sequencing and in vitro functional expression of recombinant donkey follicle-stimulating hormone receptor: a new insight into the binding specificity of gonadotrophin receptors.";
 RL J. Mol. Endocrinol. 18:193-202(1997).
 CC -1- FUNCTION: RECEPTOR FOR FOLLICLE STIMULATING HORMONE. THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE ADENYLATE CYCLASE.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS. FSH/LSH/TSH SUBFAMILY.

CC -1- SIMILARITY: CONTAINS 6 LEUCINE-RICH REPEATS (LRR).
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 CC EMBL: U73659; AAB18245.1;
 DR HSSP: P23945; 1XUN.
 DR InterPro: IPR000276; GPCR_Rhodpsn.
 DR InterPro: IPR001611; LRR.
 DR InterPro: IPR000372; LRR_Nterm.
 DR Pfam: PF00001; 7tm_1; 1.
 DR Pfam: PF00560; LRR; 3.
 DR Pfam: PF01462; LRRNT; 1.
 DR PRINTS: PR00237; GPCR_RHODPSN.
 DR SMART: SM00013; LRRNT; 1.
 DR PROSITE: PS00237; G-PROTEIN_RECEPTOR_F1_1; 1.
 DR PROSITE: PS00262; G-PROTEIN_RECEPTOR_F1_2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein; Signal; Phosphorylation; Repeat; Leucine-rich repeat.
 FT SIGNAL 1 17 POTENTIAL.
 FT CHAIN 18 687 FOLLICLE STIMULATING HORMONE RECEPTOR.
 FT DOMAIN 18 358 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 359 379 1 (POTENTIAL).
 FT DOMAIN 380 390 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 391 413 2 (POTENTIAL).
 FT DOMAIN 414 435 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 436 457 3 (POTENTIAL).
 FT DOMAIN 458 477 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 478 500 4 (POTENTIAL).
 FT DOMAIN 501 520 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 521 542 5 (POTENTIAL).
 FT DOMAIN 543 565 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 566 589 6 (POTENTIAL).
 FT DOMAIN 590 600 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 601 622 7 (POTENTIAL).
 FT DOMAIN 623 687 CYTOPLASMIC (POTENTIAL).
 FT REPEAT 69 93 LRR 1.
 FT REPEAT 99 143 LRR 2.
 FT REPEAT 170 192 LRR 3.
 FT REPEAT 193 216 LRR 4.
 FT REPEAT 218 240 LRR 5.
 FT REPEAT 240 259 LRR 6.
 FT DISULFID 434 509 BY SIMILARITY.
 FT CARBOHYD 191 191 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 199 199 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 293 293 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 687 AA; FC3AF0B5531DA9A CRC64;
 Query Match 85.6%; Score 3010.5; DB 1; Length 687;
 Best Local Similarity 86.0%; Pred. No. 2.1e-186;
 Matches 582; Conservative 38; Mismatches 48; Indels 9; Gaps 3;
 QY 1 CHHWLCHCSNRVFLCQDSKVTEIPTDLPNRIALRFLVTLKRLVTPKSGFAGDLEKIEI 60
 DB 18 CHQVCHYSNRVFLCQDSKVTEIPTDLPNRIALRFLVTLKRLVTPKSGFAGDLEKIEI 77
 QY 61 SONDVLEIADYVSNPKLHEIRIEKANNLLYINPEAFONLPRLVLLISNTGKHLPA 120
 DB 78 SONDVLEIADYVSNPKLHEIRIEKANNLLYIDHDAFONLPNLOYLLISNTGKHLPA 137
 QY 121 VKHQSLQKVLDDIODNINIHIVARNFPMGLSPESVILWLSKNGIEEIHNCAPNGTOLDE 180
 DB 138 VKHQSLQKVLDDIODNINIHIVARNFPMGLSPESVILWLSKNGIEEIHNCAPNGTOLDE 197
 QY 181 LNLSDNNLEELPNDVFGAGSGPVILDISRTKQVHSLPNHGLNKKLRSYRKLKLPN 240
 DB 198 LNLSDNNLEELPNDVFGAGSGPVILDISRTKQVHSLPNHGLNKKLRSYRKLKLPN 257

OY 241 LDKFVTLWEASITPSHCCAFANLAROISLHPICNKSTLRDDIDMDTOIGDORSLIDD 300
 Db 258 LEKFAVALLWEASITPSHCCAFANRNDVOTSELQTTCKNSILRQEV-DMTQARGERSLAD 316
 OY 301 EPSTYKGSQDMATNEFDYDLGNEVDVTCSPKPDAPNCPEDIMGILNRLVLFISILAIT 360
 Db 317 DES-----MYSZPDYDLGNEVDVTCSPKPDAPNCPEDIMGILNRLVLFISILAIT 370
 OY 361 GMTVLYVLTSTOKLTVPRFLKMLAFADICIGITLLIASYDITKTSQYHNTAIDMOT 420
 Db 371 GNIIVLVLTSTOKLTVPRFLKMLAFADICIGITLLIASYDITKTSQYHNTAIDMOT 430
 OY 421 GAGCDAAGFTVFASLSVLTATLERNHTTHMOLECKVQLRHAAVYVLTWTFAP 480
 Db 431 GAGCDAAGFTVFASLSVLTATLERNHTTHMOLECKVQLRHAAVYVLTWTFAP 490
 OY 481 AAALPFPICISYMKVSCICLPMDIDPSQLVYVALLVYVLTWTFAPVYVLTWTFAP 540
 Db 491 GVGLLPFGISTMKVSCICLPMDIDPSQLVYVALLVYVLTWTFAPVYVLTWTFAP 550
 OY 541 PTIVSSSSDTIARMAVLTFTDPLCHAPISFPAISAKVPLTVSKAKILLVLPYPIN 600
 Db 551 PNVSSSSDTIARMAVLTFTDPLCHAPISFPAISAKVPLTVSKAKILLVLPYPIN 610
 OY 601 SCANPFIYAIPTKNRDPFTLLSKFCYEMOQATYRTTSSATHNPKSHCSSAPRV 660
 Db 611 SCANPFIYAIPTKNRDPFTLLSKFCYEMOQATYRTTSTGHSHPKNGRCPPPRV 670
 OY 661 TN-SYVLPVLRHSON 675
 Db 671 TWGACTLTPVLSHLAON 687
 RESULT 10
 FSHR-CHICK STANDARD; PRT: 693 AA.
 AC P79763; 090719;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Follicle stimulating hormone receptor precursor (FSH-R) (Follitropin receptor).
 DE FSHR.
 OS Gallus gallus (Chicken).
 CC Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Chorostraea; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-Ovary;
 RX MEDLINE=97473503; PubMed=9332357;
 RA Wakabayashi N., Suzuki A., Hoshino H., Nishimori K., Mizuno S.:
 RT "The cDNA cloning and transient expression of a chicken gene encoding
 RL a follicle-stimulating hormone receptor.";
 RL Gene 197:121-127(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=White Leghorn;
 RX MEDLINE=97057887; PubMed=8902217;
 RA S. Bragman J.F., Foster D.N., Johnson A.L.:
 RT "Characterization of the chicken follicle-stimulating hormone
 RL receptor (cFSH-R) complementary DNA, and expression
 RL of cFSH-R messenger ribonucleic acid in the ovary.";
 RL Biol. Reprod. 55:1055-1062(1996).
 CC -1- FUNCTION: RECEPTOR FOR FOLLICLE STIMULATING HORMONE. THE ACTIVITY
 CC OF THIS RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE
 CC ADENYLATE CYCLASE.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 CC FSH/LSH/TSH SUBFAMILY.
 CC -1- SIMILARITY: CONTAINS 7 LEUCINE-RICH REPEATS (LRR).
 CC
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 or send an email to license@isb-ab.ch).
 EMBL: D87871; BAA13487.1;
 EMBL: U51097; AAC60030.1;
 HSSP: P23945; IXUN.
 InterPro: IPR000276; GPCR_Rhodopsn.
 InterPro: IPR001611; LRR.
 InterPro: IPR000372; LRR_Nterm.
 Pfam: PF00004; 7tmL1.1.
 Pfam: PF00004; 7tmL1.1.
 PRINTS: PR00317; GPCR_Rhodopsn.
 SMART: SM00013; LRRNT.1.
 PROSITE: PS00237; G-PROTEIN_RECEP_FL1.1.
 PROSITE: PS00262; G-PROTEIN_RECEP_FL2.1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein; Signal;
 Phosphorylation; Repeat; Leucine-rich repeat.
 FT SIGNAL 1 17 POTENTIAL.
 FT CHAIN 18 693 FOLLICLE STIMULATING HORMONE RECEPTOR.
 FT DOMAIN 18 366 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 367 387 1 (POTENTIAL).
 FT DOMAIN 388 398 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 399 421 2 (POTENTIAL).
 FT DOMAIN 422 443 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 444 465 3 (POTENTIAL).
 FT DOMAIN 466 485 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 486 506 4 (POTENTIAL).
 FT DOMAIN 507 528 5 (POTENTIAL).
 FT TRANSMEM 529 550 6 (POTENTIAL).
 FT DOMAIN 551 573 7 (POTENTIAL).
 FT TRANSMEM 574 597 8 (POTENTIAL).
 FT DOMAIN 598 609 9 (POTENTIAL).
 FT TRANSMEM 610 631 10 (POTENTIAL).
 FT DOMAIN 632 653 11 (POTENTIAL).
 FT TRANSMEM 654 675 12 (POTENTIAL).
 FT REPEAT 676 693 LRR 1.
 FT REPEAT 694 715 LRR 2.
 FT REPEAT 716 737 LRR 3.
 FT REPEAT 738 759 LRR 4.
 FT REPEAT 760 781 LRR 5.
 FT REPEAT 782 803 LRR 6.
 FT REPEAT 804 825 LRR 7.
 FT DISULFID 442 517 BY SIMILARITY.
 FT CARBOHYD 47 47 N-LINKED (GLCNAC.) (POTENTIAL).
 FT CARBOHYD 147 147 N-LINKED (GLCNAC.) (POTENTIAL).
 FT CARBOHYD 199 199 N-LINKED (GLCNAC.) (POTENTIAL).
 FT CARBOHYD 268 268 N-LINKED (GLCNAC.) (POTENTIAL).
 FT CONFLICT 88 88 G -> D (IN REF. 2).
 FT CONFLICT 140 140 K -> R (IN REF. 2).
 FT CONFLICT 174 174 I -> T (IN REF. 2).
 FT CONFLICT 191 191 N -> S (IN REF. 2).
 FT CONFLICT 329 329 V -> L (IN REF. 2).
 FT CONFLICT 329 329 V -> L (IN REF. 2).
 SQ SEQUENCE 693 AA; 78697 MW; 46P969635A1BEC CRC64;
 Query Match 73.3%; Score 2577.5; DB 1; Length 693;
 Best Local Similarity 73.6%; Pred. No. 1.5e-158;
 Matches 496; Conservative 70; Mismatches 105; Indels 3; Gaps 2;
 OY 1 CHWKLCHSNNVFLQDSKVTETPTDLPNAIEELVTLKLVTPKSPAGGDEKIEI 60
 Db 18 COHTCLCEGRIFCOEKVQVLPDPTNATELRLVTRVYPRGPTGLHDEKIEI 77
 OY 61 SONDLVETADVFSNLPKLEIRTEKANKLILNPEAFONLSRLYLLISNTGKHLP 120
 Db 78 SONDALEIEGNEVFSNLPKLEIRTEKANKLILNPEAFONLSRLYLLISNTGKHLP 137
 OY 121 VHKIOSLQVLLDIDQINITHIVARNFMSFESVILWLSKNGITEIHNCAFNCTOLDE 180
 Db 121 VHKIOSLQVLLDIDQINITHIVARNFMSFESVILWLSKNGITEIHNCAFNCTOLDE 180


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OY 152 SPESVILNLSKNGIEZHNCAFGNCTGDELNLSDNNHLELNPVDFOGACRVIDLSRT 211
Db 175 NNEISITLALVNGFEEIOSHAFNGSTTJLSLEKNALEKHNDAFRGATGPSILDSST 234
OY 212 KVHSLPHNGLNLEKLRARSTYKRLKPLNDLFTVLMKASLTYSHCACAFANLKRQISEL 271
Db 235 KQALPPTYGLSIOGTLIATFSYSKLKPSREFNLLDQATLYPSHCCAFRNL----- 287
OY 272 HPICKKILRODIDDMTOIGDQVRSUIDDPSYG---KGDMMYNEFYDLCNEVDVTC 328
Db 288 -PTNDNFSPSIFKNSKCESTARPNNETLYSAFSELSCHWDYDGLPKPT-LOC 345
OY 329 SPKPDAPNCEIDMGVNLRLVILWFLSILATGNTVTVLVVTSQVLTVPRLKMCNAP 388
Db 346 APEDNAPNCEIDMGVNLRLVILWFLSILATGNTVTVLVVTSQVLTVPRLKMCNAP 405
OY 389 ADLCIGVILLTASVDHFTSSOVHVAIDQGTGACGACGACGACGACGACGACGAC 448
Db 406 ADPCNGVILLTASVDHFTSSOVHVAIDQGTGACGACGACGACGACGACGACGAC 465
OY 449 RNIITTHAMQDCVQLRHAASVWVLGWTFAAALFPFIFGLSYKVSICLPMIDISPL 508
Db 466 RNIITTHAMQDCVQLRHAASVWVLGWTFAAALFPFIFGLSYKVSICLPMIDISPL 525
OY 509 SOLYPMALVLAFLVYICGCTHYTHYVTRPVTIVSSSDTKTKAKMATLFTDFLCA 568
Db 526 SOLYPMALVLAFLVYICGCTHYTHYVTRPVTIVSSSDTKTKAKMATLFTDFLCA 585
OY 569 SIPTFAISLAKVPLTVSGKATLVLVLPYFINSANPFLYALFTKFRDRDFLLSKFGC 628
Db 586 SIPTFAISLAKVPLTVSGKATLVLVLPYFINSANPFLYALFTKFRDRDFLLSKFGC 645
OY 629 YEMAOIYRTTSATNHFARSHCSS 656
Db 646 CYRAELVREK-----DFSNATLSNCKN 667

RESULT 12
LSHR_PIG STANDARD; PRT: 696 AA.
AC PL1582;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Lutropin-choriogonadotropic hormone receptor precursor (LH/CG-R)
GN LUCR (Luteinizing hormone receptor).
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RX MEDLINE=4933217; PubMed=250284;
RA Loosfelt H., Mirrehi M., Atger M., Salcesse R., Thi M.T.V.H.-L.,
RA Jolivet A., Guichon-Mantel A., Sar S., Jallat B., Garnier J.,
RA Milgrom E.;
RT Cloning and sequencing of porcine LH-hCG receptor cDNA: variants
RT lacking transmembrane domain.;
RL Science 245:525-528(1989).
CC -1- FUNCTION: RECEPTOR FOR LUTROPIN-CHORIOGONADOTROPIC HORMONE.
CC THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G PROTEINS WHICH
CC ARE CYTOPLASMIC ENDOPLASMIC RETICULUM TYPE C.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- ALTERNATIVE PRODUCTS: 4 ISOFORMS; A (SHOWN HERE), B, C AND D; ARE
CC PRODUCED BY ALTERNATIVE SPLICING.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC FSH/LSH/TSH SUBFAMILY.
CC -1- SIMILARITY: CONTAINS 6 LUTEININE-RICH REPEATS (LRR).
CC
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CC entities requires a license agreement. (See http://www.isb-sib.ch/announce/
CC about license and terms of use.)
CC -----
CC ENBL: M29525; AAA31062.1; -
DR ENBL: M29526; AAA31063.1; -
DR ENBL: M29527; AAA31064.1; -
DR ENBL: M29528; AAA31065.1; -
DR PIR: A41344; A41344.
DR PIR: B41344; B41344.
DR PIR: C41344; C41344.
DR PIR: D41344; D41344.
DR HSP: P22888; LUUT.
DR InterPro: IPR00276; GPCR_Rhodospn.
DR InterPro: IPR01611; LRR.
DR InterPro: IPR00372; LRR_Nterm.
DR Pfam: PF00400; LRR_1.
DR Pfam: PF00560; LRR_2.
DR SMART: SM00013; LRRNT; 1
DR PROSITE: PS00237; G-PROTEIN RECP_FL_1; 1.
DR PROSITE: PS0263; G-PROTEIN RECP_FL_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Signal;
KW Phosphorylation; Repeat; Leucine-rich repeat; Alternative splicing.
FT SIGNAL 1 27
FT CHAIN 28 696
FT DOMAIN 28 358
FT TRANSHEM 359 386
FT DOMAIN 387 395
FT TRANSHEM 396 418
FT DOMAIN 419 439
FT TRANSHEM 440 462
FT DOMAIN 463 482
FT TRANSHEM 483 506
FT DOMAIN 506 525
FT TRANSHEM 526 547
FT DOMAIN 548 570
FT TRANSHEM 571 594
FT DOMAIN 595 605
FT TRANSHEM 606 626
FT DOMAIN 627 696
FT REPEAT 48 71
FT REPEAT 122 147
FT REPEAT 149 171
FT REPEAT 172 196
FT REPEAT 198 220
FT REPEAT 221 244
FT CARBOHYD 245 254
FT CARBOHYD 255 264
FT CARBOHYD 265 274
FT CARBOHYD 275 284
FT CARBOHYD 285 294
FT CARBOHYD 295 304
FT CARBOHYD 305 314
FT CARBOHYD 315 324
FT VARSPLIC 317 329
FT VARSPLIC 330 696
FT VARSPLIC 317 331
FT VARSPLIC 332 696
FT VARSPLIC 317 628
SQ SEQUENCE 696 AA; 78092 MW; 593DEFC2F982FE CRC64;
Query Match Best Local Similarity 51.4%; Score 1807; DB:1; Length 696;
Matches 361; Conservative 98; Mismatches 142; Indels 26; Gaps 8;
OY 28 PRNATLRFVTLK--RVTPKSPAGFQDLEKIEISQNDVLEADVFNSLPKLHEIRI 85
Db 47 PRAGLS-RSLTLPKIPVPSQFRLGVNVEIKSISQSLKIEANAFONLLNLSILL 105
OY 86 EKANNLLYINPEAFONPLSLRYLLISNTGKHLPAVHKIQSLQ-KVLLDIQDNINHI 144
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Db 106 ONTKNLVYIEPGFTNLPRKLYSICNTGIRKLPDVTYKIFSSFNFILEICDNLHITVTP 165
QY 145 RNSFMGLSPFVILMLSKNGIEIHNCAPNGTOLDLNLSDNNLELPNDVQFAGSPV 204
Db 166 ANAFOGNNESITLKYNGFEBEQSHAFNGTTLISLELKENAHLKMHNDAPRGARPS 225
QY 205 ILDISRTKVLNPHGLNKLKLRARSTYRLKLPNDKRVTLMEASLYTPSHCCAFANL 264
Db 226 ILDISSTKQALSYGLSOTIATSSYSKLPLSREKFTNLDDATLTSPSHCCAFANL 285
QY 265 --RRQ-----ISELPHICKNSILRODIDMTQIGDQVSLIDDEPSYGRGSMYNEFD 316
Db 286 PTKRONFSEFIEKNSQCESTARRPNETL-----YSAIFAE-----SELSWDYD 332
QY 317 YDLCNVWVOTCSFKPDAPNCPEDINGYNILRVLIWIFISILATNTVTLVLTTSOYKL 376
Db 333 YGCSPTK-LQCAPEPDAPNCPEDIMGYDLRLVLIWILINLAIMGNTVTLVLTSHYKL 391
QY 377 TVPRFLMCLNFAFADLCIGIYLLIASVDIHTKSOYHNYAIDMOTGACDAGFTVPASE 436
Db 392 TVPRFLMCLNFAFADFCMGLYLLIASVDAQTKGYNHAIIDMOTGNCVAGFTVPASE 451
QY 437 LSVYTLTATLFRWHITTHAMOLECKVQLRHAASVMVGLWTFATAAALPFIIGISSVMKV 496
Db 452 LSVYTLTATLFRWHITTAIQLDOKLRLHRAIPMLGGWLFSTLAMLPVGVSSVMKV 511
QY 497 SICLPMDISPLSOLYVALLVNLVAFVVICCYTHIYLVTRNPTIVSSSDTKIAKRM 556
Db 512 SICLPMDVETLSQVYTLTILNVAVFIICACIKIYFVQNPMLMATNKDTKIAKRM 571
QY 557 ATLITFELCMAPISFAISAKLVPLITVSKAKILLVLPYNSCANPFLYAIFTKFR 616
Db 572 AVLITFDTCMAPISFAISAKLVPLITVSKAKILLVLPYNSCANPFLYAIFTKFR 631
QY 617 RDFILLKFGCYEQMAQIYRTETSSA 643
Db 632 RDFILLKSGCKHQALYRRKDFSA 658

RESULT 13
LSHR_MOUSE STANDARD; PRT; 700 AA.
AC P30730;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Lutropin-choriogonadotropic hormone receptor precursor (LH/CG-R)
DE (LSH-R) (Luteinizing hormone receptor).
GN LHCR OR LHR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92165799; PubMed=1311310;
RA Gudermann T., Birnbaumer M., Birnbaumer L.;
RT "Evidence for dual coupling of the murine luteinizing hormone
RT receptor to adenylyl cyclase and phosphoinositide breakdown and Ca2+
RT mobilization. Studies with the cloned murine luteinizing hormone
RT receptor expressed in L cells."
RL J. Biol. Chem. 267:4479-4488(1992).
RN [2]
RP SEQUENCE OF 1-58 FROM N.A.
RX MEDLINE=93093308; PubMed=1459341;
RA Huhtaniemi I.T., Eskola V., Pakarinen P., Matikainen T., Sprengel R.;
RT "The murine luteinizing hormone and follicle-stimulating hormone
RT receptor genes: transcription initiation sites, putative promoter
RT sequences and promoter activity."
RL Mol. Cell. Endocrinol. 88:55-66(1992).
CC -1- FUNCTION: RECEPTOR FOR LUTROPIN-CHORIOGONADOTROPIC HORMONE.
CC -1- THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G PROTEINS WHICH

CC CC ACTIVATE ADENYLATE CYCLASE.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC FSH/LSH/TSH SUBFAMILY.
CC -1- SIMILARITY: CONTAINS 4 LEUCINE-RICH REPEATS (LRR).
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CC -----
CC EMBL; S49753; AAB24402.1; -
CC EMBL; M81310; AAA39432.1; -
CC EMBL; M87571; AAA39433.1; -
CC PIR; A42395; A42395.
CC HSP; P22888; ILUT.
CC MCD; MG1:96783; Lhcgr.
CC InterPro: IPR000276; GPCR_Rhodpsn.
CC InterPro: IPR001611; LRR.
CC InterPro: IPR000372; LRR_Nterm.
CC Pfam; PF00001; 7tm_1; 1.
CC Pfam; PF00560; LRR; 1.
CC SMART; SM00013; LRRNT; 1.
CC PROSITE; PS00237; G_PROTEIN_RECPT_FL_1; 1.
CC PROSITE; PS0262; G_PROTEIN_RECPT_FL_2; 1.
CC G-protein coupled receptor; Transmembrane; Glycoprotein; Signal;
CC phosphorylation; Repeat; Leucine-rich repeat.
CC SIGNAL 1 26
CC CHAIN 27 700
CC LUTROPIN-CHORIOGONADOTROPIC HORMONE
CC RECEPTOR.
CC DOMAIN 27 362
CC TRANSMEM 363 390
CC DOMAIN 391 399
CC TRANSMEM 400 422
CC DOMAIN 423 443
CC TRANSMEM 444 466
CC DOMAIN 467 486
CC TRANSMEM 487 509
CC DOMAIN 510 529
CC TRANSMEM 530 551
CC DOMAIN 552 574
CC TRANSMEM 575 598
CC DOMAIN 599 609
CC TRANSMEM 610 631
CC DOMAIN 632 700
CC REPEAT 52 75
CC REPEAT 126 150
CC REPEAT 176 200
CC REPEAT 225 248
CC DISULFID 443 518
CC CARBOHYD 103 103
CC CARBOHYD 178 178
CC CARBOHYD 199 199
CC CARBOHYD 295 295
CC CARBOHYD 303 303
CC CARBOHYD 317 317
CC SEQUENCE 700 AA; 78214 MW; 8A6840A011E014 CRC64;
Query Match 51.2%; Score 1799; DB 1; Length 700;
Best Local Similarity 55.1%; Pred. No. 1.8e-108;
Matches 362; Conservative 108; Mismatches 153; Indels 34; Gaps 9;
QY 28 PRNAIELRVFLTKL--RVTPKGSFAGDLEKTEISONDVLEIVAEVFNLPKLHEIRI 85
Db 51 PRAGL-ARLSLTYPVKVIPSOAQRGLNEVVKISQSDSLEIRAEANFNLNLSELI 109
QY 86 EKANNLLYNPEAFONLPSIRYLLISNTGKHLPAVHKIOSLO-KVLLDQDNINHIWA 144
Db 110 QNTKNLLYEPGFTNLPRKLYSICNTGIRKLPDVTYKIFSSFNFILEICDNLHITVTP 169

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OY 145 RNSFGLSPESVILWLSKNGTETLHNCAPNGTQDLDELNSDNNHLELNDVDFQACSPV 204
DB 170 GNAPOGNNESITLKLGVNGEVSQSHAFNGTTLISLEKENYILKXHSCTTQGTOTPS 229
OY 205 ILDSIRTKVSLPHNGLEMLKLLKRASTYRLKLNLDKAFVTLMEASLTYSHCAPANL 264
DB 230 ILOVSTKLOALPSHGLESTLTIATSYSLATLPSREKFTSLVATLTYSHCAPANL 289
OY 265 KRQISELHPITCKNKSILRODIDDMTOIGDQVSLIDDEPSVG---KGSOMYNEFYDLCN 321
DB 290 PKX-----EQNFSPSIFENFSKQCESTREANNETLYSAIFENELSGSDYDFCS 341
OY 322 EYVDVTSKPAQNPCEIDNGYINLRLVFWITSLTATGNTVTLVLTSTYKTLVPRF 381
DB 342 PRT-LOCTPEPQNPCEIDNGYINLRLVFWITSLTATGNTVTLVLTSTYKTLVPRF 400
OY 382 LKCNLAPADLCIGTILYLLASVDHKSQVYATIDMGTCAGCDAGCTTFAVELSYVT 441
DB 401 LKCNLAPADLCIGTILYLLASVDHKSQVYATIDMGTCAGCDAGCTTFAVELSYVT 460
OY 442 LTAITLERHMTTHAMQCEKVLORHAASVYVGLWTEFAAALPFIGLISYKYSICLP 501
DB 461 LTVITLERHMTTAVOLOQLRLRAIPMLGGMIFSTLMATLPLVGVSYKYSICLP 520
OY 502 MDIDSPLSOLYVALLVWLAFLVVICGCTTHIYTLVTRPTIVSSSDTKIAKRNATLIF 561
DB 521 MDVESTLSQVITSLILLNAFVFCACVRYIYFAYONPELTAPKDKTKIAKRNATLIF 580
OY 562 TDPLCAPISFTASLSKVLPLTVSKAKILVLPVINSKANPFLYATFKNFRDFFI 621
DB 581 TDPLCAPISFTASLSKVLPLTVSKAKILVLPVINSKANPFLYATFKNFRDFFI 640
OY 622 LLSKCGCYEMQAIYRTSSA-----THNPARKS-----HCS--SABRV 660
DB 641 LLSKCGCYEMQAIYRTSSA-----THNPARKS-----HCS--SABRV 697

RESULT 14
LSHR_RAT
ID AC P16235; P70646; 063807; 063808; 063809;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Lutropin-choriogonadotropic hormone receptor precursor (LH/CG-R)
GN LHRH-R (Luteinizing hormone receptor).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN LHRH-R
RP SEQUENCE FROM N.A.
RA McFarland K.C., Sprengel R., Phillips H.S., Koehler M.,
RA Rosenblit N., Nikolic K., Segaloff D.L., Seeburg P.H.;
RT "Lutropin-choriogonadotropic hormone receptor: an unusual member of the G
RL Science 245:494-499(1989).
RN SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
RC MEDLINE-91332007; PubMed-2925659;
RA Alanki J.T., Pietila E., Katakapi J.T., Rajaniemi H.J.;
RT "Expression of the LH/CG receptor gene in rat ovary tissue is
RT regulated by an extensive alternative splicing of the primary
RL transcript.";
RL Mol. Cell. Endocrinol. 84:127-135(1992).
RN SEQUENCE FROM N.A.
RP MEDLINE-91209270; PubMed-2019252;
RA Foo Y.B., Slaughter R.G., Ji T.H.;
RT "Structure of the luteinizing hormone receptor gene and multiple
RT
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RT exons of the coding sequence.";
RL Endocrinology 128:2297-2308(1991).
RN SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
RX MEDLINE-91006810; PubMed-1976554;
RA Bernard M.P., Myers R.V., Molye M.R.;
RT "Cloning of rat lutropin (LH) receptor analogs lacking the soybean
RL lectin domain.";
RL Mol. Cell. Endocrinol. 71:R19-R23(1990).
RN SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
RP MEDLINE-91126285; PubMed-2281186;
RA Segaloff D.L., Sprengel R., Nikolics K., Ascoli M.;
RT "Structure of the lutropin/choriogonadotropin receptor.";
RL Recent Prog. Horm. Res. 46:261-303(1990).
RN SEQUENCE OF 295-700 FROM N.A.
RX MEDLINE-91060531; PubMed-2174034;
RA Sai-Morris C.H., Guozao E., Wang W., Dufau M.L.;
RT "A soluble C-terminus of the rat luteinizing hormone receptor gene defines
RL a soluble C-terminus of the rat luteinizing hormone binding activity.";
RL J. Biol. Chem. 265:19385-19388(1990).
RN SEQUENCE OF 27-37.
RP MEDLINE-89174723; PubMed-2925659;
RA Roche P.C., Ryan R.J.;
RT "Purification, characterization, and amino-terminal sequence of rat
RL ovarian receptor for luteinizing hormone/human chorogonadotropin.";
RL J. Biol. Chem. 264:4636-4641(1989).
RN MUTAGENESIS.
RP MEDLINE-91332007; PubMed-1714448;
RA Ji T.H.;
RT "A383 in the second transmembrane domain of the lutropin receptor
RL is important for high affinity hormone binding and cAMP production.";
RL J. Biol. Chem. 266:9531-9534(1991).
RN FUNCTION: RECEPTOR FOR LUTROPIN-CHORIOGNADOTROPIC HORMONE.
CC THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G PROTEINS WHICH
CC ACTIVATE ADENYLATE CYCLASE.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- ALTERNATIVE PRODUCTS: AT LEAST 11 ISOFORMS WHICH DIFFER IN
CC SUBCELLULAR LOCATION ARE PRODUCED BY ALTERNATIVE SPLICING
CC OF THE SAME GENE.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC FSH/LSH/TSH SUBFAMILY.
CC -1- SIMILARITY: CONTAINS 7 LEUCINE-RICH REPEATS (LRR).
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC modified and provided to other institutions as long as its content is in no way
CC entitles requires a license agreement. Usage by and for commercial
CC or send an email to license@lab-sib.ch)
CC EMBL: M26199; AAA41528.1;
CC EMBL: M61212; AAA41527.1;
CC EMBL: M61211; AAA41527.1; JOINED.
CC EMBL: S40803; AAB22680.1;
CC EMBL: S40787; AAB22680.1; JOINED.
CC EMBL: S40903; AAB22680.1; JOINED.
CC EMBL: S40904; AAB22680.1; JOINED.
CC EMBL: S40905; AAB22680.1; JOINED.
CC EMBL: S40907; AAB22680.1; JOINED.
CC EMBL: S40909; AAB22680.1; JOINED.
CC EMBL: S40920; AAB22680.1; JOINED.
CC EMBL: S40926; AAB22680.1; JOINED.
CC EMBL: S40795; AAB22680.1; JOINED.
CC EMBL: S40798; AAB22680.1; JOINED.
CC EMBL: S40795; AAB22681.1;
CC EMBL: S40787; AAB22681.1; JOINED.
CC EMBL: S40903; AAB22681.1; JOINED.
CC EMBL: S40904; AAB22681.1; JOINED.
```


GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 16, 2003, 12:58:36 ; Search time 42.4653 seconds
(without alignments)
3275.191 Million cell updates/sec

Title: US-09-877-804-7
Perfect score: 3516
Sequence: 1 CHMLCHCSNRVFLCODESKV.....SAPRVTSVLYPLNHSQSN 675

Scoring table: BLOSUM62
Gapop 10.0 ; Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum DB seq length: 100%

Listing first 45 summaries

Database : SPTRMBL21..*
1: sp-archaea.*
2: sp-archaea.*
3: sp-fungi.*
4: sp-human.*
5: sp-invertebrate.*
6: sp-mammal.*
7: sp-mhc.*
8: sp-organelle.*
9: sp-phage.*
10: sp-plant.*
11: sp-rodent.*
12: sp-virus.*
13: sp-vertebrate.*
14: sp-unclassified.*
15: sp-virus.*
16: sp-bacterioph.*
17: sp-archaeop.*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3482	99.0	688	11 Q64183	064183 rattus sp.
2	3080.5	87.6	695	11 Q8R428	Q8R428 cavia porce
3	2479	70.5	696	13 Q9DGF5	Q9DGF5 cynops pyrr
4	1936	55.6	673	13 Q9DMP8	Q9DMP8 podarcis si
5	1901.3	54.1	410	4 Q16225	Q16225 homo sapien
6	1803.5	51.3	701	5 Q8P8T4	Q8P8T4 ictalurus p
7	1798.5	51.3	701	5 Q8P8T4	Q8P8T4 ictalurus p
8	1776	50.5	699	4 Q15996	Q15996 homo sapien
9	1776	50.5	701	4 Q14751	Q14751 homo sapien
10	1685	47.9	701	13 Q9DGC6	Q9DGC6 oreochromis
11	1658	47.2	601	13 Q42500	Q42500 melargis 9
12	1658	47.1	764	6 Q9BG56	Q9BG56 sus scrofa
13	1657	47.1	764	6 Q8SPF9	Q8SPF9 sus scrofa
14	1654.5	47.1	763	6 Q9BG94	Q9BG94 felis silve
15	1647	46.8	658	13 Q9PVN9	Q9PVN9 oncorhynch
16	1647	46.8	658	13 Q9PVN9	Q9PVN9 oncorhynch

09d697 mus musculus
09d697 oreochromis
09d697 oncorhynch
09d697 oncorhynch
09d697 morone saxa
09d697 morone saxa
09d697 oreochromis
09d697 ictalurus p
09d697 sus scrofa
09d697 oncorhynch
09d697 alluoropoda
09d697 urus marit
09d697 homo sapien
09d697 homo sapien
09d697 bos taurus
09d697 canis fami
09d697 mustela vis
09d697 drosophila
09d697 drosophila
09d697 drosophila
09d697 asterina pe
09d697 asterina pe
09d697 drosophila
09d697 coturnix co
09d697 drosophila
09d697 rattus norv
09d697 salmo salar
09d697 caenorhabdi
09d697 xenopus lae

ALIGNMENTS

RESULT 1
ID 064183 PRELIMINARY; PRT: 688 AA.
AC 064183;
DT 01-NOV-1996 (TEMBLrel. 01, Created)
DT 01-NOV-1996 (TEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TEMBLrel. 19, Last annotation update)
DE Follicle-stimulating hormone receptor.
OS Rattus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10118;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE:92149579; PubMed:1738373;
RA McKert L.B., Daley I.J., Griswold M.D.;
RT Genes: Structural organization of the follicle-stimulating hormone receptor
SC Genes: Scienc.
RL Mol. Endocrinol. 6:70-80(1992).
DR EMBL: S81198; AB21415.2;
DR EMBL: S81117; AB21415.2; JOINED.
DR EMBL: S81119; AB21415.2; JOINED.
DR EMBL: S81121; AB21415.2; JOINED.
DR EMBL: S81171; AB21415.2; JOINED.
DR EMBL: S81174; AB21415.2; JOINED.
DR EMBL: S81178; AB21415.2; JOINED.
DR EMBL: S81183; AB21415.2; JOINED.
DR EMBL: S81185; AB21415.2; JOINED.
DR EMBL: S81194; AB21415.2; JOINED.
DR HSP: P33945; IXON.
DR InterPro: IPR000036; GPCR_Rhodops.
DR InterPro: IPR000036; GPCR_Rhodops.
DR InterPro: IPR000036; GPCR_Rhodops.
DR InterPro: IPR000036; GPCR_Rhodops.
DR Pfam: PF00001; 7tm.1; 1.
DR Pfam: PF00560; LRR; 3.
DR Pfam: PF01462; LRR; 1.
DR SMART: SM00013; LRRNT; 1.
DR PROSITE: PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
DR PROSITE: PS00262; G_PROTEIN_RECEP_F1_2; 1.

KW Receptor. 688 AA; 77341 MW; 441P0D9E7D01DF18 CRC64;
SQ SEQUENCE 688 AA; 77341 MW; 441P0D9E7D01DF18 CRC64;
Query Match 99.0%; Score 3482; DB 11; Length 688;
Best Local Similarity 99.3%; Pred. No. 5.4e-251;
Matches 670; Conservative 0; Mismatches 1; Indels 4; Gaps 1;
QY 1 CHWLCHCSNRVFLCQDSKVTEIPTDLPNAIELRVLTAKLRVLPKGSFAGFDGDKIEI 60
DB 18 CHWLCHCSNRVFLCQDSKVTEIPTDLPNAIELRVLTAKLRVLPKGSFAGFDGDKIEI 77
QY 61 SONDVLEIADVFSLPKLHEIRIEKANNLLYINPEAFONLPSRLYLISNTGKHLPA 120
DB 78 SONDVLEIADVFSLPKLHEIRIEKANNLLYINPEAFONLPSRLYLISNTGKHLPA 137
QY 121 VKHTOSLOKVLDDIQQNINIHIVARNFMSGLSFESVILWLSKNGIEEIHNCFAENGTOLE 180
DB 138 VKHTOSLOKVLDDIQQNINIHIVARNFMSGLSFESVILWLSKNGIEEIHNCFAENGTOLE 193
QY 181 LNSDNNLEELPNDVFOGASGPVILDSRTKVHSLPNHGLENLKLRARSTYRLKLPN 240
DB 194 LNSDNNLEELPNDVFOGASGPVILDSRTKVHSLPNHGLENLKLRARSTYRLKLPN 253
QY 241 LDKFVTLMEASLTYPSCCAAFANLKRQISELHPICNKSILRODIDMTQIGDQVSLIDD 300
DB 254 LDKFVTLMEASLTYPSCCAAFANLKRQISELHPICNKSILRODIDMTQIGDQVSLIDD 313
QY 301 EPSYKSGSDMMYNEFDYDLCEVVDVTCSPKPDAPNCPEDIMGYNILRVLIWFTSILAIT 360
DB 314 EPSYKSGSDMMYNEFDYDLCEVVDVTCSPKPDAPNCPEDIMGYNILRVLIWFTSILAIT 373
QY 361 GNTTVLVLTTSQYKLTVPFRLMCLNAPADLCIGIYLLLIASVDHTKSOYHNYAIDWOT 420
DB 374 GNTTVLVLTTSQYKLTVPFRLMCLNAPADLCIGIYLLLIASVDHTKSOYHNYAIDWOT 433
QY 421 GAGCDAAGFTTFVASELSVYTLTATLERWHTITHAMOLECKVQLRHAASVNLGWTAF 480
DB 434 GAGCDAAGFTTFVASELSVYTLTATLERWHTITHAMOLECKVQLRHAASVNLGWTAF 493
QY 481 AAALPFIPIGSISSYKMSVCLPMDIDSPLSQVYVMAALLVNLVAFVVCYTHIYLTVRN 540
DB 494 AAALPFIPIGSISSYKMSVCLPMDIDSPLSQVYVMAALLVNLVAFVVCYTHIYLTVRN 553
QY 541 PTIVSSSDTKIAKRNATLIPTDFLCMAPISFAISASLKVPPLITVSKAKILLVLFYPI 600
DB 554 PTIVSSSDTKIAKRNATLIPTDFLCMAPISFAISASLKVPPLITVSKAKILLVLFYPI 613
QY 601 SCANPFLYAIPTKRNFRDFFILLSKFCGYEMOQAIYRTTSSATHNFHARKSHCSAPRV 660
DB 614 SCANPFLYAIPTKRNFRDFFILLSKFCGYEMOQAIYRTTSSATHNFHARKSHCSAPRV 673
QY 661 TNSYVLPVPLNHSSON 675
DB 674 TNSYVLPVPLNHSSON 688

RESULT 2
Q8R428 PRELIMINARY; PRT; 695 AA.
ID Q8R428
AC Q8R428
DT 01-JUN-2002 (TRENBLrel. 21, Created)
DT 01-JUN-2002 (TRENBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TRENBLrel. 21, Last annotation update)
DE Follicle stimulating hormone receptor.
CN FSHR.
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystriocognathi; Cavidae; Cavia.
OX Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OX NCBI_TaxID=10141;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-HARTLEY; TISSUE-TESTIS;
RA Suzuki O.

RT *Guinea pig follicle stimulating hormone receptor.*
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY082514; AAL92577.1;
KW Receptor. 695 AA; 77838 MW; 9A3ECF419C45227B CRC64;
SQ SEQUENCE 695 AA; 77838 MW; 9A3ECF419C45227B CRC64;
Query Match 87.6%; Score 3080.5; DB 11; Length 695;
Best Local Similarity 87.2%; Pred. No. 4.4e-221;
Matches 591; Conservative 37; Mismatches 47; Indels 3; Gaps 2;
QY 1 CHWLCHCSNRVFLCQDSKVTEIPTDLPNAIELRVLTAKLRVLPKGSFAGFDGDKIEI 60
DB 18 CHWLCHCSNRVFLCQDSKVTEIPTDLPNAIELRVLTAKLRVLPKGSFAGFDGDKIEI 77
QY 61 SONDVLEIADVFSLPKLHEIRIEKANNLLYINPEAFONLPSRLYLISNTGKHLPA 120
DB 78 SONDVLEIADVFSLPKLHEIRIEKANNLLYINPEAFONLPSRLYLISNTGKHLPA 137
QY 121 VKHTOSLOKVLDDIQQNINIHIVARNFMSGLSFESVILWLSKNGIEEIHNCFAENGTOLE 180
DB 138 VKHTOSLOKVLDDIQQNINIHIVARNFMSGLSFESVILWLSKNGIEEIHNCFAENGTOLE 197
QY 181 LNSDNNLEELPNDVFOGASGPVILDSRTKVHSLPNHGLENLKLRARSTYRLKLPN 240
DB 198 LNSDNNLEELPNDVFOGASGPVILDSRTKVHSLPNHGLENLKLRARSTYRLKLPN 257
QY 241 LDKFVTLMEASLTYPSCCAAFANLKRQISELHPICNKSILRODIDMTQIGDQVSLI-D 299
DB 258 LDKFVTLMEASLTYPSCCAAFANLKRQISELHPICNKSILRODIDMTQIGDQVSLI-D 317
QY 300 DEFSYKSGSDMMYNEFDYDLCEVVDVTCSPKPDAPNCPEDIMGYNILRVLIWFTSILAI 359
DB 318 DEFSYKSGSDMMYNEFDYDLCEVVDVTCSPKPDAPNCPEDIMGYNILRVLIWFTSILAI 377
QY 360 TGNVAVLVLTTSQYKLTVPFRLMCLNAPADLCIGIYLLLIASVDHTKSOYHNYAIDWQ 419
DB 378 TGNVAVLVLTTSQYKLTVPFRLMCLNAPADLCIGIYLLLIASVDHTKSOYHNYAIDWQ 437
QY 420 TGAGCDAAGFTTFVASELSVYTLTATLERWHTITHAMOLECKVQLRHAASVNLGWTAF 479
DB 438 TGAGCDAAGFTTFVASELSVYTLTATLERWHTITHAMOLECKVQLRHAASVNLGWTAF 497
QY 480 AAALPFIPIGSISSYKMSVCLPMDIDSPLSQVYVMAALLVNLVAFVVCYTHIYLTVR 539
DB 498 AAALPFIPIGSISSYKMSVCLPMDIDSPLSQVYVMAALLVNLVAFVVCYTHIYLTVR 557
QY 540 NPTIVSSSDTKIAKRNATLIPTDFLCMAPISFAISASLKVPPLITVSKAKILLVLFYPI 599
DB 558 NPTIVSSSDTKIAKRNATLIPTDFLCMAPISFAISASLKVPPLITVSKAKILLVLFYPI 617
QY 600 NSCANPFLYAIPTKRNFRDFFILLSKFCGYEMOQAIYRTTSSATHNFHARKSHCSAPRV 659
DB 618 NSCANPFLYAIPTKRNFRDFFILLSKFCGYEMOQAIYRTTSSATHNFHARKSHCSAPRV 677
QY 660 VTN--SYVLPVPLNHSSON 675
DB 678 VTN--SYVLPVPLNHSSON 695

RESULT 3
Q9DGF5 PRELIMINARY; PRT; 696 AA.
ID Q9DGF5
AC Q9DGF5
DT 01-MAR-2001 (TRENBLrel. 16, Created)
DT 01-MAR-2001 (TRENBLrel. 16, Last sequence update)
DT 01-JUN-2002 (TRENBLrel. 21, Last annotation update)
DE Follicle-stimulating hormone receptor precursor.
OS Cynops pyrrhogaster (Japanese common newt).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Caudata; Salamandroidea; Salamandridae; Cynops.
OX NCBI_TaxID=8330;
RN [1]
RP SEQUENCE FROM N.A.

```
RC TISSUE-TESTIS;
RA MEDLINE=20403884; PubMed=10944452;
RX Nakayama Y., Yamamoto T., Oba Y., Nagahama Y., Abe S.-I.;
RT "Molecular cloning, functional characterization, and gene expression
of a follicle-stimulating hormone receptor in the testis of newt
Cyrops pyrrhogaster.";
RL Biochem. Biophys. Res. Commun. 275:121-128(2000).
DR HSP: P23945; 1XUN.
DR EMBL: AB005587; BAB13501.1; -.
DR InterPro: IPR000276; GPCR_Rhodan.
DR InterPro: IPR001611; LRR.
DR InterPro: IPR000372; LRR_Nterm.
DR Pfam: PF000501; 7c_m_1; 1.
DR SMART: S000237; GPCR_Rhodan.
DR PROSITE: PS00237; G-PROTEIN_RECPT_F1_1; UNKNOWN_1.
DR PROSITE: PS0262; G-PROTEIN_RECPT_F1_2; 1.
KW Receptor; Signal.
FT SIGNAL 1 17 POTENTIAL.
FT CHAIN 18 696 POTENTIAL.
FT SEQUENCE 696 AA: 78633 MW: 179A6FC800B71E57 CRC64;

Query Match 70.51; Score 2479; DB 13; Length 696;
Best Local Similarity 71.44; Pred. No. 2.8e-176;
Matches 484; Conservative 79; Mismatches 107; Indels 8; Gaps 5;

OY 1 CHRLCHSRRVFLQDSKVTETDLPRLNATLRLVTLKRVKSGFAGCDLEKIEI 60
DB II : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 18 CHP-VCLNRRVFTQESHVQIDIPRSTELRFLVTKVYIPAAFGFEDVENIEI 76
DB II : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 61 SQNVLEVEADVSNPKLHEIRIEKANLLYINPAPQMLPRLYLLISNTGKILPA 120
DB II : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 77 SQNVLEVEADVSNPKLHEIRIEKANLLYINPAPQMLPRLYLLISNTGKILPA 136
DB II : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 121 VHKIOSQVLLQDNIINHIIVARNSPGLSFVILMSKNGIEIEHNCAP 180
DB II : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 137 VSRISFHVLLVDNIINHIIVARNSPGLSFVILMSKNGIEIEHNCAP 196
DB II : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 181 LNLSDNNLELNDVDFQAGSPVLDTSRTKVLSPNGLNLEKLRARSTYRLKLPN 240
DB II : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 197 LNLSDNNLELNDVDFQAGSPVLDTSRTKVLSPNGLNLEKLRARSTYRLKLPN 256
DB II : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 241 LKRPVTLKASLTPSHCCAFANLAKROISELHPICNKSILRODIDMTQIGD 299
DB II : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 257 LKRPVTLKASLTPSHCCAFANLAKROISELHPICNKSILRODIDMTQIGD 316
DB II : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 300 DEPSYKSGSDNTH-REYD- -LCNVEYDVTCSPKPDAPNCPEDINGNLRVLPIS 355
DB II : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 317 YLSSTGFSYLVNGDFWYDILCNEVYDVTCSPKPDAPNCPEDINGNLRVLPIS 376
DB II : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 356 ILAIGNTVTVLLTTSOYKLVTPRFLMCLNAPADLCIGYLLILLASVDIHTKSOYNYA 415
DB II : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 377 ILAIGNTVTVLLTTSOYKLVTPRFLMCLNAPADLCIGYLLILLASVDIHTKSOYNYA 436
DB II : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 416 IDNQTGAGCDAAGFTVPASLSVYLTATLIERHHTITHAMOLECKVOLRHAASVYLG 475
DB II : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 437 IDNQTGAGCDAAGFTVPASLSVYLTATLIERHHTITHAMOLECKVOLRHAASVYLG 496
DB II : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 476 WTPAALPPIFGISYKVSICLPMODISPLSQLYMALLVNLVAFVYVCGCYTHY 535
DB II : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 536 LTVRNPVYSSSDTKLARNATLPTDPLCHAPISFPAISAKVPLTYSKALVYL 595
DB II : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 557 LTVRNPVYSSSDTKLARNATLPTDPLCHAPISFPAISAKVPLTYSKALVYL 616
DB II : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 596 PTPINSCANPFLYATPTKPRDFPTLLSKFCCCEMAOQYPTTSSTHFNHARKSCS 655
DB II : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 617 PTPINSCANPFLYATPTKPRDFPTLLSKFCCCEMAOQYPTTSSTHFNHARKSCS 676
DB II : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 656 SAPR--VTNSTYVLPNN 671
DB II : : : : : : : : : : : : : : : : : : : : : : : : : :

Db 677 PAKYSAASHTLPLNN 694

RESULT 4
OQ0MP8 PRELIMINARY; PRT; 673 AA.
AC OQ0MP8;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE FSH receptor.
DE FSH RECEPTOR.
GS Podarcis sicula.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Scincomorpha; Lacertoidae;
OC Lacertidae; Podarcis.
OX NCBI_TaxID=65484;
RN [1] JENSEN FROM N.A.
RC TISSUE=OVARY.
RX MEDLINE=21458565; PubMed=11574163;
RA Borrelli L., De Staels R., Parfai E., Filosa S.;
RT "Molecular cloning, sequence and expression of follicle-stimulating
hormone receptor in the lizard Podarcis sicula.";
RL "Gene 275:149-156(2000).
DR EMBL: AJ292553; CAC82173.1; -.
DR InterPro: IPR000276; GPCR_Rhodan.
DR Pfam: PF000501; 7c_m_1; 1.
DR PROSITE: PS00237; G-PROTEIN_RECPT_F1_1; UNKNOWN_1.
DR PROSITE: PS0262; G-PROTEIN_RECPT_F1_2; 1.
KW Receptor.
SQ SEQUENCE 673 AA: 76288 MW: 68994C8B5F67B5 CRC64;

Query Match 55.64; Score 1956; DB 13; Length 673;
Best Local Similarity 55.34; Pred. No. 1.5e-13;
Matches 407; Conservative 80; Mismatches 149; Indels 48; Gaps 11;

OY 3 HWLCH-CSRNVFLQDSKVTETDLPRLNATLRLVTLKRVKSGFAGCDLEKIEI 53
DB II : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 21 HPTCOPDLNMLFTQDSKVTQVOTPSQERHG-----TGIFPHQNKNIHTERAPLGLD 71
DB II : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 54 DLEKIEISQNVLEVEADVSNPKLHEIRIEKANLLYINPAPQMLPRLYLLISNT 113
DB II : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 72 EYEKIEISQNDALGTIESNVFSLPKLYEIEIEKANLLYIDRYAPQMLPRLYLLISNT 131
DB II : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 114 GIKLPAVHKIOSQVLLQDNIINHIIVARNSPGLSFVILMSKNGIEIEHNCAP 173
DB II : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 132 AHTLPVYVQIHSSVYFVLDVQDNIINHIIVARNSPGLSFVILMSKNGIEIEHNCAP 191
DB II : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 174 NGTOLDLELNDNNLELNDVDFQAGSPVLDTSRTKVLSPNGLNLEKLRARSTY 233
DB II : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 192 NGTILSDNLSDNNLEKLEKLPNEVDFQAGSPVLDTSRTKVLSPNGLNLEKLRARSTY 251
DB II : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 234 RLKLPMLDKFVTLMEASLTPSHCCAFANLAKROISELHPICNKSILRODIDMTQIGD 293
DB II : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 252 NLKVPPLDKPRASIEANLTPSHCCAFANLAKROISELHPICNKSILRODIDMTQIGD 303
DB II : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 294 RYSLIDDEFSYKSGSDM-MYREEDY--DLCNEVYDVTCSPKPDAPNCPEDINGNLRVLP 350
DB II : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 304 -----GTDFLDDEHDHYQSCKEVEVICFEPDAPNCPEDINGNLRVLP 350
DB II : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 351 IWPISILATGHTVTVLLTTSOYKLVTPRFLMCLNAPADLCIGYLLILLASVDIHTKSOY 410
DB II : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 351 IWPISILATGHTVTVLLTTSOYKLVTPRFLMCLNAPADLCIGYLLILLASVDIHTKSOY 410
DB II : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 411 YHYAIDHQTGAGCDAAGFTVPASLSVYLTATLIERHHTITHAMOLECKVOLRHAAS 470
DB II : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 411 YHYAIDHQTGAGCDAAGFTVPASLSVYLTATLIERHHTITHAMOLECKVOLRHAAS 469
DB II : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 471 VVYLGMTFAFAALPPIFGISYKVSICLPMODISPLSQLYMALLVNLVAFVYVCGCY 530
DB II : : : : : : : : : : : : : : : : : : : : : : : : : :

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Db 470 FHLVGFARFTVAIIPIFOVSYMKVSIKLPMDIETPPCQAIIMFLVLNITLAFLLISTS 529
Qy 531 YTHIYLVTRNPTIVSSSDTKIAKRMATLIITDFLCMAPISEFFAISASLKVLPIVTSKAK 590
Db 530 YISIYITVTRNPTIISNSDTKIAKRMAYLIITDFLCMAPISEFFAISASLKVLPIVTSKAK 589
Qy 591 ILLVLFPYINSCAN-PELYAIPTKFRDRFFILLSKFCYEMOQAIYRTETSSATHNPHA 649
Db 590 ILLVLFPYINRAPTVPVRH--LHQEPQDFILLSKFGLCEKQOAIYRTETSSVPTSHM 647
Qy 650 RKSHCSSAPRVTN--SYVLVPLNH 671
Db 648 KNGCHTPASKASEGPAYALVPLNY 671

RESULT 5
Q16225 PRELIMINARY; PRT; 410 AA.
AC Q16225:
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE Follicle-stimulating hormone receptor (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95000244; PubMed=7916967;
RA Gromoll J., Ried T., Holtgreve-Grez H., Nieschlag E., Gudermann T.;
RT "Localization of the human FSH receptor to chromosome 2 p21 using a
RT genomic probe comprising exon 10."
RL J. Mol. Endocrinol. 12:265-271(1994).
DR EMBL; S73526; AAB32225.1;
DR InterPro: IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODOPS.
DR PROSITE; PS00237; G_PROTEIN_RECEPT_FL_1; UNKNOWN_1.
DR PROSITE; PS0262; G_PROTEIN_RECEPT_FL_2; 1.
KW Receptor.
FT NON_TER
SQ SEQUENCE 410 AA; 46008 MW; F345E029C16BC792 CRC64;

Query Match 54.18; Score 1901.5; DB 4; Length 410;
Best Local Similarity 89.58; Pred. No. 1.5e-133;
Matches 367; Conservative 15; Mismatches 25; Indels 3; Gaps 2;

Qy 269 SELHPICNKSILRODIDMTQIGQVSLIDD-EPSSYKSGSDMMNEFDYDLCNEVDVT 327
Db 1 SELHPICNKSILROEVDVMTQRCORSLAEDNESSYRGDFMTYTFEDYDLCNEVDVT 60

Qy 328 CSPKPDAPNCPEDIMGYNLRVLWIFISILAITGTTVLVLTTSQYKLTVPFLMCLNLA 387
Db 61 CSPKPDAPNCPEDIMGYNLRVLWIFISILAITGTTVLVLTTSQYKLTVPFLMCLNLA 120

Qy 388 FADLCIGIYLLIASVDIHTKSOYHNYAIDWQTAGCDAAGFFTFVASELSVYTLTALT 447
Db 121 FADLCIGIYLLIASVDIHTKSOYHNYAIDWQTAGCDAAGFFTFVASELSVYTLTALT 180

Qy 448 ERWHTITHAMOLECKVQLRHAASVMVGLWTFAPAAALPFIQISSYMKVSLCPMDIDSP 507
Db 181 ERWHTITHAMOLECKVQLRHAASVMVGLWTFAPAAALPFIQISSYMKVSLCPMDIDSP 240

Qy 508 LSQIVMALLVNLVLAFFVVCYTHIYLVTRNPTIVSSSDTKIAKRMATLIITDFLCM 567
Db 241 LSQIVMALLVNLVLAFFVVCYTHIYLVTRNPTIVSSSDTKIAKRMATLIITDFLCM 300

Qy 568 APISFAISASLKVLPIVTSKAKILLVLFPYINSCANPFLYAIPTKFRDRFFILLSKFG 627
Db 301 APISFAISASLKVLPIVTSKAKILLVLFPYINSCANPFLYAIPTKFRDRFFILLSKFG 360

Qy 628 CYEMOQAIYRTETSSATHNPHARKSHCSSAPRV--NSVVLVPLNHSSQN 675

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Db 361 CYEMOQAIYRTETSTVHTHPNGHCSSAPRVTSGSTYILVPLSHLAQN 410

RESULT 6
Q98T84 PRELIMINARY; PRT; 662 AA.
ID Q98T84:
AC Q98T84:
DT 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
DE Follicle-stimulating hormone receptor precursor.
OS Ictalurus punctatus (Channel catfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Siluriformes;
OC Ictaluridae; Ictalurus.
OX NCBI_TaxID=7998;
RN [1]
RP SEQUENCE FROM N.A.
RA Kumar R.S., Ijiri S., Trant J.M.;
RT "Molecular Biology of Channel Catfish Gonadotropin Receptors: 2. cDNA
RT Cloning, Functional Expression, and Seasonal Gene Expression of the
RT Follicle-Stimulating Hormone Receptor."
RL Biol. Reprod. 0:0-0(2001).
DR EMBL; AF285182; AAK16067.1;
DR HSSP; P23945; 1XUN.
DR InterPro: IPR000276; GPCR_Rhodpsn.
DR InterPro: IPR001611; LRR.
DR Pfam; PF00001; 7tm_1; 1.
DR Pfam; PF00560; LRR; 4.
DR PRINTS; PR00237; GPCRHHODOPS.
DR PROSITE; PS00237; G_PROTEIN_RECEPT_FL_1; UNKNOWN_1.
DR PROSITE; PS0262; G_PROTEIN_RECEPT_FL_2; 1.
KW Receptor; Signal.
FT SIGNAL
SQ SEQUENCE 662 AA; 74846 MW; DC19F07A2CADEED CRC64;

Query Match 52.38; Score 1840.5; DB 13; Length 662;
Best Local Similarity 55.38; Pred. No. 9.7e-129;
Matches 356; Conservative 107; Mismatches 150; Indels 31; Gaps 5;

Qy 5 LCHCSNRVFLCQDSKVTEITDLPNAIEIURFVLTUKLRVLPKGSFAGGLEKTEISQND 64
Db 24 LANGTTRSFCLGSKVHMPYHIPKNTTYVEIKLTRIIMLPSPRAMSSLDLKLRLVSENG 83

Qy 65 VLEVEIADVSNLPKLEHREIKKANNLLYNPEAFONLPURLYLLISNTGKHLPAVHKI 124
Db 84 VLQRIEAYAFANLTKLEITITKSNLVCMDRHTFWGLPKRLYLTISNTGLTVPDFSKV 143

Qy 125 QSLQ-KVLLDITQDNIHIVARNSEFMGLSPESVI-LMLSKNGIEIHNCAFNQTOLDEN 182
Db 144 QSAFAEFLEEDNHNHIEVIPSNAFAGLTSGTITELRTKNGTEVDNRNAGTKIEKLF 203

Qy 183 LSDNNNLEELPNVQFQASGVVILDISRTKVHSLPNHGLENLKLRARSTYRLKLPNLD 242
Db 204 LMGNOQLKRIHNYAFLGAEGLVLDISRTAISLSPENNLRLKLLIATSVSLRWLPNLE 263

Qy 243 KFTVLMASLTYPSCCAAFANLKRQISELHPICNKSILRODIDMTQIGQVSLIDD 302
Db 264 IFTELTOANLTPSHCCAFKFNKKNSEKRLCNDSTIR-----NQEP 306

Qy 303 SYGKSGDMYNEFDYDLCNEVDVTPSPKPAFNCPEDIMGYNLRVLWIFISILAITGN 362
Db 307 -----YFEEHCKDVEIVRCEPPEPDAFNCPEDIMGTFLRLVWIFISVLAVLGN 355

Qy 363 TTVLVLTTSQYKLTVPFLMCLNLAFCADLCIGIYLLIASVDIHTKSOYHNYAIDWQTA 422
Db 356 FTVLVLVLLSSRTKLVKPKFLMCHLAFADFCMGLYLLIIGSDVLOQTRSHYNYGIEQMGV 415

Qy 423 GCDAAAGFTVFASELSVYTLTALTITLTHAMOLECKVQLRHAASVMVGLWTFAPAAAL 482
Db 416 GCGTAGFLTVFASELSVYTLTALTITLTHAMOLECKVQLRHAASVMVGLWTFAPAAAL 475

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OY 483 ALPDPICSSKNSKVSICLDPDSDPLSOLYVALLVAVLAFVIVICGCTHYTHLYVNPPT 542
DB 476 ALTPVIGVSSKATSKICLPHDVETASSOAYINLLVAVLAVTVACVYRIYLYVHPA 535
OY 543 IVSSSDTKIARAKMATLFTDFLCHAFSPFAISAKVPLITVSKAKILLVLPVPINSC 602
DB 536 SVPDASDAVARAKMAYLVFTDFLCHAFISFAISALAKOPLITVSHAKVLLVLPVPINSC 595
OY 603 ANPELYAIFETRRDRPFIILSKPFCYEMQAOIVRTETSSATHN 646
DB 596 ANPELYAIFETSKPFDVLTFRFCFESRARVYRTETSS-LHN 638

RESULT 7
QSP58 QSP58 PRELIMINARY: PRT: 701 AA.
AC QSP58: 2000 (TRENDEL, 21, Created)
DT 01-JUN-2002 (TRENDEL, 21, Last sequence update)
DT 01-JUN-2002 (TRENDEL, 21, Last sequence update)
DE Luteinizing hormone receptor.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-HOLSTEIN; TISSUE-CORPUS LUTEUM;
RA Kawada H., Tanada H., Inaba T., Sawada T.;
RT Molecular cloning of a full-length cDNA encoding bovine luteinizing
RT hormone receptor (LHR) and its expression in COS cells.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF491303; AM09535.1;
KW Receptor.
SQ SEQUENCE 701 AA: 78455 MW: D70A8662EB265CCF CRC64;
Query Watch 51.3%; Score 1803.5; DB 6; Length 701;
Best Local Similarity 56.7%; Pred. No. 5.9e-126;
Matches 356; Conservative 106; Mismatches 145; Indels 21; Gaps 6;

OY 35 RPYLTKL--RVIPKSPAGFDLEKIEISONDVLEYEADVFNLPKLEHRIEKANLL 92
DB 55 RSLTYLPKIVPQAPGLNEVIEKIEISODSLEKIEANFNLLNLSILLQNTKNLV 114
OY 93 YINPEAPNLPRLYLLISWTGKILPAPVHKIOSLQ-KVLLDQDNHIVARNSPMGL 151
DB 115 HITAGATNPRLATLISCTGILKALPVPKIFSPENFLEICDLHAITTPRNAPQ 174
OY 152 SPESYLLMLSKNGTEEHNCAPNGTOLDLNLSONNLELPNDVFCAGCPVLLDSPT 211
DB 175 NNESTILKLYGPEZIQSHAFNGTTLISLEKLEKARLEKMHNDAPRGATPSILD 234
OY 212 KYHSLPHHGLENLKLRARSTYRLKPLNLDKFTVLMKASLTYPSCCANLKRQISEL 271
DB 235 QLOALPTYGLESIGTILATSSYSKLKPSREKFTNLLDATALTPSCCAFRLN- 287
OY 272 HPICNKSILRODDMTQIGDORVSLIDDEPSYG---KGSQDMNFEFDYDLCNEVDYC 328
DB 288 -PTNDFNPSIFKNSKQCESTARPNHETLYSAFAESELSONDYDYGCLPRT-LQC 345
OY 339 SPKDAFNPCEDINGYNILVNLVNLSTILATGNTVTVLYTTQYKLTVPRLKCNAP 388
DB 346 APEPDAPNCEIDINGNPLVNLVNLVNLSTILATGNTVTVLYTTQYKLTVPRLKCN 405
OY 389 ADICIGITALLASVDIHPKSOYHNYAIDNQTGACGADGPTVPASELSVYTLTATLE 448
DB 406 ADPCNGYLLLASVDQTKQYVNHAIADNQTGSCSAAGPTVPASELSVYTLTATLE 465
OY 449 RNTHTHAKOLECVOLRHAAVYVYVYVYVYVYVYVYVYVYVYVYVYVYVYVYVY 508
DB 466 RNTHTTAYTALDOLKRLKHAIPVNLGGHLESTLIATVPLVGVSTKVSICLPHDV 525

OY 509 SOLYVALLVAVLAFVIVICGCTHYTHLYVNPPTIVSSSDTKIARAKMATLFTDFLCH 568
DB 526 SOLYVALLVAVLAFVIVICGCTHYTHLYVNPPTIVSSSDTKIARAKMATLFTDFLCH 585
OY 569 PISFPAISAKVPLITVSKAKILLVLPVPINSCANPFLVPTKFNRRPDRPFIILSKP 628
DB 586 PISFPAISAKVPLITVSKAKILLVLPVPINSCANPFLVPTKFNRRPDRPFIILSKP 645
OY 629 YEMQAOIVRTETSSATHNFAHKSCHSS 656
DB 646 CKYRAELYRRK-----DFSAYISCKN 667

RESULT 8
QSPW16 QSPW16 PRELIMINARY: PRT: 662 AA.
AC QSPW16: 2000 (TRENDEL, 13, Created)
DT 01-MAR-2002 (TRENDEL, 13, Last sequence update)
DT 01-MAR-2002 (TRENDEL, 20, Last annotation update)
DE Follicle-stimulating hormone receptor precursor.
OS Clarias gariepinus (Sharptooth catfish) (African catfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Siluriformes;
OC Clariidae; Clariinae.
OX NCBI_TaxID=13013;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-TESTIS;
RA Bogerd J., Andersson E., Blomenrohr M., Tensen C.P., Granneman J.C.,
RA Schulz R.W., Goss H.J.;
RT Cloning and functional characterization of a testicular follicle-
RT stimulating hormone receptor from the African catfish,
RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: AJ012647; CAB31907.1;
KW HSP;
DR HSP: P23945; IUN.
DR InterPro: IPR000276; GPCR_Rhodopn.
DR InterPro: IPR001611; LRR_
DR Pfam: PF00001; 7tm_1;
DR Pfam: PF00560; LRR_4;
DR PRINTS: PR00237; GPCRHHODPSN.
DR PROSITE: PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
DR PROSITE: PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor; Signal.
FT CHAIN 1..22 POTENTIAL.
FT SIGNAL 1..22 FOLLICLE-STIMULATING HORMONE RECEPTOR.
SQ SEQUENCE 662 AA: 74891 MW: 5C849EDDBDID4F5 CRC64;
Query Watch 51.2%; Score 1798.5; DB 13; Length 662;
Best Local Similarity 54.2%; Pred. No. 1.3e-125;
Matches 352; Conservative 109; Mismatches 158; Indels 31; Gaps 5;

OY 9 SNRVFLCDSKVYIEPTDLPNARIELRVLKLVIPKSPAGFDLEKIEISONDVLEV 68
DB 28 TTRSFCLAGSKVQHPHPIINTVYVEIKLTIIPFVRAMSSSLHDKRIMVSENGALQR 87
OY 69 IEADVFNLPKLEHRIEKANLLINPEAFONLPSRLYLLISNTGIRKHPAVHKIOSLQ 128
DB 88 IEAVAFANLTILEITITKSNLVSNDRDFTNGLPKRLVLTISNGLTVPDFSKVQSA 147
OY 129 -KVLLDQDNHIVARNSPMGLSPESVY-LWLSKNGIEEHNKAPNGTOLDLNLSON 186
DB 148 FEPDLEDMHIEVHISNAFACLSGTITELRTKNGIEVEFNAPNGTKMELFLMGN 207
OY 187 NPLELENDVFCAGCPVLLDSPTKYSVLSLPHHGLENLKLRARSTYRLKPLNLDKFTV 246
DB 208 QOLKRIDNHAFGAESPLVLDISRTAIISSLPENMLRLKLLIATSVYSLRMLPNELE 267
OY 247 LMEASLTYPSCCANLKRQISELHPICNKLSILRODDMTQIGDORVSLIDDEPSYCK 306
DB 268 LQANLTYPSCCAFNEKFNKLEKHLNLCNVSTIR-----NOEP----- 306
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[illegible]

RESULT 9

Q15996	PRELIMINARY; PRT; 699 AA.
ID	Q15996
AC	Q15996;
DT	01-NOV-1996 (TREMBLrel. 01, Created)
DT	01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE	Luteinizing hormone receptor.
DE	Homo sapiens (Human).
OS	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OX	NCBI_Taxid=9606;
RI	[1]
RN	SEQUENCE FROM N.A.
RP	TISSUE=OVARY;
RC	MDLLine=92017881; PubMed=1922095;
RA	Jia X.C., Oikawa M., Bo M., Tanaka T., Ny T., Boime I., Hsueh A.J.;
RX	"Expression of human luteinizing hormone (LH) receptor: interaction
RT	with LH and chorionic gonadotropin from human but not equine, rat, and
RT	ovine species"; 5:759-768(1991).
RL	Mol. Endocrinol. 5:759-768(1991).
DR	EMBL; S57793; AAB19917.2; -;
DR	HSSP; P22888; 1L0T.
DR	InterPro: IPR000276; GPCR_Rhodpsn.
DR	InterPro: IPR001611; LRR.
DR	InterPro: IPR000372; LRR_Nterm.
DR	Pfam: PF00001; 7tm.1; 1.
DR	Pfam: PF00560; LRR; 3.
DR	SMART; SM00013; LRRNT; 1.
DR	PROSITE; PS00237; G_PROTEIN_RECEPTOR_F1_1; UNKNOWN_1.
DR	PROSITE; PS00262; G_PROTEIN_RECEPTOR_F1_2; 1.
DR	Receptor.
QO	SEQUENCE 699 AA; 78642 MW; 2E3D93F64621B8A42 CRC64;

Db	171	GMNESVTLKLYNGFEEVOSHAFNGTTLTSLKLNKLVHLEKMHNGAFRGATGPKTLDIS	233
Qy	210	RTKVHSLPNHGLNKLRLARSTYRLKKLPNLDKFVTLMEASLTYPSPHCCAFANLKRKROIS	269
Db	231	STKLQALPSVGLSIOPLRIATSSYSKLKPSRETFVNLLEATLTPSPHCCAFRNL	285
Qy	270	ELHPICNKSILRQIDDMTQIGQOORVSLIDDEPSYGK---GSDMMYNEDYDLCHEVVVDV	326
Db	286	---PTKEQNFSSHISENFSKQCESTVRKVNKNTLYSSMLAESELSGMDVEYGFCLPKTP-	341
Qy	327	TCSPKPDAPNCPEDIMGYNILRVLINFISILAITGNTVTLVVLTSQYKLVLPREFLMCNL	386
Db	342	RCAPEPDAPNCPEDIMGYDFLRVLIMINILAINGNMTLVFLVLLTSRYKLVLPREFLMCNL	401
Qy	387	AFADLCIGIYLLIASVDIHTKSOYHVAIDWQTGAGCDAAGFFTFVASELSVYTLTAT	446
Db	402	SFADFCLGLYLLIASVDSQTQGYYNHAIWQTGSGCSTAGFTTFVASELSVYTLTWT	461
Qy	447	LERWHTITHAQLECKVQLRHAASVVLGWTFAFAAALFPIFGISSYMKVSTICLPMDDIS	506
Db	462	LERWHTITYAIHLDQKRLRHAILMLGGWLFSLLIAMPLVGVSNYMKVSTICPMDVET	521
Qy	507	PLSOLYVALLVNLVAFVVICGCTHYHLYTVRNPTIVSSSDTKIAKRMATLIFTDFLC	566
Db	522	TLSSQVYTLTLINVAFFITACYIKIYFAVRNPELMATNKDKIAKMAILIFTDFTC	581
Qy	567	MAPISPAISASLKVPILTVYSKAILLVLPFINSKANPFLYAIFTKFRDRDFILLSKF	626
Db	582	MAPISPAISAAKVPILTVNSKVLVLVFPINSKANPFLYAIFTKFRDRDFILLSKF	641
Qy	627	GCYEMQAQIYRTETSSATHNFHARKSHCSS	656
Db	642	GCCKRRAELYRRK-----DESAYTSNCKN	665

RESULT 10

Q14751 PRELIMINARY; PRT; 701 AA.

ID AC Q14751;

DT 01-NOV-1996 (TREMBLrel. 01, Created)

DT 01-JUN-2001 (TREMBLrel. 01, Last sequence update)

DE DE LUTEINIZING hormone-chorogonadotropin receptor (Luteinizing hormone receptor).

GN LHCGR OR LHR.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

NCBI_Taxid=9606;

[1]

RN SEQUENCE FROM N.A.

RX MEDLINE=96023956; PubMed=7556872;

RA Alger M., Misrahi M., Sar S., Leflem L., Dessen P., Milgrom E.;

RT "Structure of the human luteinizing hormone-chorogonadotropin receptor gene: unusual promoter and 5' non-coding regions.";

RL Mol. Cell. Endocrinol. 111:113-123(1995).

RN [2]

RP SEQUENCE OF 1-56 FROM N.A.

RA Tsai-Morris C.H., Geng Y., Buczko E., Dufau M.L.;

RT "Human luteinizing hormone receptor gene containing 6 bp insertion in exon 1 coding region with identical 5' flanking sequence as LHR2 exon 1 coding region."

RL Hum. Hered. 49:0-0(1999).

DR EMBL; X84753; CAA59234.1; JOINED.

DR EMBL; X84754; CAA59234.1; JOINED.

DR EMBL; X84755; CAA59234.1; JOINED.

DR EMBL; X84756; CAA59234.1; JOINED.

DR EMBL; X84757; CAA59234.1; JOINED.

DR EMBL; X84758; CAA59234.1; JOINED.

DR EMBL; X84759; CAA59234.1; JOINED.

DR EMBL; X84760; CAA59234.1; JOINED.

DR EMBL; X84761; CAA59234.1; JOINED.

DR EMBL; X84762; CAA59234.1; JOINED.


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DB 564 AKVSIQLPMDTEPLALAYILVLLLVNVAITVCSYVYIYVIRNPQVNGOKOTKIA 623
OY 554 KRMATLITPTDPLCMAPISFPAISASLKVLPTVTSKAKITLLVLPYDINSCANPFLYAIPTK 613
DB 624 KMAVLITPTDPMCMAPISFPAISASLKVLPTVTSKAKITLLVLPYDINSCANPFLYAIPTK 603
OY 614 NFRDFFILLSKFGCYENAOIYR-----TETSSATNHFARKSHCSAPRVTN 662
DB 684 AFORDVILLSKFGCKROAQAYRCORVSPKNSGTGVOKVTQNNR-----QSLPNMOD 737
OY 663 SYVLVPLNH 671
DB 738 DYELLENSH 746

RESULT 14
OSPP9 PRELIMINARY; PRT: 764 AA.
AC OSPP9
AC OSPP9
DT 01-JUN-2002 (TREMblrel. 21, Created)
DT 01-JUN-2002 (TREMblrel. 21, Last sequence update)
DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)
DE Thyroid stimulating hormone receptor.
GN TSHR.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Suidae; Sus.
OX NCBI_TaxId=9683;
RN [1]
RP Sequence from N.A.
RA Igarashi M., Nagata A.; to the EMBL/GenBank/DBJ databases.
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AL082601; AAL92560.1;
KW RECEPTOR.
SQ SEQUENCE 764 AA; 86647 MW; 1E8ED0B617E7052 CRC64;
Query Match 47.1%; Score 1657; DB 6; Length 764;
Best Local Similarity 47.2%; Pred. No. 54e-115;
Matches 344; Conservative 113; Mismatches 198; Indels 74; Gaps 13;
OY 6 CHCSN-----RVFLQDSKVTETPTDLPNATLRFVLTKLRLVTPKSGFAGCDLEKIETS 61
DB 29 CECHQEDDFRV-TCKD--IHSIP-PLPPTOTLKFETHLTKTPSRAFSNLPNISRIYLS 84
OY 62 QNDVLEIADVPSNLPKLHEIRIEKANNILLYINPEAFONLPISRLYLLISMTGKHLPAV 121
DB 85 IDATQLOESQSPNLSMTHIEIRNTRSLTYINPCALKDPLKFLGTFNGTGLVPPOL 144
OY 122 HKIOSLOK-VLLDIOONTNTHIVARNSPGLSFESVILMSKNGIEEIHNCAPNGTOLDE 180
DB 145 TKVISTDVFLEITDNPMTSIPANAFQGLCNETLTKLYNNGFTSIOGHAFNGTKLDA 204
OY 181 LNLSDNNILELNDPVGGA-SGPVLDISRTKVSHPNGLNKLKLRATYTRKLLUP 239
DB 205 VYLNKKYLTVDQAFQGVSPFTLDDYSTVTAFLPSKGLNKLKLRATYTRKLLUP 264
OY 240 NLDKFTVTLMEASITPSHCCAFANLKRQISELHP-ICNKSILRQ-----DI 284
DB 434 ASLSVYTLTALTIERNHITTHAMQLECKVQLRHAASVNVLTGFAPAAALPIPIGTSY 493
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DB 504 ASLSVYTLTALTIERNHITTHAMQLECKVQLRHAASVNVLTGFAPAAALPIPIGTSY 563
OY 494 KWSICLQMDISPLSOLVYALVNLVLAIVYOCCTHILTVRNPVTSVSSSOTKIA 553
DB 564 AKVSIQLPMDTEPLALAYILVLLLVNVAITVCSYVYIYVIRNPQVNGOKOTKIA 623
OY 554 KRMATLITPTDPLCMAPISFPAISASLKVLPTVTSKAKITLLVLPYDINSCANPFLYAIPTK 613
DB 624 KMAVLITPTDPMCMAPISFPAISASLKVLPTVTSKAKITLLVLPYDINSCANPFLYAIPTK 603
OY 614 NFRDFFILLSKFGCYENAOIYR-----TETSSATNHFARKSHCSAPRVTN 662
DB 684 AFORDVILLSKFGCKROAQAYRCORVSPKNSGTGVOKVTQNNR-----QSLPNMOD 737
OY 663 SYVLVPLNH 671
DB 738 DYELLENSH 746

RESULT 15
OSPP9 PRELIMINARY; PRT: 763 AA.
AC OSPP9
AC OSPP9
DT 01-JUN-2001 (TREMblrel. 17, Created)
DT 01-JUN-2001 (TREMblrel. 17, Last sequence update)
DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)
DE Thyrotropin receptor.
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX NCBI_TaxId=9685;
RN [1]
RP SEQUENCE FROM N.A.
RA Nguyen L.O., Karamanoglu Arseven O., Gerber H., Stein B.S.,
RA Cloning of the cat thyrotropin receptor and evidence against an
RT autoantibody binding to the extracellular domain of feline hyperthyroidism.;
RT Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF218264; AAK00133.1;
DR HSP: P16473; LXUN
DR InterPro: IPR00276; GPCR_Rhodopsin.
DR InterPro: IPR001611; LRR.
DR Pfam: PF00560; LRR; 1.
DR PRINTS: PR00237; GPCRHHODOPS.
DR PROSITE: PS00237; G_PROTEIN_RECP_F1; UNKNOWN_1.
DR PROSITE: PS0262; G_PROTEIN_RECP_F2; 1.
DR RECEPTOR.
KW RECEPTOR.
SQ SEQUENCE 763 AA; 86588 MW; 937P60A140487D60 CRC64;
Query Match 47.1%; Score 1654.5; DB 6; Length 763;
Best Local Similarity 46.9%; Pred. No. 8.3e-115;
Matches 343; Conservative 112; Mismatches 205; Indels 71; Gaps 11;
OY 6 CHCSN-----RVFLQDSKVTETPTDLPNATLRFVLTKLRLVTPKSGFAGCDLEKIETS 61
DB 29 CECHQEDDFRV-TCKD--IHRIPS-LPPSTQTLKFETHLTKTPSRAFSNLPNISRIYLS 84
OY 62 QNDVLEIADVPSNLPKLHEIRIEKANNILLYINPEAFONLPISRLYLLISMTGKHLPAV 121
DB 85 IDATQLOESQSPNLSMTHIEIRNTRSLTYINPCALKDPLKFLGTFNGTGLVPPOL 144
OY 122 HKIOSLOK-VLLDIOONTNTHIVARNSPGLSFESVILMSKNGIEEIHNCAPNGTOLDE 180
DB 145 TKVISTDVFLEITDNPMTSIPANAFQGLCNETLTKLYNNGFTSIOGHAFNGTKLDA 204
OY 181 LNLSDNNILELNDPVGGA-SGPVLDISRTKVSHPNGLNKLKLRATYTRKLLUP 239
DB 205 VYLNKKYLTVDQAFQGVSPFTLDDYSTVTAFLPSKGLNKLKLRATYTRKLLUP 264
OY 240 NLDKFTVTLMEASITPSHCCAFANLKRQISELHP-ICNKSILRQ-----DI 284
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DB 265 LTLSEHLTRADLSYPSHCFAKNOKIKIGLESFMCNDSIRSLRQRKSVNALNGPFDQ 324
OY 285 DDMTOIGORVSLIDDEPSYKGSMDMY-----NEF 315
DB 325 EYEXYLGDSHAGYKDNSSKFRQDTRSNSHYVFFEEODEILGFGOEKLNPOEETLQAFDSHY 384
OY 316 DYDLCEVVDVTCSPKPDAPNFCEDIMGYNILRVLIIMFISILAITGNTVLVVLFTSOYK 375
DB 385 DYTVCGNEDMCTKSPKDEPNCEIDIMGKFLRIYVWVSLALGNFVLITLITSHYK 444
OY 376 LTVPRFLMCNLAFAADLCIGIYLLLIASVDIHTKSOYHNYAIDMOTGAGCDAAGFTVFAS 435
DB 445 LTVPRFLMCNLAFADECMGMYLLLIASVDLYTHSEYNNHAIIDMOTGPCNAGFTVFAS 504
OY 436 ELSVYTLTAITLERHHTTHAMOLECKVOLRHAASVVLGWTFAFAALFPIFGISSYMK 495
DB 505 ELSVYTLTAITLERHHTTHAMOLECKVOLRHAASVVLGWTFAFAALFPIFGISSYMK 564
OY 496 VSTCLPMOISPLSQLYVVALVNLVAFVVICGCTHYLTVRNPYIVSSSDTKIAKR 555
DB 565 VSTCLPMOISPLSQLYVVALVNLVAFVVICGCTHYLTVRNPYIVSSSDTKIAKR 624
OY 556 MATLIFTDFLCAPISFPAISASLKYPLITVSKAKILLVFPINSCANPFLYAITFTKNF 615
DB 625 MAVLIFTDFLCAPISFPAISASLKYPLITVSKAKILLVFPINSCANPFLYAITFTKNF 684
OY 616 RRDFFILSKFCGCEYMOAOIYR-----TETSSATVHNPARKSHCSSAPRVYNSY 664
DB 685 ORDVFILSKFCGCEYMOAOIYR-----TETSSATVHNPARKSHCSSAPRVYNSY 738
OY 665 VLVPLNHSN 675
DB 739 ELLENSHLTPN 749
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Job time : 44.4653 secs